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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 21:57:09 ; Search time 700 Seconds
(without alignments)
10736.472 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgactctagcctcactg.....agaacccaanaaagaacc 4228Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2606114

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4228	100.0	4228	3	US-09-227-421-3
2	4228	100.0	4228	3	US-09-479-855-3
3	268	6.3	2148	3	US-09-227-421-1
4	268	6.3	2148	3	US-09-479-855-1
5	55	1.3	2408	2	US-08-486-013-69
6	55	1.3	2408	2	US-08-482-279-69
7	55	1.3	2408	2	US-08-342-268-69
8	55	1.3	2408	2	US-09-397-386-69
9	55	1.3	2408	2	US-09-015-968-69
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54	25	0.6	48	3	US-10-037-986-37	Sequence 37, Appl
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56	25	0.6	48	6	PCT-US95-05600-141	Sequence 141, App
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58	25	0.6	59	3	US-09-816-089A-3	Sequence 7, Appl
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99 24 0.6 53 3 US-08-465-679-56 Sequence 56, Appli
100 24 0.6 54 2 US-08-446-919A-7 Sequence 7, Appli

ALIGNMENTS

RESULT 1

US-09-227-421-3
; Sequence 3, Application US/09227421
; Patent No. 6559357
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
; TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
; FILE REFERENCE: 023070-090700PC
; CURRENT APPLICATION NUMBER: US/09/227,421
; PRIOR FILING DATE: 1999-01-08
; PRIOR FILING DATE: 1999-01-08
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4228
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)-(4228)
; OTHER INFORMATION: ANT promoter
US-09-227-421-3

Query Match 100.0%; Score 4228; DB 3; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGTTGTTGTTGTTGTTACCAATGATGGGT 4140
Db 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGTTGTTGTTGTTGTTACCAATGATGGGT 4140
Qy 4141 TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGAGTGAAGATTCATTATAGAAAG 4200
Db 4141 TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGAGTGAAGATTCATTATAGAAAG 4200
Qy 4201 AGAGAACCAAAACCAAAAAGAAACC 4228
Db 4201 AGAGAACCAAAACCAAAAAGAAACC 4228

RESULT 2

US-09-479-855-3
; Sequence 3, Application US/09479855
; Patent No. 6639128
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
; FILE REFERENCE: 023070-090720US
; CURRENT APPLICATION NUMBER: US/09/479,855
; CURRENT FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 4228
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: ANT gene 5' promoter
US-09-479-855-3

Query Match 100.0%; Score 4228; DB 3; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCTCACTGACCTAATACGACTCATATAGGAGCTCGAGATCCTTTA 60
Db 1 GTGACTCTAGGCTCACTGACCTAATACGACTCATATAGGAGCTCGAGATCCTTTA 60
Qy 61 GTTAGAAAAAATCTTCTTTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 61 GTTAGAAAAAATCTTCTTTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy 121 ACATGTGATTCACATATATATATATGAATGGAATTTATTCATATTAATGAGTTGCAT 180
Db 121 ACATGTGATTCACATATATATATGAATGGAATTTATTCATATTAATGAGTTGCAT 180
Qy 181 TAAATATATACGCTGACATTAACAACCAATGTTCTGCTTTATGATGATTCATAT 240
Db 181 TAAATATATACGCTGACATTAACAACCAATGTTCTGCTTTATGATGATTCATAT 240

Db 181 TAAATATATACGCTGACATTAACAACCAATGTTCTGCTTTATGATGATTCATAT 240
Qy 241 GTTGACATGATTATATGATATATATATAAATCGGGTTTATTTAAATCCGTACCATAC 300
Db 241 GTTGACATGATTATATGATATATATAAATCGGGTTTATTTAAATCCGTACCATAC 300
Qy 301 AAAAGTGAACAAACGAGATCCATGTTTTGTGTGTTACTTTGTTGTTTAAACAGATAT 360
Db 301 AAAAGTGAACAAACGAGATCCATGTTTTGTGTGTTACTTTGTTGTTTAAACAGATAT 360
Qy 361 ATGATTTAGGAATTAATCTTTACTAAATTTAATAATTTGAAAAACCAACTTA 420
Db 361 ATGATTTAGGAATTAATCTTTACTAAATTTAATAATTTGAAAAACCAACTTA 420
Qy 421 ATATGTTAGTGCTTCAGTGCTCACTGTTCAGAAATATCTGAGTTATCTACTTGAA 480
Db 421 ATATGTTAGTGCTTCAGTGCTCACTGTTCAGAAATATCTGAGTTATCTACTTGAA 480
Qy 481 CTAGAAATGATATACATTAACAACGTGAATATTTTAAAGACGTACATTAACAATGAT 540
Db 481 CTAGAAATGATATACATTAACAACGTGAATATTTTAAAGACGTACATTAACAATGAT 540
Qy 541 CGATCAATACAAATTTATATGAGACTAGATCCAGATGAGATGACTCTAGCAGATA 600
Db 541 CGATCAATACAAATTTATATGAGACTAGATCCAGATGAGATGACTCTAGCAGATA 600
Qy 601 TACACAGCTTAGAATTTGTACAAAGAGTGAAGAAATAGATTCTAATTTAAAAAGA 660
Db 601 TACACAGCTTAGAATTTGTACAAAGAGTGAAGAAATAGATTCTAATTTAAAAAGA 660
Qy 661 TATGATTTCACTTACGATGATTAATTAATTAATTAATTAATTAATTAATTAATTTT 720
Db 661 TATGATTTCACTTACGATGATTAATTAATTAATTAATTAATTAATTAATTAATTTT 720
Qy 721 TGTGTTGTTTTCACGATTAATGAGAAATGTTGTGTTAAAAATGTTGTTTCTAA 780
Db 721 TGTGTTGTTTTCACGATTAATGAGAAATGTTGTGTTAAAAATGTTGTTTCTAA 780
Qy 781 AACTGTTTTATGTTAATCTATATATATGCTTTCCGATGTAATTTGAAACAAACGTGA 840
Db 781 AACTGTTTTATGTTAATCTATATATATGCTTTCCGATGTAATTTGAAACAAACGTGA 840
Qy 841 TACAATTTATGTTAAGCCATTCGATTAATAAATCCACGGTATGTAATCTTCAGAAAT 900
Db 841 TACAATTTATGTTAAGCCATTCGATTAATAAATCCACGGTATGTAATCTTCAGAAAT 900
Qy 901 TATGTTAAGCTTACAAATTTCTCTTATGATTAATGTTGAGACCAAAATATGATA 960
Db 901 TATGTTAAGCTTACAAATTTCTCTTATGATTAATGTTGAGACCAAAATATGATA 960
Qy 961 CCTTGACGGGATTAAGGTCATGATGTCAGATCAGCAATGAAGCCAAAGATCGTC 1020
Db 961 CCTTGACGGGATTAAGGTCATGATGTCAGATCAGCAATGAAGCCAAAGATCGTC 1020
Qy 1021 TCTGTCCTAAGATATCTACAGCTGCTTCGCTGTGTAATAGAGAAATTTGAATGTA 1080
Db 1021 TCTGTCCTAAGATATCTACAGCTGCTTCGCTGTGTAATAGAGAAATTTGAATGTA 1080
Qy 1081 GAGATCCCATCTAGGCTTCAAGTTGCGTTCCGTCCGCACTTTGGCGGTGTGACT 1140
Db 1081 GAGATCCCATCTAGGCTTCAAGTTGCGTTCCGTCCGCACTTTGGCGGTGTGACT 1140
Qy 1141 TTTTCTTATATGTCGTTGTTTATCTAATTTTCCAGAGTGAAGTGAATCAAGAAACT 1200
Db 1141 TTTTCTTATATGTCGTTGTTTATCTAATTTTCCAGAGTGAAGTGAATCAAGAAACT 1200
Qy 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATATATGTCGAAAGACATTAATGAC 1260
Db 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATATATGTCGAAAGACATTAATGAC 1260
Qy 1261 ACTAAAAATGATTAATTAATAATGATATATGTTGTGGAATTTATATCATTAACAA 1320
Db 1261 ACTAAAAATGATTAATTAATAATGATATATGTTGTGGAATTTATATCATTAACAA 1320

QY 1321 AATCAAGGAAGAGAGGAGCCTCTGCTGCTTATGATTTCCCTCTTAAACAATGCT 1380
DB 1321 AATCAAGGAAGAGAGGAGCCTCTGCTGCTTATGATTTCCCTCTTAAACAATGCT 1380
QY 1381 CCCACTATCTTTTACTTCTCAACAAATATCATCAACGAGAAATCTGCTGATC 1440
DB 1381 CCCACTATCTTTTACTTCTCAACAAATATCATCAACGAGAAATCTGCTGATC 1440
QY 1441 ACTTCATGCAAAATTAACATAATTTGGTATTTTGTCAAGTCTGCTGTTTAAAG 1500
DB 1441 ACTTCATGCAAAATTAACATAATTTGGTATTTTGTCAAGTCTGCTGTTTAAAG 1500
QY 1501 TCGATTTATTTGTAATCTATATATGTAATACATCACTCACTATCAATATGAT 1560
DB 1501 TCGATTTATTTGTAATCTATATGTAATACATCACTCACTATCAATATGAT 1560
QY 1561 CTCCTTCTGCTTATCAATTAATACACATAGCTATCACTATTAATTAACCA 1620
DB 1561 CTCCTTCTGCTTATCAATTAATACACATAGCTATCACTATTAATTAACCA 1620
QY 1621 CATCTCTTATCAATTTTATATGTAATTAATAAACAACGACTATAGGCTACAGATT 1680
DB 1621 CATCTCTTATCAATTTTATATGTAATTAATAAACAACGACTATAGGCTACAGATT 1680
QY 1681 GGTATTAAGGATTAATGCTTCTAGTCAAGAAATTTTGTATGATTAACCTGCTG 1740
DB 1681 GGTATTAAGGATTAATGCTTCTAGTCAAGAAATTTTGTATGATTAACCTGCTG 1740
QY 1741 GGAAAAAATCAGCCTTAATATGCTCAATTAAGGATTAATGATTAATGCTTAATCA 1800
DB 1741 GGAAAAAATCAGCCTTAATATGCTCAATTAAGGATTAATGATTAATGCTTAATCA 1800
QY 1801 TTAATAATAAGTATTTTGTCTTAAAGTTACACGCTTAAATTCATTAAGAGAT 1860
DB 1801 TTAATAATAAGTATTTTGTCTTAAAGTTACACGCTTAAATTCATTAAGAGAT 1860
QY 1861 ATTATCTTGTATGCAATTTCCAAATATCTTTTAAACATTAAGAAATTTTCAGATT 1920
DB 1861 ATTATCTTGTATGCAATTTCCAAATATCTTTTAAACATTAAGAAATTTTCAGATT 1920
QY 1921 TTAATAATAAGGATTAATGCTTCAATTAATGCTTCAAGTAAAGTTGAGGT 1980
DB 1921 TTAATAATAAGGATTAATGCTTCAATTAATGCTTCAAGTAAAGTTGAGGT 1980
QY 1981 TTAACAATGATTTTGTATTAATAAACAATTAATTTCTAGTATTAACATT 2040
DB 1981 TTAACAATGATTTTGTATTAATAAACAATTAATTTCTAGTATTAACATT 2040
QY 2041 TTTAACCGTCAATCAATGTAATTAAGTACAAATCTGAAACATTTTTTTCTTG 2100
DB 2041 TTTAACCGTCAATCAATGTAATTAAGTACAAATCTGAAACATTTTTTTCTTG 2100
QY 2101 AATTTGTTAAATTTCTCTGCTGCAATCTTGACGATTTGACAAAGCTATTAACA 2160
DB 2101 AATTTGTTAAATTTCTCTGCTGCAATCTTGACGATTTGACAAAGCTATTAACA 2160
QY 2161 TTTGAAACAAATATCAACAGGATGATAGGTTAGATCCCAATTCATTAATCTTTGT 2220
DB 2161 TTTGAAACAAATATCAACAGGATGATAGGTTAGATCCCAATTCATTAATCTTTGT 2220
QY 2221 CTTTGTATTTATGAAAAAACAATATTTATCAAGAAAAAAGCTTCTCTGAGGTGA 2280
DB 2221 CTTTGTATTTATGAAAAAACAATATTTATCAAGAAAAAAGCTTCTCTGAGGTGA 2280
QY 2281 TAAATATTAAGTATTAACAAATTTAATCTAGTATGTAATGATTAATCTGAACTT 2340
DB 2281 TAAATATTAAGTATTAACAAATTTAATCTAGTATGTAATGATTAATCTGAACTT 2340
QY 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTATCAACATCTTCACTA 2400
DB 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTATCAACATCTTCACTA 2400

QY 2401 AAAAATGCAAAAGAGATATATTTAAGTCAAAAGTATTAAGATGAGGTGAT 2460
DB 2401 AAAAATGCAAAAGAGATATATTTAAGTCAAAAGTATTAAGATGAGGTGAT 2460
QY 2461 TCTTCAGCAAAACGCGCCGAGAGGTGCTTATCTTACATTAACGCTGGTTGCGAG 2520
DB 2461 TCTTCAGCAAAACGCGCCGAGAGGTGCTTATCTTACATTAACGCTGGTTGCGAG 2520
QY 2521 ACATCATAGGCGCTAGATATTTAGCTTTACTGTAAGCTTAACATATCTAGT 2580
DB 2521 ACATCATAGGCGCTAGATATTTAGCTTTACTGTAAGCTTAACATATCTAGT 2580
QY 2581 TAGTTCTCATGTAACAAACAAATCCAATTCGTAACATATTAACAAATCTACTA 2640
DB 2581 TAGTTCTCATGTAACAAACAAATCCAATTCGTAACATATTAACAAATCTACTA 2640
QY 2641 GTACTAGATTAACGTAATGATACATGCTTTTTCGCAAAATTTCTAACTATCTATCAA 2700
DB 2641 GTACTAGATTAACGTAATGATACATGCTTTTTCGCAAAATTTCTAACTATCTATCAA 2700
QY 2701 CAATCTGAATGTTGTTGTAATTTATCTTAAACAAAGTTTGAATGTCATTTGGG 2760
DB 2701 CAATCTGAATGTTGTTGTAATTTATCTTAAACAAAGTTTGAATGTCATTTGGG 2760
QY 2761 AGCTACACTAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTAAAGT 2820
DB 2761 AGCTACACTAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTAAAGT 2820
QY 2821 ATTTAAACCAAAATTTTAAATTTGTGCTGAAGTCAAAACATGTCATATATAGAGA 2880
DB 2821 ATTTAAACCAAAATTTTAAATTTGTGCTGAAGTCAAAACATGTCATATATAGAGA 2880
QY 2881 CAGCATGTTTATTAACAAATATGTTGATGTAATGGAATCAAAATTAATGCAATTA 2940
DB 2881 CAGCATGTTTATTAACAAATATGTTGATGTAATGGAATCAAAATTAATGCAATTA 2940
QY 2941 GCGACTCATGTTGTAATGTTGGAAGATTAAGAAATTAAGAAATGAAATGAAAGTAA 3000
DB 2941 GCGACTCATGTTGTAATGTTGGAAGATTAAGAAATTAAGAAATGAAATGAAAGTAA 3000
QY 3001 CAGAGCTATATATGTCGGGTCAATTTAGAGCCGTGACCAAAAGTTTCGTATTAAC 3060
DB 3001 CAGAGCTATATATGTCGGGTCAATTTAGAGCCGTGACCAAAAGTTTCGTATTAAC 3060
QY 3061 GGTGCTCATTAAGAAATTTGGAATTTTCACTTTTATGAACTTCTGATATGTTT 3120
DB 3061 GGTGCTCATTAAGAAATTTGGAATTTTCACTTTTATGAACTTCTGATATGTTT 3120
QY 3121 TGTGGAATTAATATTTGTAATGTAATTTTGTCTTAATTAAGTAACTGTAATCA 3180
DB 3121 TGTGGAATTAATATTTGTAATGTAATTTTGTCTTAATTAAGTAACTGTAATCA 3180
QY 3181 CGATTAAGAAAGCTTCTTTTATTTAATTTGAATTAACCTTTGTTTGAATGACT 3240
DB 3181 CGATTAAGAAAGCTTCTTTTATTTAATTTGAATTAACCTTTGTTTGAATGACT 3240
QY 3241 CATACACAAGGTTAAAGTTGATGTAATCAATTTTACAAAAATGTTTGAAGTGGCTC 3300
DB 3241 CATACACAAGGTTAAAGTTGATGTAATCAATTTTACAAAAATGTTTGAAGTGGCTC 3300
QY 3301 GAGTGTCTTACACATGTAACCACTGTAAGGTTTATTAATGTTTCTTCTT 3360
DB 3301 GAGTGTCTTACACATGTAACCACTGTAAGGTTTATTAATGTTTCTTCTT 3360
QY 3361 TTTCCAAATGCTTTATTAATTAAGACCACTTAATTTCTTTTATTAATGTTAAGAT 3420
DB 3361 TTTCCAAATGCTTTATTAATTAAGACCACTTAATTTCTTTTATTAATGTTAAGAT 3420
QY 3421 CTTGAATTTTCTGTTGAATTTTAAACAAGGTTTCAATCTCTTACACAAAAAATAA 3480
DB 3421 CTTGAATTTTCTGTTGAATTTTAAACAAGGTTTCAATCTCTTACACAAAAAATAA 3480
QY 3481 AAAAGTTTCAATTAATTAAGAAATCTAAATTTTGTGAGTTCAAGAGTTTAATGATGCT 3540

D	b		3481	AAAAAGTTTCAATTAATTAAAGAATCTAAAATTTTTTGAGTTCAAGAGTTTAATGATACCT	3540
Q	y		3541	GAAAAGTTATGAATGATTCGAAGTTTGGACAAGAAATGGTCAGTAGTACTATCTCAAAA	3600
D	b		3541	GAAAAGTTATGAATGATTCGAAGTTTGGACAAGAAATGGTCAGTAGTACTATCTCAAAA	3600
Q	y		3601	CATGCATCAAAATAAATTAATGTGCTTGCGCAAGAGAAACGATTTGAAATTAACAGAACAT	3666
D	b		3601	CATGCATCAAAATAAATTAATGTGCTTGCGCAAGAGAAACGATTTGAAATTAACAGAACAT	3666
Q	y		3661	CGTTAACCACTTAAAAATCTTGAATAATTTTGTAGTATATTTCTGTAAAGAGAGG	3720
D	b		3661	CGTTAACCACTTAAAAATCTTGAATAATTTTGTAGTATATTTCTGTAAAGAGAGG	3720
Q	y		3721	TATCATATCTTACAAAAAAAATCTCATTCCAGATTAATAATGTTGCCAATCGTTACA	3780
D	b		3721	TATCATATCTTACAAAAAAAATCTCATTCCAGATTAATAATGTTGCCAATCGTTACA	3780
Q	y		3781	AGTAAAGTTTTCGCTGCATCAGTTGATATGTAACCTGCCTATGACCATAATGTTCTAAG	3840
D	b		3781	AGTAAAGTTTTCGCTGCATCAGTTGATATGTAACCTGCCTATGACCATAATGTTCTAAG	3840
Q	y		3841	TTTTAAATGTTTTCAAAGACTTTACAAAATAAATAATAATAAGTGAATTTGTAGG	3900
D	b		3841	TTTTAAATGTTTTCAAAGACTTTACAAAATAAATAATAATAAGTGAATTTGTAGG	3900
Q	y		3901	CTAAAGGGAATAATTAATAATTAATAAGTAAAGGAGCTCTTCTCAATTAAGAACAC	3966
D	b		3901	CTAAAGGGAATAATTAATAATTAATAAGTAAAGGAGCTCTTCTCAATTAAGAACAC	3966
Q	y		3961	AGATCCCAACGATTCACAAACAGCAAAATTTGTGCTTGTCTCTCTTATTAATATATC	4020
D	b		3961	AGATCCCAACGATTCACAAACAGCAAAATTTGTGCTTGTCTCTCTTATTAATATATC	4020
Q	y		4021	CTCTCAAAAAACCTCTCTCTATATCTCTTAAGCCCCCTTCCTGTTTCTCTACCGCAA	4080
D	b		4021	CTCTCAAAAAACCTCTCTCTATATCTCTTAAGCCCCCTTCCTGTTTCTCTACCGCAA	4080
Q	y		4081	CAAAAGAAAAACAAGGTTGAGAAAAATGGAGTGTGTTGTTGTATACCAATGATGGGT	4140
D	b		4081	CAAAAGAAAAACAAGGTTGAGAAAAATGGAGTGTGTTGTTGTATACCAATGATGGGT	4140
Q	y		4141	TTTAGCTTACTTCTCGAGAGATTATAGAAAAGAAAGTAGAAGTACATTATAGAAAGA	4200
D	b		4141	TTTAGCTTACTTCTCGAGAGATTATAGAAAAGAAAGTAGAAGTACATTATAGAAAGA	4200
Q	y		4201	AGAGAGAGAAACCAAAAAAGAAACC 4228	
D	b		4201	AGAGAGAGAAACCAAAAAAGAAACC 4228	

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1      RESULT 3
2      US-09-227-421-1
3      ; Sequence 1, Application US/09227421
4      ; Patent No. 6559357
5      ; GENERAL INFORMATION:
6      ; APPLICANT: Fischer, Robert L.
7      ; APPLICANT: Mizukami, Yukiko
8      ; APPLICANT: The Regents of the University of California
9      ; TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
10     ; TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
11     ; FILE REFERENCE: 023070-090700PC
12     ; CURRENT APPLICATION NUMBER: US/09/227,421
13     ; CURRENT FILING DATE: 1999-01-08
14     ; PRIOR APPLICATION NUMBER: US 09/227,421
15     ; PRIOR FILING DATE: 1999-01-08
16     ; NUMBER OF SEQ ID NOS: 8
17     ; SOFTWARE: PatentIn Ver. 2.1
18     ; SEQ ID NO 1
19     ; LENGTH: 2148
20     ; Type: DNA
21     ; ORGANISM: Arabidopsis thaliana

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (269)..(1936)
; OTHER INFORMATION: AINTEGUMENTA (ANT)
; NAME/KEY: misc feature
; LOCATION: (1109)..(1339)
; OTHER INFORMATION: encodes first AP2 domain
; NAME/KEY: misc feature
; LOCATION: (1340)..(1414)
; OTHER INFORMATION: encodes linker region
; NAME/KEY: misc feature
; LOCATION: (1415)..(1621)
; OTHER INFORMATION: encodes second AP2 domain
US-09-227-421-1

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Query	March	5.3#	Score 268	DB 3	Length 2148
Best Local Similarity	100.0%	Prod. No.	5.3e-96		
Matches 268	Conservative 0	Mismatches 0	Indels 0	Gaps 0	
QY	3961	AGATCCACGAGATCCAAACGACAAATTTGTGCTTTGCTCTCTCTTATATATATC	4020		
DB	1	AGATCCCAACGATTCAAACAGCAAAATTTGTGCTTTGCTCTCTCTTATATATATC	60		
QY	4021	CTCTCAAAAAACCTCTCTCTATATCTCTTAAAGCCCCCTCTGTGTTCTCTACCGCA	4080		
DB	61	CTCTCAAAAAACCTCTCTATATCTCTTAAAGCCCCCTCTGTGTTCTCTACCGCA	120		
QY	4081	CAAAGAAAAACAAAGTTTGAGAAAAATGTGTGTTGCTTGTAACCAATGATGGGT	4140		
DB	121	CAAAGAAAAACAAAGTTTGAGAAAAATGTGTGTTGCTTGTAACCAATGATGGGT	180		
QY	4141	TTTAGCTTACTCTCGAGATATATAAGAAAGAGAGTAAATACATTATAGAAAGA	4200		
DB	181	TTTAGCTTACTCTCGAGATATATAAGAAAGAGTAAATACATTATAGAAAGA	240		
QY	4201	AGAGAGCAAAACCAAAAAAGAAACC	4228		
DB	241	AGAGAGCAAAACCAAAAAAGAAACC	268		

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QY      361 AGATCCACGAGATTCAAACGCAAAATTGTGCTTTGCTCTCTCTATTATATATC 4020
DB      1 AGATCCACGAGATTCAAACGCAAAATTGTGCTTTGCTCTCTCTATTATATATC 60

; Sequence 1, Application US/09479855
; Patent No. 6639128
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; TITLE OF INVENTION: Methods for the Universal Organ Mass, Controlling Fertility
; TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
; FILE REFERENCE: 023070-090720US
; CURRENT FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2148
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA
; NAME/KEY: CDS
; LOCATION: (269)..(1936)
; OTHER INFORMATION: AINTEGUMENTA (ANT)
US-09-479-855-1

Query Match      6.3%; Score 268; DB 3; Length 2148;
Best Local Similarity 100.0%; Pred. No. 5,3e-96;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	CTCTCAAAAACCCCTCCTATATCTCCTAAAGCCCCCTCTCTGTTTCTCTACCGGA	4082
Db	CTCTCAAAAACCCCTCCTATATCTCCTAAAGCCCCCTCTCTGTTTCTCTACCGGA	120
QY	CAAGAAAAAACAAGATTGTAGAAAAATGCTGTGTTCTGTGTAAACAATGATTGGGT	4140
Db	CAAGAAAAAACAAGATTGTAGAAAAATGCTGTGTTCTGTGTAAACAATGATTGGGT	180
QY	TTTAGCTTACTACTTCGAGAGATTATAGAAAAAGTGAAGATACATTATAGAAAGA	4200
Db	TTTAGCTTACTACTTCGAGAGATTATAGAAAAAGTGAAGATACATTATAGAAAGA	240
QY	AGAGAGCAGAAACCAAAAAAAGAAACC	4228
Db	AGAGAGCAGAAACCAAAAAAAGAAACC	268

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RESULT 5
US-08-486-013-69
Sequence 69, Application US/08486013
Patent No. 5731149
GENERAL INFORMATION:
APPLICANT: Selected, Michael E.
APPLICANT: Ouellette, Andre J.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of their use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,013
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-486-013-69

Query Match 1.3%; Score 55; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCACTTAGGGCTCACTGACCTTAATGCACTCACTATAGGAGAGCTGAGAGATC 55

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Db      666  GTGACCTCTAGGGCCTCACTGGCCTTAATACGACTCACTAATAGGGAGCTCGAGATC  720

RESULT 6
US-08-482-279--69
: Sequence 69, Application US/08482279
: Patent No. 5840498
: GENERAL INFORMATION:
: APPLICANT: Selseled, Michael E.
: APPLICANT: Quellette, Andre J.
: TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
: TITLE OF INVENTION: of Their Use
: NUMBER OF SEQUENCES: 70
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell and Flores
: STREET: 4370 La Jolla Village Drive, Suite 700
: CITY: San Diego
: STATE: California
: COUNTRY: USA
: ZIP: 92122
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/482,279
: FILING DATE:
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/342,268
: FILING DATE: 18-NOV-1994
: APPLICATION NUMBER: US 07/930,649
: FILING DATE: 14-AUG-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/889,020
: FILING DATE: 26-MAY-1992
: ATTORNEY/AGENT INFORMATION A:
: NAME: Campbell, Cathryn A.
: REGISTRATION NUMBER: 31,815
: REFERENCE/DOCKET NUMBER: P-UC 1206
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (619) 535-9001
: TELEFAX: (619) 535-8949
: INFORMATION FOR SEQ ID NO: 69:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2408 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: US-08-482-279--69

Query Match      1.3%; Score 55; DB 2; Length 2408;
Best Local Similarity 100.0%; Fied. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      1  GTGACCTCTAGGGCCTCACTGGCCTTAATACGACTCACTAATAGGGAGCTCGAGATC  55
Db      666  GTGACCTCTAGGGCCTCACTGGCCTTAATACGACTCACTAATAGGGAGCTCGAGATC  720

RESULT 7
US-08-342-268--69
: Sequence 69, Application US/08342268
: Patent No. 5844072
: GENERAL INFORMATION:
: APPLICANT: Selseled, Michael E.
: APPLICANT: Quellette, Andre J.
: TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
: TITLE OF INVENTION: of Their Use
: NUMBER OF SEQUENCES: 70
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Campbell and Flores

```

STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/342,268
FILING DATE: 18-NOV-1994
CLASSIFICATION: 435
PRIORITY/AGENT INFORMATION:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 1206
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-342-268-69

Query Match 1.3%; Score 55; DB 2; Length 2408;
Best local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGACTTAGGCTCAGCTGCGCTTAATAGACTCACTATTAGGAGCTCGAGATC 55
DB 666 GTGGACTTAGGCTCAGCTGCGCTTAATAGACTCACTATTAGGAGCTCGAGATC 720

RESULT 8
US-09-015-968-69
Sequence 69, Application US/09015968
Patent No. 6057425
GENERAL INFORMATION:
APPLICANT: Seisted, Michael E.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-015-968-69

Query Match 1.3%; Score 55; DB 3; Length 2408;
Best local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGGACTTAGGCTCAGCTGCGCTTAATAGACTCACTATTAGGAGCTCGAGATC 55
DB 666 GTGGACTTAGGCTCAGCTGCGCTTAATAGACTCACTATTAGGAGCTCGAGATC 720

RESULT 9
US-09-397-386-69
Sequence 69, Application US/09397386
Patent No. 6300470
GENERAL INFORMATION:
APPLICANT: Seisted, Michael E.
TITLE OF INVENTION: Antibiotic Cryptdin Peptides and Methods
TITLE OF INVENTION: of Their Use
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/397,386
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/015,968
FILING DATE:
APPLICATION NUMBER: US 08/482,279
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/342,268
FILING DATE: 18-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/930,649
FILING DATE: 14-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/889,020
FILING DATE: 26-MAY-1992

ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-UC 3003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 2408 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-397-386-69

Query Match 1.3%; Score 55; DB 3; Length 2408;
Best Local Similarity 100.0%; Pred. No. 4.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 666 GTGACTTATGGCTCTACTGGCTTATACGACTCACTATATAGGAGCTCGAGATC 55
1 GTGACTTATGGCTCTACTGGCTTATACGACTCACTATATAGGAGCTCGAGATC 55

RESULT 10
US-08-459-448A-26/C
Sequence 26, Application US/08459448A
Patent No. 5859336
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Deesl, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launig, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Sutcliffe, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 5859336artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent-in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,448A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.

REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CTP/DIV4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 541-8582
TELEFAX: (919) 541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
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NAME/KEY: exon
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NAME/KEY: intron
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FEATURE:
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LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-448A-26

Query Match 0.8%; Score 32; DB 2; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 4162 TTGGCTTATAGCACTCACTATATAGGAGCTCGA 50
19 TTGGCTTATAGCACTCACTATATAGGAGCTCGA 50

RESULT 11
US-08-459-595A-26/C
Sequence 26, Application US/08459595A
Patent No. 6018104
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launib, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSES:
ADDRESSEE: No. 6018104artis Corporation
STREET: Patent & Trademark Dept., 520 White Plains
STREET: Rd., POB 2005
CITY: Tarrytown
STATE: New York
COUNTRY: USA
ZIP: 10591-9005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,595A
FILING DATE: 02-JUN-1995
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA: US 07/772,027
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Pace, Gary M.
REGISTRATION NUMBER: 40403
REFERENCE/DOCKET NUMBER: CGC 1577/CIP/DIV3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8582
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451

FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
FEATURE:
NAME/KEY: promoter
LOCATION: 1..1477
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /partial
OTHER INFORMATION: /function= "pollen-specific promoter region"
OTHER INFORMATION: /evidence= EXPERIMENTAL
US-08-459-595A-26
Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TGGCTTAATACGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTTAATACGACTCACTATAGGAGCTCGA 4131
RESULT 12
US-08-459-504B-26/C
Sequence 26, Application US/08459504B
Patent No. 6075185
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
APPLICANT: Desai, Nalini M.
APPLICANT: Lewis, Kelly S.
APPLICANT: Kramer, Vance C.
APPLICANT: Warren, Gregory W.
APPLICANT: Evola, Stephen V.
APPLICANT: Crossland, Lyle D.
APPLICANT: Wright, Martha S.
APPLICANT: Merlin, Ellis J.
APPLICANT: Launib, Karen L.
APPLICANT: Rothstein, Steven J.
APPLICANT: Bowman, Cindy G.
APPLICANT: Dawson, John L.
APPLICANT: Dunder, Erik M.
APPLICANT: Pace, Gary M.
APPLICANT: Suttie, Janet L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED

TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6075185artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,504B
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mel98, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: CGC1577/CIP/DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
FAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHEetical: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:

NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
US-08-459-504B-26
Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cv 19 TGGCTATATGACTGCTATAGGAGCTCGA 50
Db 4162 TGGCTATATGACTGCTATAGGAGCTCGA 4131
RESULT 13
US-08-459-444-26/c
Sequence 26, Application US/08459444A
Patent No. 6121014
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.
TITLE OF INVENTION: METHOD FOR PRODUCING A PLANT-OPTIMIZED
NUCLEIC ACID CODING SEQUENCE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6121014artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,444A
FILING DATE: 02-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mel98, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805/PL/CGC1577/CIP/DIV6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
FAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-08-459-444-26
Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TGGCTTAATGAGCTCACTATAGGAGCTCGA 50
DB 4162 TGGCTTAATGAGCTCACTATAGGAGCTCGA 4131
RESULT 14
US-09-547-422-26/c
Sequence 26, Application US/09547422
Patent No. 6320100
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Deeal, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 6320100artis Agribusiness Biotechnology Research, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/547,422
FILING DATE: 11-Apr-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/459,595
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-18805H
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:

NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-547-422-26

Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCTAATAGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTAATAGACTCACTATAGGAGCTCGA 4131

RESULT 15
US-09-988-462-26/C
Sequence 26, Application US/09988462
Patent No. 6720488
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Launis, Karen L.

TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE

NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-No. 6720488-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-APR-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-JUN-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-SEP-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-OCT-1991

ATTORNEY/AGENT INFORMATION:
NAME: Mel198, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689

INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"

FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811

SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-09-988-462-26

Query Match 0.8%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0053;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCTAATAGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTAATAGACTCACTATAGGAGCTCGA 4131

RESULT 16
US-07-951-715A-26/C
Sequence 26, Application US/07951715A
Patent No. 5625136
GENERAL INFORMATION:
APPLICANT: Koziel, Michael G.
Desai, Nalini M.
Kramer, Vance C.
Warren, Gregory W.

```

? APPLICANT: Evola, Stephen V.
? APPLICANT: Crossland, Lyle D.
? APPLICANT: Wright, Martha S.
? APPLICANT: Merlin, Ellis J.
? APPLICANT: Launle, Karen L.
? APPLICANT: Rothelein, Steven J.
? APPLICANT: Bowman, Cindy G.
? APPLICANT: Dawson, John L.
? APPLICANT: Dunder, Erik M.
? APPLICANT: Pace, Gary M.
? APPLICANT: Suttle, Janet L.
? TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
? TITLE OF INVENTION: INSECTICIDAL ACTIVITY IN MAIZE
? NUMBER OF SEQUENCES: 94
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: CIBA-GEIGY Corporation
? STREET: 7 Skyline Drive
? CITY: Hawthorne
? STATE: New York
? COUNTRY: USA
? ZIP: 10532
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.308
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/07/951,715A
? FILING DATE: 25-SEP-1992
? CLASSIFICATION: 800
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 07/772,027
? FILING DATE: 04-OCT-1991
? ATTORNEY/AGENT INFORMATION:
? NAME: Sprull, W. Murray
? REGISTRATION NUMBER: 32,943
? REFERENCE/DOCKET NUMBER: S-18805/A/CGC 1577/CIP
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (919)541-8615
? TELEFAX: (919)541-8689
? INFORMATION FOR SEQ ID NO: 26:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 4165 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: 1416..1425
? OTHER INFORMATION: /note= "start of mRNA"
? FEATURE:
? NAME/KEY: exon
? LOCATION: 1481..2366
? FEATURE:
? NAME/KEY: intron
? LOCATION: 2367..2449
? FEATURE:
? NAME/KEY: exon
? LOCATION: 2450..2602
? FEATURE:
? NAME/KEY: intron
? LOCATION: 2603..2688
? FEATURE:
? NAME/KEY: exon
? LOCATION: 2689..2804
? FEATURE:
? NAME/KEY: intron
? LOCATION: 2805..2906
? FEATURE:
? NAME/KEY: exon
? LOCATION: 2907..3074

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? FEATURE:
? NAME/KEY: intron
? LOCATION: 3075..3177
? FEATURE:
? NAME/KEY: exon
? LOCATION: 3178..3305
? FEATURE:
? NAME/KEY: intron
? LOCATION: 3306..3397
? FEATURE:
? NAME/KEY: exon
? LOCATION: 3398..3497
? FEATURE:
? NAME/KEY: intron
? LOCATION: 3498..3712
? FEATURE:
? NAME/KEY: exon
? LOCATION: 3713..3811
? US-07-951-715A-26

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Query Match 0.7%; Score 31; DB 2; Length 4165;

Best Local Similarity 100.0%; Pred. No. 0.013; Mismatches 0; Indels 0; Gaps 0;

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Qy 20 GGCTAATAGACTCACTATAGGAGCTCGA 50
Db 4165 GGCTAATAGACTCACTATAGGAGCTCGA 4135

```

RESULT 17

US-09-308-090-1

Sequence 1, Application US/09308090

Patent No. 6395963

GENERAL INFORMATION:

APPLICANT: OHL, Stephan

APPLICANT: Van Der Lee, Frederique

APPLICANT: Goddijn, Oscar

APPLICANT: Klap, Joke

APPLICANT: Sijmons, Peter

TITLE OF INVENTION: Nematode-Inducible Regulatory DNA Sequences

FILE REFERENCE: MOG 57680

CURRENT APPLICATION NUMBER: US/09/308,090

CURRENT FILING DATE: 1999-05-14

EARLIER APPLICATION NUMBER: PCT/EP97/06472

EARLIER FILING DATE: 1997-11-18

EARLIER APPLICATION NUMBER: EP 96203213.2

EARLIER FILING DATE: 1996-11-18

NUMBER OF SEQ ID NOS: 10

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 1

LENGTH: 3484

TYPE: DNA

ORGANISM: Arabidopsis thaliana

FEATURE:

NAME/KEY: CDS

LOCATION: (3482)..(3484)

US-09-308-090-1

Query Match 0.7%; Score 28; DB 3; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 23 CTAATAGACTCACTATAGGAGCTCGA 50
Db 698 CTAATAGACTCACTATAGGAGCTCGA 725

```

RESULT 18

US-09-380-090A-1

Sequence 1, Application US/09380090A

Patent No. 6555529

GENERAL INFORMATION:

APPLICANT: OHL, Stephan Andreas

;; SIMONS, Peter Christiaan
;; KLEIN-VAN DER LEE, Frederique
;; Marianne
;; GODDARD, Oscar
;; Klap, Joke
;; TITLE OF INVENTION: NEMATODE-INDUCIBLE REGULATORY DNA
;; SEQUENCES
;;
;; NUMBER OF SEQUENCES: 10
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Hale and Dorr LLP
;; STREET: 60 State Street
;; CITY: Boston
;; STATE: Massachusetts
;; COUNTRY: United States
;; ZIP: 02109
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/380,090A
;; FILING DATE: 17-May-1999
;; CLASSIFICATION: <Unknown>
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: WO PCT/EP97/06472
;; FILING DATE: 18-NOV-1997
;; APPLICATION NUMBER: EP 9620323.2
;; FILING DATE: 18-NOV-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Superko, Colleen
;; REGISTRATION NUMBER: 39,850
;; REFERENCE/DOCKET NUMBER: SYN-010
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (617) 526-6000
;; TELEFAX: (617) 526-5000
;;
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 3484 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
;; HYPOTHETICAL: NO
;; ANTI-SENSE: NO
;; ORIGINAL SOURCE:
;; ORGANISM: Arabidopsis thaliana
;; STRAIN: C24
;;
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 3481..3484
;; OTHER INFORMATION: /codon_start= 3482
;;
;; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
;;
;; US-09-380-090A-1
;;
Query Match 0.74; Score 28; DB 3; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.2;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAGCTCGA 50
Db 698 CTAATAGACTCACTATAGGAGCTCGA 725

RESULT 19
PCT-US96-11473A-23
; Sequence 23; Application PC/TUS9611473A
; GENERAL INFORMATION:
; APPLICANT: LARRY GOLD
; APPLICANT: MICHAEL LOCHRIE
; APPLICANT: HANG CHEN
; APPLICANT: CRAIG TUERK
; TITLE OF INVENTION: INTRACELLULAR ACTION OF

;; TITLE OF INVENTION: NUCLEIC ACID LIGANDS
;; NUMBER OF SEQUENCES: 31
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Swanson and Bratschum, L.L.C.
;; STREET: 8400 East Prentice Avenue, Suite #200
;; CITY: Englewood
;; STATE: Colorado
;; COUNTRY: USA
;; ZIP: 80111
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
;; OPERATING SYSTEM: MS-DOS
;; SOFTWARE: WordPerfect 6.0
;;
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US96/11473A
;; FILING DATE:
;; CLASSIFICATION:
;;
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/521,515
;; FILING DATE: 30-AUGUST-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/000,872
;; FILING DATE: 11-JULY-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Barry J. Swanson
;; REGISTRATION NUMBER: 33,215
;; REFERENCE/DOCKET NUMBER: NEX45/PCT
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (303) 793-3333
;; TELEFAX: (303) 793-3433
;;
;; INFORMATION FOR SEQ ID NO: 23:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 239 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: RNA
;;
;; PCT-US96-11473A-23
;;
Query Match 0.64; Score 26; DB 6; Length 239;
Best Local Similarity 76.9%; Pred. No. 1.6;
Matches 20; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAGCTC 48
Db 94 CTAATAGACTCACTATAGGAGCTC 119

RESULT 20
US-09-949-016-55437
; Sequence 55437; Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55437
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-55437

Query Match 0.6%; Score 26; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAAATATAATATAAGTAAA 3935
DB 500 AAAAAATATAATATAAGTAAA 525

RESULT 21

US-09-949-016-13362/c
; Sequence 13362, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTNER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ. ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13362
; LENGTH: 285478
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(285478)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13362

Query Match 0.6%; Score 26; DB 3; Length 285478;
Best Local Similarity 100.0%; Pred. No. 0.83;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAAATATAATATAAGTAAA 3935
DB 97296 AAAAAATATAATATAAGTAAA 97271

RESULT 22

US-08-458-423A-11/c
; Sequence 11, Application US/08458423A
; Patent No. 5731144
; GENERAL INFORMATION:
; APPLICANT: PENELOPE J. TOOTHMAN
; APPLICANT: STEVEN RINGQUIST
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY TGFA NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,423A

FILING DATE: 2-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992

ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn

REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 34-1

TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:

LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

US-08-458-423A-11
MOLECULE TYPE: DNA

Query Match 0.6%; Score 25; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCATATAGGAGGCTC 48
DB 33 TATACGACTCATATAGGAGGCTC 9

RESULT 23

US-08-458-424B-11/c
; Sequence 11, Application US/08458424B
; Patent No. 5731424
; GENERAL INFORMATION:
; APPLICANT: PENELOPE J. TOOTHMAN
; APPLICANT: STEVEN RINGQUIST
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY TGFA NUCLEIC
; TITLE OF INVENTION: ACID LIGANDS AND INHIBITORS
; NUMBER OF SEQUENCES: 89
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,424B
; FILING DATE: 2-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McLearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 34-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-458-424B-11

Query Match 0.6%; Score 25; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 24 TAATACGACTCAGCTATAGGAGCTC 48
Db 33 TAATACGACTCAGCTATAGGAGCTC 9

RESULT 24
US-08-973-124-11/c
Sequence 11, Application US/08973124
Patent No. 6207816
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594

FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-973-124-11

Query Match 0.6%; Score 25; DB 3; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 24 TAATACGACTCAGCTATAGGAGCTC 48
Db 33 TAATACGACTCAGCTATAGGAGCTC 9

RESULT 25
PCT-US96-08014-11/c
Sequence 11, Application PC/TUS9608014
GENERAL INFORMATION:
APPLICANT: LARRY GOLD, NEBOJSA JANJIC, STEVEN RINGQUIST;
APPLICANT: PAGARITS, PENELOPE J. TOOTHMAN
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO TRANSFORMING GROWTH
TITLE OF INVENTION: FACTOR (TGF), PLATELET-DERIVED
TITLE OF INVENTION: GROWTH FACTOR (PDGF) AND HUMAN
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA: 08/479,763
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION NUMBER: 08/618,633
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US96-08014-11

Query Match 0.6%; Score 25; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTCACTATAGGAGCTC 48
Db 33 TAATAGACTCACTATAGGAGCTC 9

RESULT 26
US-09-268-710-1
Sequence 1, Application US/09268710
Patent No. 6261773
GENERAL INFORMATION:
APPLICANT: Segawa, Masaya
APPLICANT: Kondo, Motohiro
TITLE OF INVENTION: Reagent for Nucleic Acid Amplification and Process for
FILE REFERENCE: 10089/8
CURRENT APPLICATION NUMBER: US/09/268,710
CURRENT FILING DATE: 1999-03-16
EARLIER APPLICATION NUMBER: JP P1998/66988
EARLIER FILING DATE: 1998-03-17
EARLIER APPLICATION NUMBER: JP P1999/18434
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 47
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: misc_binding
LOCATION: (28)..(47)
OTHER INFORMATION: DNA sequence complementary to a sequence of
OTHER INFORMATION: Mycobacterium tuberculosis 16S rRNA gene
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(27)
OTHER INFORMATION: promoter for T7 RNA polymerase
US-09-268-710-1

Query Match 0.6%; Score 25; DB 3; Length 47;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTATAGCACTCACTATAGGAGCT 47
Db 5 CTATAGCACTCACTATAGGAGCT 29

RESULT 27
US-07-931-473B-37
Sequence 37, Application US/07931473B
Patent No. 5270163
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Tueck
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 335
CORRESPONDENCE ADDRESS:
ADDRESSER: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/931,473B
FILING DATE: 19920817
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
US-07-931-473B-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTCACTATAGGAGCTC 48
Db 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 28
US-08-199-507B-55
Sequence 55, Application US/08199507B
Patent No. 5472841
GENERAL INFORMATION:
APPLICANT: JAYASENA, S. AND GOLD, L.
TITLE OF INVENTION: NUCLEIC ACID LIGAND INHIBITORS
TITLE OF INVENTION: OF HUMAN NEUTROPHIL ELASTASE
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado

COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/199,507B
FILING DATE: 22 FEBRUARY 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-199-507B-55

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTATAGGAGCTC 48
Db 9 TAATACGACTCATTATAGGAGCTC 33

RESULT 29
US-07-714-131C-37
Sequence 37, Application US/07714131C
Patent No. 5475096
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Therk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/714,131C
FILING DATE: June 10, 1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900

TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-07-714-131C-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTATAGGAGCTC 48
Db 9 TAATACGACTCATTATAGGAGCTC 33

RESULT 30
US-08-243-870-1
Sequence 1, Application US/08243870
Patent No. 5527894
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY M.
APPLICANT: TUEK, CRAIG
TITLE OF INVENTION: LIGANDS OF HIV-1 tat PROTEIN
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Beaton & Swanson, P.C.
STREET: 4582 South Ulster Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,870
FILING DATE:
CLASSIFICATION: 536

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/953,694
FILING DATE: 29-SEPTEMBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-243-870-1

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTATAGGAGCTC 48
Db 9 TAATACGACTCATTATAGGAGCTC 33

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RESULT 31
US-08-442-572-58
; Sequence 58, Application US/08442572
; Patent No. 5587468
; GENERAL INFORMATION:
; APPLICANT: Allen, Patrick, and Gold, Larry
; TITLE OF INVENTION: High Affinity HIV
; TITLE OF INVENTION: Integrase Inhibitors
; NUMBER OF SEQUENCES: 61
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratechun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/442,572
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/177,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX25
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 58:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-442-572-58

Query Match      0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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QY      24 TAATAGACTCACTATAGGAGCTC 48
      |||
Db      9  TAATAGACTCACTATAGGAGCTC 33
```

```
RESULT 32
US-08-477-530-2
; Sequence 2, Application US/08477530
```

```
; Patent No. 5635400
; GENERAL INFORMATION:
; APPLICANT: PATRICK ALLEN
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY HIV
; TITLE OF INVENTION: NUCLEOCAPSID NUCLEIC ACID LIGANDS
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratechun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,530
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,474
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/477,172
; FILING DATE: 19-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McClearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX 44-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA
;
US-08-477-530-2

Query Match      0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      24 TAATAGACTCACTATAGGAGCTC 48
      |||
Db      9  TAATAGACTCACTATAGGAGCTC 33
```

```
RESULT 33
US-08-477-530-2
; Sequence 2, Application US/08477530
; Patent No. 5635615
```


GENERAL INFORMATION:
APPLICANT: PATRICK ALLEN
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY HIV
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,530
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,474
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,172
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 44-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-477-530-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCATATAGGAGCTC 48
Db 9 TAATACGACTCATATAGGAGCTC 33

RESULT 34
US-08-409-439A-1
Sequence 1, Application US/08409439A
Patent No. 5637461
GENERAL INFORMATION:

APPLICANT: GOLD, LARRY M.
APPLICANT: TIERK, CRAIG
TITLE OF INVENTION: LIGANDS OF HIV-1 tat PROTEIN
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,439A
FILING DATE: 24-MARCH-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/953,694
FILING DATE: 29-SEPTEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX03/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-409-439A-1

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCATATAGGAGCTC 48
Db 9 TAATACGACTCATATAGGAGCTC 33

RESULT 35
US-08-441-591-2
Sequence 2, Application US/08441591
Patent No. 5637682
GENERAL INFORMATION:
APPLICANT: NIEMIANDT, D., GOLD, L. AND WECKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage

COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,591
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 9-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21/C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-591-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 36
US-08-384-708A-2
Sequence 2, Application US/08384708A
Patent No. 5639868
GENERAL INFORMATION:
APPLICANT: Gold, Larry
TITLE OF INVENTION: High-Affinity RNA Ligands of Basic
TITLE OF INVENTION: Fibroblast Growth Factors
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/384,708A

FILING DATE: 02-FEBRUARY-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-384-708A-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 37
US-08-303-362A-2
Sequence 2, Application US/08303362A
Patent No. 5648214
GENERAL INFORMATION:
APPLICANT: NIEMULANDT, D., GOLD, L. AND WICKER, M.
TITLE OF INVENTION: HIGH-AFFINITY
TITLE OF INVENTION: OLIGONUCLEOTIDE LIGANDS
TITLE OF INVENTION: TO THE TACHYKININ
TITLE OF INVENTION: SUBSTANCE P
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/303,362A
FILING DATE: 9-SEPTEMBER-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER 1993
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-303-362A-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCCTATAGGAGCTC 48
Db 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 38
US-08-477-830-2
Sequence 2, Application US/08477830
Patent No. 5654151
GENERAL INFORMATION:
APPLICANT: PATRICK ALLEN
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY HIV
TITLE OF INVENTION: NUCLEOSAPSID NUCLEIC ACID LIGANDS
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,830
FILING DATE: 7-JUNE-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,474
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/477,172
FILING DATE: 19-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McLearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX 44-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-477-830-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCCTATAGGAGCTC 48
Db 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 39
US-08-412-110-37
Sequence 37, Application US/08412110
Patent No. 5670637
GENERAL INFORMATION:
APPLICANT: Larry Gold
APPLICANT: Craig Therk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 344
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/412,110
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-412-110-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 40
US-08-409-442A-37
Sequence 37, Application US/08409442A
Patent No. 5696249
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,442A
FILING DATE:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-409-442A-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 41
US-08-441-828-55
Sequence 55, Application US/08441828
Patent No. 5734034
GENERAL INFORMATION:
APPLICANT: JAYASENA, S. AND GOLD, L.
TITLE OF INVENTION: NUCLEIC ACID LIGAND INHIBITORS
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/441,828
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/199,507
FILING DATE: 22 FEBRUARY 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 55:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-441-828-55

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 42
US-08-361-795-58
Sequence 58, Application US/08361795
Patent No. 5756287
GENERAL INFORMATION:
APPLICANT: Allen, Patrick, and Gold, Larry
TITLE OF INVENTION: High Affinity HIV
NUMBER OF SEQUENCES: 61
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/361,795
FILING DATE:

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/177,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 48
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-361-795-58

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTCCTATAGGAGCTC 48
Db 9 TAATAGACTCCTATAGGAGCTC 33

RESULT 43

US-08-447-169A-2
Sequence 2, Application US/08447169A
Patent No. 5811533
GENERAL INFORMATION:
APPLICANT: JANJIC, N. and GOLD, L.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO VASCULAR ENDOTHELIAL
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Place, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/447,169A
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-447-169A-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTCCTATAGGAGCTC 48
Db 9 TAATAGACTCCTATAGGAGCTC 33

RESULT 44

US-08-469-609A-37
Sequence 37, Application US/08469609A
Patent No. 5843653
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,609A
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/CS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-469-609A-37

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
Db 9 TATACGACTCACTATAGGAGCTC 33

RESULT 45
US-08-233-012C-2
Sequence 2, Application US/08233012C
Patent No. 5849479
GENERAL INFORMATION:
APPLICANT: JANJIC, N. and GOLD, L.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO VASCULAR
TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR
TITLE OF INVENTION:
NUMBER OF SEQUENCES: 146
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Place, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,012C
FILING DATE: 25-APRIL-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA: 07/964,624
APPLICATION NUMBER: 21-OCTOBER-1992
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-233-012C-2

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
Db 9 TATACGACTCACTATAGGAGCTC 33

RESULT 46
US-08-477-527A-208
Sequence 208, Application US/08477527A
Patent No. 5972599
GENERAL INFORMATION:
APPLICANT: DIANE TASSET
APPLICANT: NIKOS PAGRATIS
APPLICANT: SUMEDHA JAYASENA
APPLICANT: LARRY GOLD
TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
TITLE OF INVENTION: OF CYTOKINES
NUMBER OF SEQUENCES: 258
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,527A
FILING DATE: 7-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 8-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Diane H. McClearn
REGISTRATION NUMBER: 33,960
REFERENCE/DOCKET NUMBER: NEX41-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-477-527A-208

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48

Db 9 TAATACGACTCATATAGGAGCTC 33

RESULT 47

US-08-481-710-208
; Sequence 208, Application US/08481710
; Patent No. 6028186
; GENERAL INFORMATION:
; APPLICANT: DIANE TASSET
; APPLICANT: NIKOS PAGRATIS
; APPLICANT: SUMEDHA JAYASENA
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS
; TITLE OF INVENTION: OF CYTOKINES
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/481,710
; FILING DATE: 7-JUNE-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 8-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Diane H. McClearn
; REGISTRATION NUMBER: 33,960
; REFERENCE/DOCKET NUMBER: NEX41-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 208:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; US-08-481-710-208

Query Match 0.6%; Score 25; DB 3; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATATAGGAGCTC 48
Db 9 TAATACGACTCATATAGGAGCTC 33

RESULT 48

US-09-143-190-37

; Sequence 37, Application US/09143190
; Patent No. 6110900
; GENERAL INFORMATION:
; APPLICANT: Larry Gold
; APPLICANT: Craig Tuerk
; TITLE OF INVENTION: Nucleic Acid Ligands
; NUMBER OF SEQUENCES: 374
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 8.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/143,190
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/469,609
; FILING DATE: June 6, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/428,964
; FILING DATE: April 25, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/412,110
; FILING DATE: March 27, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/409,442
; FILING DATE: March 24, 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: June 10, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: June 11, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX01/C6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 48 nucleotides
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-143-190-37

Query Match 0.6%; Score 25; DB 3; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATATAGGAGCTC 48
Db 9 TAATACGACTCATATAGGAGCTC 33

RESULT 49

US-08-687-421-2
; Sequence 2, Application US/08687421
; Patent No. 6177557
; GENERAL INFORMATION:
; APPLICANT: Gold, Larry
; APPLICANT: Janjic, Nebojsa
; APPLICANT: Taseet, Diane

TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF BASIC
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
TITLE OF INVENTION: THROMBIN
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/687,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/219,012
FILING DATE: 28-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-687-421-2
Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATAGCACTACTATAGGAGCTC 48
DB 9 TATAGCACTACTATAGGAGCTC 33

RESULT 50
US-09-502-344-37
Sequence 37, Application US/09502344
Patent No. 6331398
GENERAL INFORMATION:
APPLICANT: Larry Gold
ADDRESSEE: Craig Turk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.

STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/502,344
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3333
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-502-344-37
Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATAGCACTACTATAGGAGCTC 48
DB 9 TATAGCACTACTATAGGAGCTC 33

RESULT 51
US-09-860-474-2
Sequence 2, Application US/09860474
Patent No. 6696252
GENERAL INFORMATION:
APPLICANT: GOLD, L. and JANIC, N.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TO VASCULAR ENDOTHELIAL GROWTH
FACTOR (VEGF)
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado

COUNTRY: USA
ZIP: 80129
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,474
FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/156,824
FILING DATE: 18-SEPTEMBER-1998
APPLICATION NUMBER: 08/447,169
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14/CIP-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-09-860-474-2
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 24 TAATACGACTCATTATGAGGAGCTC 48
Db 9 TAATACGACTCATTATGAGGAGCTC 33
RESULT 52
US-08-442-423-2
Sequence 2: Application US/08442423
Patent No. 675392
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Janjic, Nebojsa
TITLE OF INVENTION: High-Affinity RNA ligands of Basic
TITLE OF INVENTION: Fibroblast Growth Factors
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/442,423
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-442-423-2

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 24 TAATACGACTCATTATGAGGAGCTC 48
Db 9 TAATACGACTCATTATGAGGAGCTC 33

RESULT 53
US-09-449-204-16
Sequence 16: Application US/09449204A
Patent No. 6927024
GENERAL INFORMATION:
APPLICANT: Simicop, Dominick V.
APPLICANT: Williams, P. Mickey
APPLICANT: Meng, Yu-Ju G.
APPLICANT: Dodge, Anthony H.
APPLICANT: Sims, Paul W.
APPLICANT: Wong, Wei Lee Tan
TITLE OF INVENTION: PCR ASSAY
FILE REFERENCE: P1543R1
CURRENT APPLICATION NUMBER: US/09/449,204A
CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: US 60/110,259
EARLIER FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 16
LENGTH: 48
TYPE: DNA
ORGANISM: artificial sequence
FEATURES:
OTHER INFORMATION: Sequence source: synthetic primer
Patent No. 6927024
US-09-449-204-16

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 24 TAATACGACTCATTATGAGGAGCTC 48
Db 9 TAATACGACTCATTATGAGGAGCTC 33

RESULT 54
US-10-037-986-37
Sequence 37, Application US/10037986
Patent No. 693316
GENERAL INFORMATION:
APPLICANT: Larry Gold
Craig Therk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-10-037-986-37
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-037-986-37
Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 24 TAATACGACTCATATAGGAGCTC 48
9 TAATACGACTCATATAGGAGCTC 33

RESULT 55
PCT-US95-05600-19
Sequence 19, Application PC/TUS9505600
GENERAL INFORMATION:
APPLICANT: GOLD, LARRY
APPLICANT: NIEWLANDT, DAN
APPLICANT: WECKER, MATTHEW
APPLICANT: SCHNEIDER, DANIEL J.

APPLICANT: FEIGON, JULI
APPLICANT: ALLEN, PATRICK
APPLICANT: SULENGER, BRUCE A.
APPLICANT: DOUDNA, JENNIFER, A.
TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/05600
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/238,863
FILING DATE: 06-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/248,632
FILING DATE: 24-MAY-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/303,362
FILING DATE: 09-SEPTEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/361,795
FILING DATE: 21-DECEMBER-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,991
FILING DATE: 08-SEPTEMBER-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/931,473
FILING DATE: 17-AUGUST-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX17/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05600-19
Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTACTATAGGAGCTC 48
|||||
Db 9 TAATAGACTACTATAGGAGCTC 33

RESULT 56
PCT-US95-05600-141
; Sequence 141, Application PC/TUS9505600
; GENERAL INFORMATION:
; APPLICANT: GOLD, LARRY
; APPLICANT: NIEMULANDT, DAN
; APPLICANT: WECKER, MATTHEW
; APPLICANT: SCHNEIDER, DANIEL J.
; APPLICANT: FEIGON, JULI
; APPLICANT: ALLEN, PATRICK
; APPLICANT: SULLINGER, BRUCE A.
; APPLICANT: DOUDNA, JENNIFER, A.
; TITLE OF INVENTION: HIGH-AFFINITY LIGANDS OF
; TITLE OF INVENTION: INSULIN RECEPTOR ANTIBODIES, TACHYKININ SUBSTANCE
; TITLE OF INVENTION: P, HIV INTEGRASE AND HIV-1 REVERSE TRANSCRIPTASE
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson & Bratschun, L.L.C.
; STREET: 8400 E. Prentice Avenue, Suite 200
; CITY: Englewood
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG
; MEDIUM TYPE: Storage
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05600
; FILING DATE:
; CLASSIFICATION:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/238,863
; FILING DATE: 06-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/248,632
; FILING DATE: 24-MAY-1994
; CLASSIFICATION:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/303,362
; FILING DATE: 09-SEPTEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/361,795
; FILING DATE: 21-DECEMBER-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/117,991
; FILING DATE: 08-SEPTEMBER-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/931,473
; FILING DATE: 17-AUGUST-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/964,624
; FILING DATE: 21-OCTOBER-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/714,131
; FILING DATE: 10-JUNE-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/536,428
; FILING DATE: 11-JUNE-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX17/PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US95-05600-141

Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATAGACTACTATAGGAGCTC 48
|||||
Db 9 TAATAGACTACTATAGGAGCTC 33

RESULT 57
PCT-US96-09537-208
; Sequence 208, Application PC/TUS9609537
; GENERAL INFORMATION:
; APPLICANT: NEXSTAR PHARMACEUTICALS, INC.
; APPLICANT: DIANE TASSET
; APPLICANT: NIKOS PAGRATIS
; APPLICANT: SUMEDHA JAYASENA
; APPLICANT: LARRY GOLD
; TITLE OF INVENTION: HIGH AFFINITY NUCLEIC ACID LIGANDS OF
; TITLE OF INVENTION: CYTOKINES
; NUMBER OF SEQUENCES: 258
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Swanson and Bratschun, L.L.C.
; STREET: 8400 East Prentice Avenue, Suite #200
; CITY: Denver
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: MS-DOS
; SOFTWARE: WordPerfect 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/09537
; FILING DATE:
; CLASSIFICATION:
; APPLICATION DATA:
; APPLICATION NUMBER: 08/477,829
; FILING DATE: 07-JUNE-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/481,710
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Barry J. Swanson
; REGISTRATION NUMBER: 33,215
; REFERENCE/DOCKET NUMBER: NEX14/PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 793-3333
; TELEFAX: (303) 793-3433
; INFORMATION FOR SEQ ID NO: 208:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
PCT-US96-09537-208

Query Match 0.6%; Score 25; DB 6; Length 48;

Best Local Similarity 100.0%; Pred. No. 4.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
|||||
DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 58

US-09-816-089A-7
; Sequence 7, Application US/09816089A
; Patent No. 6558906
; GENERAL INFORMATION:
; APPLICANT: OBOKATA, Junichi et al.
; TITLE OF INVENTION: Methods of Screening Potential
; TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
; FILE REFERENCE: 10235/9
; CURRENT APPLICATION NUMBER: US/09/816,089A
; PRIOR FILING DATE: 2001-03-26
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 59
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-816-089A-7

Query Match 0.6%; Score 25; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATAGACTCACTATAGGGA 44
|||||
DB 4 GGCCTAATAGACTCACTATAGGGA 28

RESULT 59

US-09-816-089A-3
; Sequence 3, Application US/09816089A
; Patent No. 6558906
; GENERAL INFORMATION:
; APPLICANT: OBOKATA, Junichi et al.
; TITLE OF INVENTION: Methods of Screening Potential
; TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
; FILE REFERENCE: 10235/9
; CURRENT APPLICATION NUMBER: US/09/816,089A
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: JP 2000-291084
; PRIOR FILING DATE: 2000-09-25
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 63
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; US-09-816-089A-3

Query Match 0.6%; Score 25; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 4.5;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATAGACTCACTATAGGGA 44
|||||
DB 9 GGCCTAATAGACTCACTATAGGGA 33

RESULT 60

5436330-1
; Patent No. 5436330
; APPLICANT: TAIRA, KAZUMARI;ODA, MASANO;SHINSHI, HIDEAKI;
; FURUKAWA, KENSUKE;MAEDA, HIDEKATSU
; TITLE OF INVENTION: HAMMERHEAD RIBOZYMES WITH ENHANCED
; STABILITY PROVIDED BY AN ADDITIONAL 3' HAIRPIN SEQUENCE
; NUMBER OF SEQUENCES: 5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/111,444
; FILING DATE: 24-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 499,787
; FILING DATE: 27-MAR-1990
; APPLICATION NUMBER:
; FILING DATE:
; SEQ ID NO:1
; LENGTH: 136
5436330-1

Query Match 0.6%; Score 25; DB 9; Length 136;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATACGACTCACTATAGGAGCTC 48
|||||
DB 11 TATACGACTCACTATAGGAGCTC 35

RESULT 61

US-08-652-369A-2
; Sequence 2, Application US/08652369A
; Patent No. 5861268
; GENERAL INFORMATION:
; APPLICANT: Dean G. Tang, Kenneth V. Honn
; TITLE OF INVENTION: Induction of Tumor
; TITLE OF INVENTION: Cell Apoptosis With Chemical Inhibitors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ian C. McLeod
; STREET: 2190 Commons Parkway
; CITY: Okemos
; STATE: Michigan
; COUNTRY: USA
; ZIP: 48864
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette 5.25 inch,
; MEDIUM TYPE: 360 kb storage
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: MS-DOS (version
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/652,369A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Ian C. McLeod
; REGISTRATION NUMBER: 20,931
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (517) 347-4100
; TELEFAX: (517) 347-4103
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 Bases
; TYPE: Nucleic Acid
; STRANDEDNESS: Single
; TOPOLOGY: Linear
; MOLECULE TYPE:

DESCRIPTION: DNA primer for
DESCRIPTION: a segment of 12-lipoxygenase.
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Human
IMMEDIATE SOURCE:
LIBRARY: Genomic
US-08-652-369A-2

Query Match 0.6%; Score 24; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 62
US-09-302-620B-109
Sequence 109, Application US/09302620B
Patent No. 6331420
GENERAL INFORMATION:
APPLICANT: Wilson, C. Ron
APPLICANT: Craft, David L.
APPLICANT: Eirich, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450
TITLE OF INVENTION: OXIDOREDUCTASE GENES AND PROTEINS RELATED TO THE OMEGA
TITLE OF INVENTION: HYDROXYLASE COMPLEX OF CANDIDA TROPICALIS AND METHODS
TITLE OF INVENTION: RELATING THERETO
FILE REFERENCE: 1010-16, seq
CURRENT APPLICATION NUMBER: US/09/302,620B
CURRENT FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 109
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-09-302-620B-109

Query Match 0.6%; Score 24; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 63
US-08-755-587-203
Sequence 203, Application US/08755587
Patent No. 6045997
GENERAL INFORMATION:
APPLICANT: Futreal, Phillip A
APPLICANT: Wooster, Richard F
APPLICANT: Ashworth, Alan
APPLICANT: Stratton, Michael R
TITLE OF INVENTION: Materials and methods relating to the BRCA2 cancer
TITLE OF INVENTION: Identification and sequencing of the BRCA2 cancer
NUMBER OF SEQUENCES: 222
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell Seltzer Park & Gibson

STREET: 310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
CITY: Raleigh
STATE: NC
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/755,587
FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9525555.0
FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9617961.9
FILING DATE: 28-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
REGISTRATION NUMBER: 31,665
REFERENCE/DOCKET NUMBER: 5405-135
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-755-587-203

Query Match 0.6%; Score 24; DB 3; Length 37;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 64
US-08-169-303-23
Sequence 23, Application US/08169303
Patent No. 5709998
GENERAL INFORMATION:
APPLICANT: KINZLER, KENNETH W.
APPLICANT: VOGELSTEIN, BERT
TITLE OF INVENTION: MOLECULAR DIAGNOSIS OF FAMILIAL
TITLE OF INVENTION: ADENOMATOUS POLYPOSIS
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: BANNER, BIRCH, MCKIE AND BECKETT
STREET: 1001 G STREET, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/169,303
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KAGAN, SARAH A.
REGISTRATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 1107.44447
TELECOMMUNICATION INFORMATION:

TELEPHONE: 202.508.9100
TELEFAX: 202.508.9299
TELEX: 197430 BMB UT
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: YES
US-08-169-303-23

Query Match 0.6%; Score 24; DB 2; Length 38;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 65
US-08-771-781-1
Sequence 1, Application US/08771781
Patent No. 6027886
GENERAL INFORMATION:
APPLICANT: LEYING, Hermann
APPLICANT: HINZPETER, Matthias
APPLICANT: WITTOR, Heiko
APPLICANT: FRITTON, Hans-Peter
TITLE OF INVENTION: METHOD FOR THE QUANTITATIVE
TITLE OF INVENTION: DETECTION OF SPECIFIC NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSER: Nikaido, Marmelstein, Murray & Oram LLP
STREET: 655 Fifteenth Street N.W. Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/771,781
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 195 48 680.3
FILING DATE: 23-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Murray, Robert B.
REGISTRATION NUMBER: 22,980
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)638-5000
TELEFAX: (202)638-4810
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 41 base pairs
TYPE: nucleotide
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: nucleic acid
US-08-771-781-1

Query Match 0.6%; Score 24; DB 3; Length 41;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 CCTAATACGACTCATTATAGGAG 45

DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 66
US-09-181-706-6
Sequence 6, Application US/09181706
Patent No. 6130068
GENERAL INFORMATION:
APPLICANT: Melanie K. Spriggs, Michael R. Comeau,
APPLICANT: Robert F. Dubose, Richard S. Johnson
TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: Janis C. Henry
STREET: 51 University St.
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/181,706
FILING DATE: October 28, 1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/958,598 (converted to a
APPLICATION NUMBER: Provisional, see below)
FILING DATE: October 28, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: --to be assigned-- (US 08/958,598
APPLICATION NUMBER: conversion to Provisional application)
FILING DATE: October 26, 1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2631-A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206)470-4189
TELEFAX: (206)233-0644
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: primer
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-181-706-6

Query Match 0.6%; Score 24; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 67
US-09-458-791-6
Sequence 6, Application US/09458791
Patent No. 6174689
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie


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1 TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
2 RECEPTOR DNA AND POLYPEPTIDES
3
4 NUMBER OF SEQUENCES: 10
5
6 CORRESPONDENCE ADDRESSES:
7 ADDRESSSEE: Janis C. Henry
8 STREET: 51 University St.
9 CITY: Seattle
10 STATE: WA
11 COUNTRY: US
12 ZIP: 98101
13
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: Floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: MS-DOS/Windows 95
18 SOFTWARE: Word for Windows 95, 7.0a
19
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/09/458,791
22 FILING DATE: 10-Dec-1999
23 CLASSIFICATION: <Unknown>
24
25 PRIOR APPLICATION DATA:
26 APPLICATION NUMBER: 08/958,598
27 FILING DATE: 28-OCT-1997
28 ATTORNEY/AGENT INFORMATION:
29 NAME: Henry, Janis C
30 REGISTRATION NUMBER: 34,347
31 REFERENCE/DOCKET NUMBER: 2631
32 TELECOMMUNICATION INFORMATION:
33 TELEPHONE: (206)470-4189
34 TELEFAX: (206)233-0644
35
36 INFORMATION FOR SEQ ID NO: 6:
37
38 SEQUENCE CHARACTERISTICS:
39 LENGTH: 43 base pairs
40 TYPE: nucleic acid
41 STRANDEDNESS: single
42 TOPOLOGY: linear
43 MOLECULE TYPE: primer
44 HYPOTHEICAL: NO
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46 ANTI-SENSE: NO
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48 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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50 US-09-458-791-6
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52 Query Match 0.6% Score 24; DB 3; Length 43;
53 Best Local Similarity 100.0%; Pred. No. 12;
54 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
55
56 QY 22 CCTATACGACTCACTATAGGAG 45
57 |||||
58 Db 5 CCTATACGACTCACTATAGGAG 28
59
60
61 RESULT 68
62 US-09-459-066-6
63 Sequence 6, Application US/09459066
64 Patent No. 6187909
65
66 GENERAL INFORMATION:
67 APPLICANT: Spr1999, Melanie
68 TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
69 TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
70 NUMBER OF SEQUENCES: 10
71
72 CORRESPONDENCE ADDRESSES:
73 ADDRESSSEE: Janis C. Henry
74 STREET: 51 University St.
75 CITY: Seattle
76 STATE: WA
77 COUNTRY: US
78 ZIP: 98101
79
80 COMPUTER READABLE FORM:
81 MEDIUM TYPE: Floppy disk
82 COMPUTER: IBM PC compatible
83 OPERATING SYSTEM: MS-DOS/Windows 95
84 SOFTWARE: Word for Windows 95, 7.0a
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86 CURRENT APPLICATION DATA:
87 APPLICATION NUMBER: US/09/459,066
88 FILING DATE: 10-Dec-1999
89 CLASSIFICATION: <Unknown>
90
91 PRIOR APPLICATION DATA:
92 APPLICATION NUMBER: 08/958,598
93 FILING DATE: 28-OCT-1997
94 ATTORNEY/AGENT INFORMATION:
95 NAME: Henry, Janis C
96 REGISTRATION NUMBER: 34,347
97 REFERENCE/DOCKET NUMBER: 2631
98 TELECOMMUNICATION INFORMATION:
99 TELEPHONE: (206)470-4189
100 TELEFAX: (206)233-0644
101
102 INFORMATION FOR SEQ ID NO: 6:
103
104 SEQUENCE CHARACTERISTICS:
105 LENGTH: 43 base pairs
106 TYPE: nucleic acid
107 STRANDEDNESS: single
108 TOPOLOGY: linear
109 MOLECULE TYPE: primer
110 HYPOTHEICAL: NO
111
112 ANTI-SENSE: NO
113
114 SEQUENCE DESCRIPTION: SEQ ID NO: 6:
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116 US-09-459-066-6

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1  CLASSIFICATION:
2  PRIOR APPLICATION DATA:
3  APPLICATION NUMBER: 08/958,598
4  FILING DATE:
5  ATTORNEY/AGENT INFORMATION:
6  NAME: Henry, Janis C
7  REGISTRATION NUMBER: 34,347
8  REFERENCE/DOCKET NUMBER: 2631
9  TELECOMMUNICATION INFORMATION:
10 TELEPHONE: (206)470-4189
11 TELEFAX: (206)233-0644
12 INFORMATION FOR SEQ ID NO: 6:
13 SEQUENCE CHARACTERISTICS:
14 LENGTH: 43 base pairs
15 TYPE: nucleic acid
16 STRANDEDNESS: single
17 MOLECULAR TYPE: primer
18 HYPOTHETICAL: NO
19 ANTI-SENSE: NO
20 US-09-459-066-6
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22 Query Match 0.6%; Score 24; DB 3; Length 43;
23 Best Local Similarity 100.0%; Pred. No. 12;
24 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
25
26 QY 22 CCTAATACGACTCACTATAGCGAG 45
27 |||||||
28 Db 5 CCTAATACGACTCACTATAGCGAG 28
29
30 RESULT 69
31 US-09-459-065-6
32 Sequence 6, Application US/09459065
33 Patent No. 6562949
34
35 GENERAL INFORMATION:
36 APPLICANT: Spriggs, Melanie
37 TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
38 TITLE OF INVENTION: RECEPTOR DNA AND POLYPEPTIDES
39 NUMBER OF SEQUENCES: 10
40 CORRESPONDENCE ADDRESS:
41 ADDRESSER: Janis C. Henry
42 STREET: 51 University St.
43 CITY: Seattle
44 STATE: WA
45 COUNTRY: US
46 ZIP: 98101
47
48 COMPUTER READABLE FORM:
49 MEDIUM TYPE: floppy disk
50 COMPUTER: IBM PC compatible
51 OPERATING SYSTEM: MS-DOS/Windows 95
52 SOFTWARE: Word for Windows 95, 7.0a
53 CURRENT APPLICATION DATA:
54 APPLICATION NUMBER: US/09/459,065
55 FILING DATE:
56 CLASSIFICATION:
57 PRIOR APPLICATION DATA:
58 APPLICATION NUMBER: 08/958,598
59
60 FILING DATE:
61 ATTORNEY/AGENT INFORMATION:
62 NAME: Henry, Janis C
63 REGISTRATION NUMBER: 34,347
64 REFERENCE/DOCKET NUMBER: 2631
65 TELECOMMUNICATION INFORMATION:
66 TELEPHONE: (206)470-4189
67 TELEFAX: (206)233-0644
68 INFORMATION FOR SEQ ID NO: 6:
69 SEQUENCE CHARACTERISTICS:
70 LENGTH: 43 base pairs
71 TYPE: nucleic acid
72 STRANDEDNESS: single
73 TOPOLOGY: linear
74

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/ MOLECULE TYPE: primer
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
US-09-459-065-6

Query Match 0.6%; Score 24; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 70
US-08-623-428D-40
Sequence 40, Application US/08623428D
Patent No. 6312890
GENERAL INFORMATION:
APPLICANT: W. MARSTON LINEHAN, MICHAEL
LEHMAN, FARIDA LATIF AND BERTON
ZBAR

TITLE OF INVENTION: PARTIAL INTRON SEQUENCE
OF VHL DISEASE GENE AND ITS USE IN DIAGNOSIS
OF DISEASE CARRIERS

NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
STREET: 345 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10154

COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MICROSOFT WORD 97
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/623,428D
FILING DATE: 05-Sep-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/623,428
FILING DATE: MARCH 28, 1996
APPLICATION NUMBER: 08/061,889
FILING DATE: MAY 14, 1993

ATTORNEY/AGENT INFORMATION:
NAME: Kachlya M. Brown
REGISTRATION NUMBER: 34,556
REFERENCE/DOCKET NUMBER: 2026-4078US3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 758-4800
TELEFAX: (212) 751-6849
TELEX: 421792

INFORMATION FOR SEQ ID NO: 40:
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 40:

US-08-623-428D-40

Query Match 0.6%; Score 24; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 71
US-09-689-012-6
Sequence 6, Application US/09689012
Patent No. 6670135
GENERAL INFORMATION:
APPLICANT: Spriggs, Melanie K.
TITLE OF INVENTION: NOVEL SEMAPHORIN POLYPEPTIDES
FILE REFERENCE: 2634-US
CURRENT APPLICATION NUMBER: US/09/689,012
CURRENT FILING DATE: 2000-10-12
PRIOR APPLICATION NUMBER: PCT/US99/09831
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: US 60/085,497
PRIOR FILING DATE: 1998-05-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 44
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PRIMER
US-09-689-012-6

Query Match 0.6%; Score 24; DB 3; Length 44;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 6 CCTAATACGACTCATTATAGGAG 29

RESULT 72
US-08-270-314-6
Sequence 6, Application US/08270314
Patent No. 5683888
GENERAL INFORMATION:
APPLICANT: CAMPBELL, Anthony K.
TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND
THEIR USE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: VA
COUNTRY: US
ZIP: 22202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/270,314
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 89 16806.6
FILING DATE: 22-JUL-1989
APPLICATION NUMBER: PCT/GB90/01131
FILING DATE: 23-JUL-1990
APPLICATION NUMBER: US 07/820,867
FILING DATE: 22-JAN-1992
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-270-314-6

Query Match      0.6%; Score 24; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATAGCACTCACTAATAGGAG 45
Db      3 CCTAATAGCACTCACTAATAGGAG 26

RESULT 73
US-08-270-314-9
; Sequence 9, Application US/08270314
; Patent No. 568388
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, Anthony K.
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND
; TITLE OF INVENTION: THEIR USE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: YOUNG & THOMPSON
; STREET: 745 South 23rd Street
; CITY: Arlington
; STATE: VA
; COUNTRY: US
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/270,314
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 89 16806.6
; FILING DATE: 22-JUL-1989
; APPLICATION NUMBER: PCT/GB90/01131
; FILING DATE: 23-JUL-1990
; APPLICATION NUMBER: US 07/820,867
; FILING DATE: 22-JAN-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PATCH, Andrew J.
; REGISTRATION NUMBER: 32,925
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 521-2297
; TELEFAX: (703) 585-0573
; TELEX: 248425 EMBON
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-270-314-9

Query Match      0.6%; Score 24; DB 2; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATAGCACTCACTAATAGGAG 45
Db      3 CCTAATAGCACTCACTAATAGGAG 26
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RESULT 74
US-09-225-302-6
; Sequence 6, Application US/09225302
; Patent No. 644065
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, ANTHONY KEITH
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
; FILE REFERENCE: 09/225,302
; CURRENT APPLICATION NUMBER: US/09/225,302
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 08/957,135
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 6
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-225-302-6

Query Match      0.6%; Score 24; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATAGCACTCACTAATAGGAG 45
Db      3 CCTAATAGCACTCACTAATAGGAG 26

RESULT 75
US-09-225-302-9
; Sequence 9, Application US/09225302
; Patent No. 644065
; GENERAL INFORMATION:
; APPLICANT: CAMPBELL, ANTHONY KEITH
; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
; FILE REFERENCE: 09/225,302
; CURRENT APPLICATION NUMBER: US/09/225,302
; CURRENT FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 08/957,135
; PRIOR FILING DATE: 1998-09-14
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 9
; LENGTH: 45
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-225-302-9

Query Match      0.6%; Score 24; DB 3; Length 45;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATAGCACTCACTAATAGGAG 45
Db      3 CCTAATAGCACTCACTAATAGGAG 26
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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

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Title: US-10-623-477-3

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Post-processing: Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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2	26	0.6	625	6 US-09-925-065A-275529	Sequence 275529,
3	26	0.6	625	6 US-09-925-065A-275530	Sequence 275530,
4	24	0.6	52	12 US-11-183-294-1	Sequence 1, Appl1
5	24	0.6	53	12 US-11-183-294-3	Sequence 3, Appl
6	24	0.6	94	7 US-10-903-612B-138	Sequence 138, App
7	24	0.6	99	7 US-10-903-612B-146	Sequence 146, App
8	24	0.6	114	7 US-10-903-612B-141	Sequence 141, App
9	24	0.6	115	7 US-10-903-612B-144	Sequence 144, App
10	24	0.6	582	6 US-09-925-065A-269639	Sequence 269639,
11	24	0.6	585	6 US-09-925-065A-330079	Sequence 330079,
12	24	0.6	585	6 US-09-925-065A-330080	Sequence 330080,
13	23	0.5	28	12 US-11-169-809-11	Sequence 11, Appl
14	23	0.5	31	8 US-10-500-831-385	Sequence 385, App
15	23	0.5	46	12 US-11-148-593-2	Sequence 2, Appl1
16	23	0.5	47	8 US-10-773-440A-1	Sequence 1, Appl1
17	23	0.5	47	12 US-11-176-795-81	Sequence 81, App
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26	23	0.5	49	8 US-10-500-831-233	Sequence 233, App
27	23	0.5	49	12 US-11-176-795-72	Sequence 72, Appl
28	23	0.5	49	12 US-11-176-795-76	Sequence 76, Appl
29	23	0.5	50	7 US-10-991-803-20	Sequence 20, Appl
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37	23	0.5	50	12 US-11-176-795-51	Sequence 51, Appl
38	23	0.5	51	8 US-10-500-831-137	Sequence 137, App
39	23	0.5	51	8 US-10-500-831-163	Sequence 163, App
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46	23	0.5	51	8 US-10-500-831-215	Sequence 215, App
47	23	0.5	51	8 US-10-500-831-217	Sequence 217, App
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50	23	0.5	51	8 US-10-500-831-264	Sequence 264, App
51	23	0.5	51	8 US-10-500-831-269	Sequence 269, App
52	23	0.5	51	8 US-10-500-831-271	Sequence 271, App
53	23	0.5	51	8 US-10-500-831-285	Sequence 285, App
54	23	0.5	52	8 US-10-500-831-195	Sequence 195, App
55	23	0.5	52	8 US-10-500-831-248	Sequence 248, App
56	23	0.5	52	12 US-11-176-795-59	Sequence 59, Appl
57	23	0.5	53	8 US-10-500-831-135	Sequence 135, App
58	23	0.5	53	8 US-10-500-831-160	Sequence 160, App
59	23	0.5	53	8 US-10-500-831-181	Sequence 181, App
60	23	0.5	53	8 US-10-500-831-224	Sequence 224, App
61	23	0.5	53	8 US-10-500-831-254	Sequence 254, App
62	23	0.5	53	8 US-10-500-831-262	Sequence 262, App
63	23	0.5	53	8 US-10-500-831-277	Sequence 277, App
64	23	0.5	53	8 US-10-500-831-279	Sequence 279, App
65	23	0.5	53	12 US-11-176-795-55	Sequence 55, Appl
66	23	0.5	53	12 US-11-176-795-79	Sequence 79, Appl
67	23	0.5	54	8 US-10-500-831-235	Sequence 235, App
68	23	0.5	54	12 US-11-195-109-32	Sequence 32, Appl
69	23	0.5	55	8 US-10-500-831-166	Sequence 166, App
70	23	0.5	55	8 US-10-500-831-256	Sequence 256, App
71	23	0.5	55	8 US-10-500-831-260	Sequence 260, App
72	23	0.5	55	8 US-10-500-831-275	Sequence 275, App
73	23	0.5	56	8 US-10-500-831-157	Sequence 157, App
74	23	0.5	56	12 US-11-176-795-63	Sequence 63, Appl
75	23	0.5	57	8 US-10-500-831-187	Sequence 187, App
76	23	0.5	60	10 US-11-174-042-1	Sequence 1, Appl1
77	23	0.5	60	12 US-11-119-869-11	Sequence 11, Appl1
78	23	0.5	99	8 US-10-989-723-5	Sequence 5, Appl1
79	23	0.5	101	8 US-10-989-723-8	Sequence 8, Appl1
80	23	0.5	104	8 US-10-989-723-2	Sequence 2, Appl1
81	23	0.5	122	8 US-10-989-723-1	Sequence 1, Appl1
82	23	0.5	525	6 US-09-925-065A-18438	Sequence 18438, A
83	23	0.5	588	6 US-09-925-065A-892537	Sequence 892537,
84	23	0.5	594	6 US-09-925-065A-354079	Sequence 354079,
85	23	0.5	597	6 US-09-925-065A-620716	Sequence 620716,
86	23	0.5	597	6 US-09-925-065A-895007	Sequence 895007,
87	23	0.5	599	6 US-09-925-065A-894173	Sequence 894173,
88	23	0.5	614	6 US-09-925-065A-836169	Sequence 836169,
89	23	0.5	614	6 US-09-925-065A-836170	Sequence 836170,
90	23	0.5	650	6 US-09-925-065A-875759	Sequence 875759,
91	23	0.5	2219	12 US-11-151-601-24	Sequence 24, Appl
92	23	0.5	2838	12 US-11-151-601-14	Sequence 14, Appl
93	23	0.5	6860	8 US-10-949-720-406	Sequence 406, App

94 23 0.5 6921 8 US-10-949-720-420 Sequence 420, App
95 23 0.5 7164 8 US-10-949-720-411 Sequence 411, App
96 23 0.5 7387 12 US-11-154-421-28 Sequence 28, App
97 23 0.5 7429 8 US-10-949-720-413 Sequence 413, App
98 23 0.5 48000 12 US-11-159-597-20 Sequence 20, App
99 22 0.5 23 12 US-11-128-440-53 Sequence 53, App
100 22 0.5 26 12 US-11-089-805-1 Sequence 1, App

ALIGNMENTS

RESULT 1

US-10-755-092-26/c
Sequence 26, Application US/10755092
Publication No. US20060021095A1
GENERAL INFORMATION:
APPLICANT: Kozziel, Michael G.
Desai, Nalini M.
Lewis, Kelly S.
Kramer, Vance C.
Warren, Gregory W.
Evola, Stephen V.
Crossland, Lyle D.
Wright, Martha S.
Merlin, Ellis J.
Lauris, Karen L.
TITLE OF INVENTION: SYNTHETIC DNA SEQUENCE HAVING ENHANCED
INSECTICIDAL ACTIVITY IN MAIZE
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Syngenta Biotechnology, Inc.
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: NC
COUNTRY: USA
ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/755,092
FILING DATE: 08-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/988,462
FILING DATE: 20-Nov-2001
APPLICATION NUMBER: US 09/547,422
FILING DATE: 11-Apr-2000
APPLICATION NUMBER: US 08/459,504
FILING DATE: 02-Jun-1995
APPLICATION NUMBER: US 07/951,715
FILING DATE: 25-Sep-1992
APPLICATION NUMBER: US 07/772,027
FILING DATE: 04-Oct-1991
ATTORNEY/AGENT INFORMATION:
NAME: Weigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: S-188051
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8587
TELEFAX: (919)541-8689
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 4162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
FEATURE:

NAME/KEY: misc feature
LOCATION: 1418..1427
OTHER INFORMATION: /note= "start of mRNA"
FEATURE:
NAME/KEY: exon
LOCATION: 1481..2366
FEATURE:
NAME/KEY: intron
LOCATION: 2367..2451
FEATURE:
NAME/KEY: exon
LOCATION: 2452..2602
FEATURE:
NAME/KEY: intron
LOCATION: 2603..2690
FEATURE:
NAME/KEY: exon
LOCATION: 2691..2804
FEATURE:
NAME/KEY: intron
LOCATION: 2805..2906
FEATURE:
NAME/KEY: exon
LOCATION: 2907..3075
FEATURE:
NAME/KEY: intron
LOCATION: 3076..3177
FEATURE:
NAME/KEY: exon
LOCATION: 3178..3304
FEATURE:
NAME/KEY: intron
LOCATION: 3305..3398
FEATURE:
NAME/KEY: exon
LOCATION: 3399..3498
FEATURE:
NAME/KEY: intron
LOCATION: 3499..3713
FEATURE:
NAME/KEY: exon
LOCATION: 3714..3811
SEQUENCE DESCRIPTION: SEQ ID NO: 26:
US-10-755-092-26
Query Match 0.8%; Score 32; DB 7; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 19 TGGCCTAATGACGCTCACTATAGGAGGCTCGA 50
Db 4162 TGGCCTAATGACGCTCACTATAGGAGGCTCGA 4131
RESULT 2
US-09-925-065A-275529
Sequence 275529, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16

```

; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275529
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-275529

Query Match      0.6%; Score 26; DB 6; Length 625;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3910 AAAAAATAAAAATAAATAAAGTAA 3935
Db      161 AAAAAATAAAAATAAATAAAGTAA 186

RESULT 3
US-09-925-065A-275530
; Sequence 275530, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 10837.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275530
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-275530

Query Match      0.6%; Score 26; DB 6; Length 625;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3910 AAAAAATAAAAATAAATAAAGTAA 3935
Db      161 AAAAAATAAAAATAAATAAAGTAA 186

RESULT 4
US-11-183-294-1
; Sequence 1, Application US/11183294
; Publication No. US20060019383A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Grasso, Luigi
; APPLICANT: Saes, Philip M.
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0475
; CURRENT APPLICATION NUMBER: US/11/183,294
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 09/760,285
; PRIOR FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 1
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; US-11-183-294-1

Query Match      0.6%; Score 24; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28

RESULT 5
US-11-183-294-3
; Sequence 3, Application US/11183294
; Publication No. US20060019383A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C.
; APPLICANT: Grasso, Luigi
; APPLICANT: Saes, Philip M.
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0475
; CURRENT APPLICATION NUMBER: US/11/183,294
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 09/760,285
; PRIOR FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 3
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Oligonucleotide Primer
; US-11-183-294-3

Query Match      0.6%; Score 24; DB 12; Length 53;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATCGACTCACTATAGGAG 45
Db      5 CCTAATCGACTCACTATAGGAG 28

RESULT 6
US-10-903-612B-138
; Sequence 138, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gilte, Sadanand
; APPLICANT: Berge, Vladislav B.
; APPLICANT: Rothschild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 138
; LENGTH: 94
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-10-903-612B-138
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Query Match 0.6%; Score 24; DB 7; Length 94;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 7
US-10-903-612B-146
; Sequence 146, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gite, Sadanand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rotshchild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 146
; LENGTH: 99
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-146

US-10-903-612B-141
; Sequence 141, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gite, Sadanand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rotshchild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-141

Query Match 0.6%; Score 24; DB 7; Length 99;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 8
US-10-903-612B-141
; Sequence 141, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gite, Sadanand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rotshchild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 141
; LENGTH: 114
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-141

Query Match 0.6%; Score 24; DB 7; Length 114;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 9
US-10-903-612B-144
; Sequence 144, Application US/10903612B
; Publication No. US20060024781A1
; GENERAL INFORMATION:
; APPLICANT: Garvin, Alex M.
; APPLICANT: Gite, Sadanand
; APPLICANT: Bergo, Vladislav B.
; APPLICANT: Rotshchild, Kenneth J.
; TITLE OF INVENTION: Detection of Truncation Mutations by Mass Spectrometry
; FILE REFERENCE: AMBER-08599
; CURRENT APPLICATION NUMBER: US/10/903,612B
; CURRENT FILING DATE: 2004-07-30
; NUMBER OF SEQ ID NOS: 167
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 144
; LENGTH: 115
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-903-612B-144

Query Match 0.6%; Score 24; DB 7; Length 115;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 5 CCTAATACGACTCCTATAGGAG 28

RESULT 10
US-09-925-065A-269639/C
; Sequence 269639, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 269639
; LENGTH: 582
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-269639

Query Match 0.6%; Score 24; DB 6; Length 582;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAATPAAAAATPAAAAAGTA 3933
DB 425 AAAAATPAAAAATPAAAAAGTA 402

RESULT 11
US-09-925-065A-330079/C
; Sequence 330079, Application US/09925065A


```
Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330079
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-330079

Query Match      0.6%; Score 24; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      2019 AATTTCTAGTAATACACATTTT 2042
Db      426 AATTTCTAGTAATACACATTTT 403

RESULT 12
US-09-925-065A-330080/C
; Sequence 330080, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 330080
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-330080
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```
Query Match      0.6%; Score 24; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2019 AATTTCTAGTAATACACATTTT 2042
Db      426 AATTTCTAGTAATACACATTTT 403
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```
RESULT 13
US-11-169-809-11
; Sequence 11, Application US/11169809
; Publication No. US20060014141A1
; GENERAL INFORMATION:
; APPLICANT: Ohnaka, Satoru
; TITLE OF INVENTION: METHOD OF DETECTING AND QUANTIFYING CYTOMEGALOVIRUS
; FILE REFERENCE: 274564US0
; CURRENT FILING DATE: 2005-06-30
; PRIOR APPLICATION NUMBER: JP2004-194367
; PRIOR FILING DATE: 2004-06-30
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: Synthetic DNA
US-11-169-809-11

Query Match      0.5%; Score 23; DB 12; Length 28;
Best Local Similarity 100.0%; Pred. No. 1,9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      23 CTAATACGACTCCTACTATGAGGAG 45
Db      5 CTAATACGACTCCTACTATGAGGAG 27
```

```
RESULT 14
US-10-500-831-385
; Sequence 385, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 385
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial
; OTHER INFORMATION: T7 promoter sequence
US-10-500-831-385
```

```
Query Match      0.5%; Score 23; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 1,9e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      23 CTAATACGACTCCTACTATGAGGAG 45
Db      5 CTAATACGACTCCTACTATGAGGAG 27
```

```
RESULT 15
US-11-148-593-2
; Sequence 2, Application US/11148593
; Publication No. US20060014182A1
; GENERAL INFORMATION:
; APPLICANT: Kurih, Norich
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; AMPLIFICATION OF RNA SEQUENCES
```

```
; FILE REFERENCE: 492692000701
; CURRENT APPLICATION NUMBER: US/11/148,593
; CURRENT FILING DATE: 2005-06-08
; PRIOR APPLICATION NUMBER: 10/096,221
; PRIOR FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: 60/274,236
; PRIOR FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 46
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 46
; OTHER INFORMATION: 3' thymine is biotinylated
US-11-148-593-2
```

```
Query Match          0.5%; Score 23; DB 12; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       7  CTAATACGACTCACTATAGGAG 29
```

```
RESULT 16
US-10-773-440A-1
; Sequence 1, Application US/10773440A
; Publication No. US20050282170A1
; GENERAL INFORMATION:
; APPLICANT: Fradet, Yves
; APPLICANT: Chypre, Camille
; APPLICANT: Piche, Lyvon
; APPLICANT: Garon, Genevieve
; TITLE OF INVENTION: Method to Detect Prostate Cancer in a Sample
; FILE REFERENCE: 1619.0180001
; CURRENT APPLICATION NUMBER: US/10/773,440A
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 60/445,436
; PRIOR FILING DATE: 2003-02-07
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-773-440A-1
```

```
Query Match          0.5%; Score 23; DB 8; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       5  CTAATACGACTCACTATAGGAG 27
```

```
RESULT 17
US-11-176-795-81
; Sequence 81, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Mammaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
```

```
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 47
; TYPE: DNA
; ORGANISM: Listeria monocytogenes
US-11-176-795-81
```

```
Query Match          0.5%; Score 23; DB 12; Length 47;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       5  CTAATACGACTCACTATAGGAG 27
```

```
RESULT 18
US-10-500-831-138
; Sequence 138, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 138
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-138
```

```
Query Match          0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23  CTAATACGACTCACTATAGGAG 45
Db       5  CTAATACGACTCACTATAGGAG 27
```

```
RESULT 19
US-10-500-831-139
; Sequence 139, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 139
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-139
```

```
Query Match          0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23 CTAATAGCACTCACTATAGGAG 45
|||||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 20
US-10-500-831-140
; Sequence 140, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 140
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-140

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 175
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 18
US-10-500-831-175

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23 CTAATAGCACTCACTATAGGAG 45
|||||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 21
US-10-500-831-141
; Sequence 141, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 141
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-141

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 221
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Human papillomavirus type 52
US-10-500-831-221

Query Match      0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23 CTAATAGCACTCACTATAGGAG 45
|||||
Db      5 CTAATAGCACTCACTATAGGAG 27

RESULT 22
US-10-500-831-175
; Sequence 175, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
```

```
RESULT 24
US-10-500-831-227
; Sequence 227, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
```

SEQ ID NO 227
LENGTH: 49
TYPE: DNA
ORGANISM: Human papillomavirus type 58
US-10-500-831-227

Query Match 0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45
DB 5 CTAATAGCACTCACTATAGGAG 27

RESULT 25
US-10-500-831-229
Sequence 229, Application US/10500831
Publication No. US2005024481A1
GENERAL INFORMATION:

APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

FILE REFERENCE: B0192.700520S00

CURRENT APPLICATION NUMBER: US/10/500,831

CURRENT FILING DATE: 2004-07-07

PRIOR APPLICATION NUMBER: GB 0200258.2

PRIOR FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: GB 0214124.0

PRIOR FILING DATE: 2002-06-19

NUMBER OF SEQ ID NOS: 387

SOFTWARE: Patentin version 3.2

SEQ ID NO 229

LENGTH: 49

TYPE: DNA

ORGANISM: Human papillomavirus type 58

US-10-500-831-229

Query Match 0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45
DB 5 CTAATAGCACTCACTATAGGAG 27

RESULT 26
US-10-500-831-233
Sequence 233, Application US/10500831
Publication No. US2005024481A1
GENERAL INFORMATION:

APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

FILE REFERENCE: B0192.700520S00

CURRENT APPLICATION NUMBER: US/10/500,831

CURRENT FILING DATE: 2004-07-07

PRIOR APPLICATION NUMBER: GB 0200258.2

PRIOR FILING DATE: 2002-01-07

PRIOR APPLICATION NUMBER: GB 0214124.0

PRIOR FILING DATE: 2002-06-19

NUMBER OF SEQ ID NOS: 387

SOFTWARE: Patentin version 3.2

SEQ ID NO 233

LENGTH: 49

TYPE: DNA

ORGANISM: Human papillomavirus

US-10-500-831-233

Query Match 0.5%; Score 23; DB 8; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45

DB 5 CTAATAGCACTCACTATAGGAG 27

RESULT 27
US-11-176-795-72
Sequence 72, Application US/11176795
Publication No. US2005025517A1
GENERAL INFORMATION:

APPLICANT: Gerdes, John C

APPLICANT: Marmaro, Jeffrey M

TITLE OF INVENTION: Method and Device for Multiplex Amplification System

FILE REFERENCE: 1

CURRENT APPLICATION NUMBER: US/11/176,795

CURRENT FILING DATE: 2005-07-07

NUMBER OF SEQ ID NOS: 84

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 72

LENGTH: 49

TYPE: DNA

ORGANISM: Escherichia coli

US-11-176-795-72

Query Match 0.5%; Score 23; DB 12; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45
DB 4 CTAATAGCACTCACTATAGGAG 26

RESULT 28
US-11-176-795-76
Sequence 76, Application US/11176795
Publication No. US2005025517A1
GENERAL INFORMATION:

APPLICANT: Gerdes, John C

APPLICANT: Marmaro, Jeffrey M

TITLE OF INVENTION: Method and Device for Multiplex Amplification System

FILE REFERENCE: 1

CURRENT APPLICATION NUMBER: US/11/176,795

CURRENT FILING DATE: 2005-07-07

NUMBER OF SEQ ID NOS: 84

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 76

LENGTH: 49

TYPE: DNA

ORGANISM: Escherichia coli

US-11-176-795-76

Query Match 0.5%; Score 23; DB 12; Length 49;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGCACTCACTATAGGAG 45
DB 4 CTAATAGCACTCACTATAGGAG 26

RESULT 29
US-10-991-803-20
Sequence 20, Application US/10991803
Publication No. US20060008817A1
GENERAL INFORMATION:

APPLICANT: INVITROGEN CORPORATION

APPLICANT: CARRINO, John

APPLICANT: FAN, James

APPLICANT: BENNETT, Robert P.

APPLICANT: CHESNOT, Jonathan D.

APPLICANT: GLEESON, Martin A.

APPLICANT: MADDERN, Knut R.

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING RECOMBINANT NUCLEIC ACID

```

/ TITLE OF INVENTION: MOLECULES
/ FILE REFERENCE: INVIT1290-4
/ CURRENT APPLICATION NUMBER: US/10/991,803
/ CURRENT FILING DATE: 2004-11-17
/ PRIOR APPLICATION NUMBER: US 60/520,946
/ PRIOR FILING DATE: 2003-11-17
/ PRIOR APPLICATION NUMBER: US 10/014,128
/ PRIOR FILING DATE: 2001-12-07
/ PRIOR APPLICATION NUMBER: US 60/326,092
/ PRIOR FILING DATE: 2001-09-28
/ PRIOR APPLICATION NUMBER: US 60/254,510
/ PRIOR FILING DATE: 2000-12-08
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 20
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PRIMER T7top
US-10-991-803-20
```

```
Query Match          0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      24 TAATAGCACTCACTATAGGAGC 46
      |||||||
Db       8 TAATAGCACTCACTATAGGAGC 30
```

```

RESULT 30
US-10-991-803-21/c
/ Sequence 21, Application US/10991803
/ Publication No. US2006008817A1
/ GENERAL INFORMATION:
/ APPLICANT: INVITROGEN CORPORATION
/ APPLICANT: CARRINO, John
/ APPLICANT: FAN, James
/ APPLICANT: BENNETT, Robert P.
/ APPLICANT: CHESNUT, Jonathan D.
/ APPLICANT: GLEESON, Martin A.
/ APPLICANT: MADDEN, Knut R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR GENERATING RECOMBINANT NUCLEIC ACID
/ FILE REFERENCE: INVIT1290-4
/ CURRENT APPLICATION NUMBER: US/10/991,803
/ CURRENT FILING DATE: 2004-11-17
/ PRIOR APPLICATION NUMBER: US 60/520,946
/ PRIOR FILING DATE: 2003-11-17
/ PRIOR APPLICATION NUMBER: US 10/014,128
/ PRIOR FILING DATE: 2001-12-07
/ PRIOR APPLICATION NUMBER: US 60/326,092
/ PRIOR FILING DATE: 2001-09-28
/ PRIOR APPLICATION NUMBER: US 60/254,510
/ PRIOR FILING DATE: 2000-12-08
/ NUMBER OF SEQ ID NOS: 62
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 21
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: PRIMER T7bottom
US-10-991-803-21
```

```
Query Match          0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      24 TAATAGCACTCACTATAGGAGC 46
      |||||||
Db       43 TAATAGCACTCACTATAGGAGC 21
```

```

RESULT 31
US-10-014-128-20
/ Sequence 20, Application US/10014128
/ Publication No. US20060029935A1
/ GENERAL INFORMATION:
/ APPLICANT: INVITROGEN CORPORATION
/ APPLICANT: CARRINO, John
/ APPLICANT: FAN, James
/ APPLICANT: BENNETT, Robert
/ APPLICANT: CHESNUT, Jonathan
/ APPLICANT: GLEESON, Martin
/ APPLICANT: MADDEN, Knut
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR RAPIDLY GENERATING
/ FILE REFERENCE: INVIT1290-2
/ CURRENT APPLICATION NUMBER: US/10/014,128
/ CURRENT FILING DATE: 2001-12-07
/ PRIOR APPLICATION NUMBER: US 60/254,510
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: US 60/326,092
/ PRIOR FILING DATE: 2001-09-28
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 20
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: ARTIFICIAL SEQUENCE
/ FEATURE:
/ OTHER INFORMATION: PRIMER T7top
US-10-014-128-20
```

```
Query Match          0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      24 TAATAGCACTCACTATAGGAGC 46
      |||||||
Db       8 TAATAGCACTCACTATAGGAGC 30
```

```

RESULT 32
US-10-014-128-21/c
/ Sequence 21, Application US/10014128
/ Publication No. US20060029935A1
/ GENERAL INFORMATION:
/ APPLICANT: INVITROGEN CORPORATION
/ APPLICANT: CARRINO, John
/ APPLICANT: FAN, James
/ APPLICANT: BENNETT, Robert
/ APPLICANT: CHESNUT, Jonathan
/ APPLICANT: GLEESON, Martin
/ APPLICANT: MADDEN, Knut
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR RAPIDLY GENERATING
/ FILE REFERENCE: INVIT1290-2
/ CURRENT APPLICATION NUMBER: US/10/014,128
/ CURRENT FILING DATE: 2001-12-07
/ PRIOR APPLICATION NUMBER: US 60/254,510
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: US 60/326,092
/ PRIOR FILING DATE: 2001-09-28
/ NUMBER OF SEQ ID NOS: 47
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 21
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: ARTIFICIAL SEQUENCE
/ FEATURE:
/ OTHER INFORMATION: PRIMER T7bottom
US-10-014-128-21
```

```
Query Match      0.5%; Score 23; DB 7; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCACTATAGGAGC 46
Db 43 TAATACGACTCACTATAGGAGC 21

RESULT 33
US-10-500-831-197
; Sequence 197, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.700520S00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 197
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human papillomavirus type 33
US-10-500-831-197

Query Match      0.5%; Score 23; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAG 45
Db 5 CTAATACGACTCACTATAGGAG 27

RESULT 34
US-10-500-831-239
; Sequence 239, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.700520S00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 239
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-500-831-239

Query Match      0.5%; Score 23; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAG 45
Db 5 CTAATACGACTCACTATAGGAG 27

RESULT 35
US-10-500-831-245

; Sequence 245, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.700520S00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 245
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Human papillomavirus type 39
US-10-500-831-245

Query Match      0.5%; Score 23; DB 8; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAG 45
Db 5 CTAATACGACTCACTATAGGAG 27

RESULT 36
US-11-176-795-47
; Sequence 47, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 47
; LENGTH: 50
; TYPE: DNA
; ORGANISM: Chlamydia trachomatis
US-11-176-795-47

Query Match      0.5%; Score 23; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAG 45
Db 5 CTAATACGACTCACTATAGGAG 27

RESULT 37
US-11-176-795-51
; Sequence 51, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Gerdes, John C
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 51
; LENGTH: 50
; TYPE: DNA
```

ORGANISM: *Nisseria gonorrhoea*
US-11-176-795-51

Query Match 0.5%; Score 23; DB 12; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 38
US-10-500-831-137

Sequence 137, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 137
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 16
US-10-500-831-137

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 39
US-10-500-831-163

Sequence 163, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 163
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 18
US-10-500-831-163

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 40
US-10-500-831-173

Sequence 173, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 173
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 18
US-10-500-831-173

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 41
US-10-500-831-178

Sequence 178, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 178
LENGTH: 51
TYPE: DNA
ORGANISM: Human papillomavirus type 31
US-10-500-831-178

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAG 45
|||||
DB 5 CTAATACGACTCACTATAGGAG 27

RESULT 42
US-10-500-831-184

Sequence 184, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07

```
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 184
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 31
US-10-500-831-184
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATAGCACTCACTATAGGAG 45
Db      5 CTAATAGCACTCACTATAGGAG 27
```

```
RESULT 43
US-10-500-831-200
; Sequence 200, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 200
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 33
US-10-500-831-200
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATAGCACTCACTATAGGAG 45
Db      5 CTAATAGCACTCACTATAGGAG 27
```

```
RESULT 44
US-10-500-831-209
; Sequence 209, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 209
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 33
US-10-500-831-209
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATAGCACTCACTATAGGAG 45
Db      5 CTAATAGCACTCACTATAGGAG 27
```

```
RESULT 45
US-10-500-831-212
; Sequence 212, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 212
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 35
US-10-500-831-212
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATAGCACTCACTATAGGAG 45
Db      5 CTAATAGCACTCACTATAGGAG 27
```

```
RESULT 46
US-10-500-831-215
; Sequence 215, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 215
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 35
US-10-500-831-215
```

```
Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      23 CTAATAGCACTCACTATAGGAG 45
Db      5 CTAATAGCACTCACTATAGGAG 27
```

RESULT 47


```
US-10-500-831-217
; Sequence 217, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 217
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 35
US-10-500-831-217

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 48
US-10-500-831-242
; Sequence 242, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 242
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus
US-10-500-831-242

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 49
US-10-500-831-251
; Sequence 251, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
```

```
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 251
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 39
US-10-500-831-251

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 50
US-10-500-831-264
; Sequence 264, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 264
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-264

Query Match          0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTATACGACTCACTATAGGAG 45
Db      5 CTATACGACTCACTATAGGAG 27

RESULT 51
US-10-500-831-269
; Sequence 269, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; PRIOR FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 269
; LENGTH: 51
; TYPE: DNA
; ORGANISM: Human papillomavirus type 51
US-10-500-831-269

Query Match          0.5%; Score 23; DB 8; Length 51;
```

Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 52
US-10-500-831-271

; Sequence 271, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.700520S00

; CURRENT APPLICATION NUMBER: US/10/500,831

; CURRENT FILING DATE: 2004-07-07

; PRIOR APPLICATION NUMBER: GB 0200258.2

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: GB 0214124.0

; PRIOR FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 387

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 271

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Human papillomavirus type 51

US-10-500-831-271

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 53
US-10-500-831-285

; Sequence 285, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.700520S00

; CURRENT APPLICATION NUMBER: US/10/500,831

; CURRENT FILING DATE: 2004-07-07

; PRIOR APPLICATION NUMBER: GB 0200258.2

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: GB 0214124.0

; PRIOR FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 387

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 285

; LENGTH: 51

; TYPE: DNA

; ORGANISM: Human papillomavirus type 56

US-10-500-831-285

Query Match 0.5%; Score 23; DB 8; Length 51;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 54
US-10-500-831-195

; Sequence 195, Application US/10500831

; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.700520S00

; CURRENT APPLICATION NUMBER: US/10/500,831

; CURRENT FILING DATE: 2004-07-07

; PRIOR APPLICATION NUMBER: GB 0200258.2

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: GB 0214124.0

; PRIOR FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 387

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 195

; LENGTH: 52

; TYPE: DNA

; ORGANISM: Human papillomavirus type 31

US-10-500-831-195

Query Match 0.5%; Score 23; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 55
US-10-500-831-248

; Sequence 248, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:

; APPLICANT: Frank KARLSEN

; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.700520S00

; CURRENT APPLICATION NUMBER: US/10/500,831

; CURRENT FILING DATE: 2004-07-07

; PRIOR APPLICATION NUMBER: GB 0200258.2

; PRIOR FILING DATE: 2002-01-07

; PRIOR APPLICATION NUMBER: GB 0214124.0

; PRIOR FILING DATE: 2002-06-19

; NUMBER OF SEQ ID NOS: 387

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 248

; LENGTH: 52

; TYPE: DNA

; ORGANISM: Human papillomavirus type 39

US-10-500-831-248

Query Match 0.5%; Score 23; DB 8; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATAGACTCACTATAGGAG 45
|||||
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 56
US-11-176-795-59

; Sequence 59, Application US/11176795
; Publication No. US20050255517A1
; GENERAL INFORMATION:

; APPLICANT: Gardes, John C

; TITLE OF INVENTION: Method and Device for Multiplex Amplification System

; FILE REFERENCE: 1

; CURRENT APPLICATION NUMBER: US/11/176,795

; CURRENT FILING DATE: 2005-07-07

; NUMBER OF SEQ ID NOS: 84

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 59

LENGTH: 52
TYPE: DNA
ORGANISM: Coliform Bacteria
US-11-176-795-59

Query Match 0.5%; Score 23; DB 12; Length 52;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 4 CTAATAGCACTCACTATAGGAG 26

RESULT 57
US-10-500-831-135
Sequence 135, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 135
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus
US-10-500-831-135

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 58
US-10-500-831-160
Sequence 160, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 160
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus type 16
US-10-500-831-160

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 59
US-10-500-831-181
Sequence 181, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 181
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus type 31
US-10-500-831-181

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 60
US-10-500-831-224
Sequence 224, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00
CURRENT APPLICATION NUMBER: US/10/500,831
CURRENT FILING DATE: 2004-07-07
PRIOR APPLICATION NUMBER: GB 0200258.2
PRIOR FILING DATE: 2002-01-07
PRIOR APPLICATION NUMBER: GB 0214124.0
PRIOR FILING DATE: 2002-06-19
NUMBER OF SEQ ID NOS: 387
SOFTWARE: PatentIn version 3.2
SEQ ID NO 224
LENGTH: 53
TYPE: DNA
ORGANISM: Human papillomavirus type 52
US-10-500-831-224

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATAGCACTCACTATAGGAG 45
Db 5 CTAATAGCACTCACTATAGGAG 27

RESULT 61
US-10-500-831-254
Sequence 254, Application US/10500831
Publication No. US20050244813A1
GENERAL INFORMATION:
APPLICANT: Frank KARLSEN
TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
FILE REFERENCE: B0192.70052US00

; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 254
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-254

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 62
US-10-500-831-262
; Sequence 262, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 262
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-262

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 63
US-10-500-831-277
; Sequence 277, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 277
; LENGTH: 53
; TYPE: DNA

; ORGANISM: Human papillomavirus type 56
US-10-500-831-277

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 64
US-10-500-831-279
; Sequence 279, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 279
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Human papillomavirus type 56
US-10-500-831-279

Query Match 0.5%; Score 23; DB 8; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 65
US-11-176-795-55
; Sequence 55, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Coliform Bacteria
US-11-176-795-55

Query Match 0.5%; Score 23; DB 12; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 66
US-11-176-795-79

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/ Sequence 79, Application US/11176795
/ Publication No. US20050255517A1
/ GENERAL INFORMATION:
/ APPLICANT: Gerdes, John C
/ APPLICANT: Marmaro, Jeffrey M
/ TITLE OF INVENTION: Method and Device for Multiplex Amplification System
/ FILE REFERENCE: 1
/ CURRENT APPLICATION NUMBER: US/11/176,795
/ CURRENT FILING DATE: 2005-07-07
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 79
/ LENGTH: 53
/ TYPE: DNA
/ ORGANISM: Escherichia coli
US-11-176-795-79

Query Match          0.5%; Score 23; DB 12; Length 53;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 CTAATACGACTCACTATAGGAG 45
Db 5 CTAATACGACTCACTATAGGAG 27

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RESULT 67
US-10-500-831-235
/ Sequence 235, Application US/10500831
/ Publication No. US20050244813A1
/ GENERAL INFORMATION:
/ APPLICANT: Frank KARLSEN
/ TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
/ FILE REFERENCE: B0192.70052US00
/ CURRENT APPLICATION NUMBER: US/10/500,831
/ CURRENT FILING DATE: 2004-07-07
/ PRIOR APPLICATION NUMBER: GB 0200258.2
/ PRIOR FILING DATE: 2002-01-07
/ PRIOR APPLICATION NUMBER: GB 0214124.0
/ PRIOR FILING DATE: 2002-06-19
/ NUMBER OF SEQ ID NOS: 387
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 235
/ LENGTH: 54
/ TYPE: DNA
/ ORGANISM: Human papillomavirus
US-10-500-831-235

Query Match          0.5%; Score 23; DB 8; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 CTAATACGACTCACTATAGGAG 45
Db 5 CTAATACGACTCACTATAGGAG 27

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RESULT 68
US-11-195-109-32
/ Sequence 32, Application US/11195109
/ Publication No. US20050265975A1
/ GENERAL INFORMATION:
/ APPLICANT: Miles, Vincent J.
/ APPLICANT: Mathew, Michael B.
/ APPLICANT: Katze, Michael G.
/ APPLICANT: Witherell, Gary
/ APPLICANT: Watson, Julia C.
/ TITLE OF INVENTION: METHOD FOR SELECTIVE INACTIVATION
/ TITLE OF INVENTION: OF VIRAL REPLICATION
/ NUMBER OF SEQUENCES: 33
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
```

```

/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036/2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/11/195,109
/ FILING DATE: 01-Aug-2005
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/10/867,798
/ FILING DATE: 14-Jun-2004
/ APPLICATION NUMBER: US/10/109,368
/ FILING DATE: 27-Mar-2002
/ APPLICATION NUMBER: US/08/221,816
/ FILING DATE: 01-Apr-1994
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Coruzzi, Laura A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7960-030
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864
/ TELE: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 32:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 54 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-11-195-109-32

Query Match          0.5%; Score 23; DB 12; Length 54;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 CTAATACGACTCACTATAGGAG 45
Db 8 CTAATACGACTCACTATAGGAG 30

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RESULT 69
US-10-500-831-166
/ Sequence 166, Application US/10500831
/ Publication No. US20050244813A1
/ GENERAL INFORMATION:
/ APPLICANT: Frank KARLSEN
/ TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
/ FILE REFERENCE: B0192.70052US00
/ CURRENT APPLICATION NUMBER: US/10/500,831
/ CURRENT FILING DATE: 2004-07-07
/ PRIOR APPLICATION NUMBER: GB 0200258.2
/ PRIOR FILING DATE: 2002-01-07
/ PRIOR APPLICATION NUMBER: GB 0214124.0
/ PRIOR FILING DATE: 2002-06-19
/ NUMBER OF SEQ ID NOS: 387
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 166
/ LENGTH: 55
/ TYPE: DNA
/ ORGANISM: Human papillomavirus type 18
US-10-500-831-166

Query Match          0.5%; Score 23; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 23 CTAATACGACTCACTATAGGAG 45

Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 70
US-10-500-831-256
; Sequence 256, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 256
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-256

Query Match 0.5%; Score 23; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 71
US-10-500-831-260
; Sequence 260, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 260
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Human papillomavirus type 45
US-10-500-831-260

Query Match 0.5%; Score 23; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 72
US-10-500-831-275
; Sequence 275, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA

; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 275
; LENGTH: 55
; TYPE: DNA
; ORGANISM: Human papillomavirus type 56
US-10-500-831-275

Query Match 0.5%; Score 23; DB 8; Length 55;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 73
US-10-500-831-157
; Sequence 157, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: Frank KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 157
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Human papillomavirus type 16
US-10-500-831-157

Query Match 0.5%; Score 23; DB 8; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATAGACTCACTATAGGAG 45
Db 5 CTAATAGACTCACTATAGGAG 27

RESULT 74
US-11-176-795-63
; Sequence 63, Application US/11176795
; Publication No. US2005025517A1
; GENERAL INFORMATION:
; APPLICANT: Marmaro, Jeffrey M
; TITLE OF INVENTION: Method and Device for Multiplex Amplification System
; FILE REFERENCE: 1
; CURRENT APPLICATION NUMBER: US/11/176,795
; CURRENT FILING DATE: 2005-07-07
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 56
; TYPE: DNA
; ORGANISM: Coliform Bacteria
US-11-176-795-63

Query Match 0.5%; Score 23; DB 12; Length 56;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCACTATAGGAG 45
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Db 5 CTATACGACTCACTATAGGAG 27

RESULT 75

US-10-500-831-187
; Sequence 187, Application US/10500831
; Publication No. US20050244813A1
; GENERAL INFORMATION:
; APPLICANT: FRANK KARLSEN
; TITLE OF INVENTION: DETECTION OF HUMAN PAPILLOMAVIRUS E6 mRNA
; FILE REFERENCE: B0192.70052US00
; CURRENT APPLICATION NUMBER: US/10/500,831
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: GB 0200258.2
; PRIOR FILING DATE: 2002-01-07
; PRIOR APPLICATION NUMBER: GB 0214124.0
; PRIOR FILING DATE: 2002-06-19
; NUMBER OF SEQ ID NOS: 387
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 187
; LENGTH: 57
; TYPE: DNA
; ORGANISM: Human papillomavirus type 31
US-10-500-831-187

Query Match 0.5%; Score 23; DB 8; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCACTATAGGAG 45
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Db 5 CTATACGACTCACTATAGGAG 27

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Job time : 747 secs

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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 23:47:12 ; Search time 3139 Seconds
(without alignments)
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Title: US-10-623-477-3

Perfect score: 4228
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Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 413468905 residue

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Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

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- Published Applications NA_Main:*
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 - 3: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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3	268	6.3	2148	6 US-10-059-911-1	Sequence 1, Appli
4	268	6.3	2148	9 US-10-623-477-1	Sequence 1, Appli
5	55	1.3	3049	7 US-10-432-148-4	Sequence 4, Appli
6	32	0.8	4162	3 US-09-988-462-26	Sequence 26, Appli
7	27	0.6	6975	6 US-10-431-252-17	Sequence 17, Appli
8	26	0.6	625	4 US-09-925-065A-275529	Sequence 275529,
9	26	0.6	625	4 US-09-925-065A-275530	Sequence 275530,
10	26	0.6	6337	6 US-10-223-646-58	Sequence 58, Appli
11	26	0.6	96499	5 US-10-087-192-2011	Sequence 456, App
12	26	0.6	301477	7 US-10-324-281-456	Sequence 11, Appli
13	25	0.6	33	6 US-10-223-666-11	Sequence 11, Appli
14	25	0.6	48	3 US-09-449-204-16	Sequence 2, Appli
15	25	0.6	48	3 US-09-860-474-2	Sequence 37, Appli
16	25	0.6	48	6 US-10-037-986-37	Sequence 2, Appli
17	25	0.6	48	6 US-10-409-365-2	Sequence 37, Appli
18	25	0.6	48	8 US-10-408-085-37	Sequence 2, Appli
19	25	0.6	59	3 US-09-816-089A-7	Sequence 7, Appli
20	25	0.6	63	3 US-09-816-089A-3	Sequence 109, App
21	25	0.6	29	3 US-09-976-800-109	Sequence 109, App
22	24	0.6	29	3 US-10-138-838-109	Sequence 109, App
23	24	0.6	29	5 US-10-138-838-109	Sequence 109, App

24	24	0.6	29	5	US-10-139-031-109	Sequence 109, App
25	24	0.6	29	5	US-10-138-905-109	Sequence 109, App
26	24	0.6	29	5	US-10-138-916-109	Sequence 109, App
27	24	0.6	29	6	US-10-139-296-109	Sequence 109, App
28	24	0.6	29	6	US-10-139-218-109	Sequence 109, App
29	24	0.6	29	6	US-10-405-660-109	Sequence 109, App
30	24	0.6	29	6	US-10-138-898-109	Sequence 109, App
31	24	0.6	43	5	US-10-284-055-6	Sequence 6, Appli
32	24	0.6	43	5	US-10-983-198-33	Sequence 3, Appli
33	24	0.6	44	8	US-10-740-773-6	Sequence 6, Appli
34	24	0.6	45	5	US-10-154-801-6	Sequence 6, Appli
35	24	0.6	45	5	US-10-154-801-9	Sequence 9, Appli
36	24	0.6	48	3	US-09-816-089A-6	Sequence 6, Appli
37	24	0.6	48	6	US-10-094-507-32	Sequence 32, Appli
38	24	0.6	49	3	US-09-976-800-59	Sequence 59, Appli
39	24	0.6	49	3	US-09-976-800-71	Sequence 71, Appli
40	24	0.6	49	3	US-09-976-800-75	Sequence 75, Appli
41	24	0.6	49	5	US-10-138-838-59	Sequence 59, Appli
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43	24	0.6	49	5	US-10-138-838-75	Sequence 75, Appli
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59	24	0.6	49	6	US-10-405-660-59	Sequence 59, Appli
60	24	0.6	49	6	US-10-405-660-71	Sequence 71, Appli
61	24	0.6	49	6	US-10-405-660-75	Sequence 75, Appli
62	24	0.6	49	6	US-10-138-898-59	Sequence 59, Appli
63	24	0.6	49	6	US-10-138-898-71	Sequence 71, Appli
64	24	0.6	49	6	US-10-138-898-75	Sequence 75, Appli
65	24	0.6	50	6	US-10-212-476-16	Sequence 16, Appli
66	24	0.6	51	6	US-10-094-507-1	Sequence 1, Appli
67	24	0.6	52	3	US-09-760-285-1	Sequence 1, Appli
68	24	0.6	52	3	US-10-079-429-65	Sequence 65, Appli
69	24	0.6	52	6	US-10-369-845-1	Sequence 1, Appli
70	24	0.6	53	3	US-09-976-800-69	Sequence 69, Appli
71	24	0.6	53	3	US-09-760-285-3	Sequence 3, Appli
72	24	0.6	53	5	US-10-079-429-56	Sequence 56, Appli
73	24	0.6	53	5	US-10-138-838-69	Sequence 69, Appli
74	24	0.6	53	5	US-10-139-031-69	Sequence 69, Appli
75	24	0.6	53	5	US-10-138-905-69	Sequence 69, Appli
76	24	0.6	53	5	US-10-138-916-69	Sequence 69, Appli
77	24	0.6	53	6	US-10-139-296-69	Sequence 69, Appli
78	24	0.6	53	6	US-10-139-218-69	Sequence 69, Appli
79	24	0.6	53	6	US-10-405-660-69	Sequence 69, Appli
80	24	0.6	53	6	US-10-369-845-3	Sequence 3, Appli
81	24	0.6	53	6	US-10-138-898-69	Sequence 69, Appli
82	24	0.6	54	3	US-09-790-399-14	Sequence 14, Appli
83	24	0.6	54	3	US-09-976-800-61	Sequence 61, Appli
84	24	0.6	54	3	US-09-976-800-66	Sequence 66, Appli
85	24	0.6	54	3	US-10-138-838-61	Sequence 61, Appli
86	24	0.6	54	5	US-10-138-838-66	Sequence 66, Appli
87	24	0.6	54	5	US-10-139-031-61	Sequence 61, Appli
88	24	0.6	54	5	US-10-139-031-66	Sequence 66, Appli
89	24	0.6	54	5	US-10-138-905-61	Sequence 61, Appli
90	24	0.6	54	5	US-10-138-905-66	Sequence 66, Appli
91	24	0.6	54	5	US-10-138-916-61	Sequence 61, Appli
92	24	0.6	54	5	US-10-138-916-66	Sequence 66, Appli
93	24	0.6	54	6	US-10-139-296-61	Sequence 61, Appli
94	24	0.6	54	6	US-10-139-296-66	Sequence 66, Appli
95	24	0.6	54	6	US-10-139-218-61	Sequence 61, Appli
96	24	0.6	54	6	US-10-139-218-66	Sequence 66, Appli

ALIGNMENTS

; Sequence 3, Application US/10623477

Query Match	100.0%;	Score 4228;	DB 9;	Length 4228;
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1 GTTCGACTTAGGCCCTCACTGGCTATACGACTCATATAGGAGCTCGAGGATCCTTTA 60

61 GTTAGAAAAAATTCTTTGTGACGTCGTGTGTTTAACTCAAATTATACTAGTC 120

121 ACATGTGATTCACAATATATATATTTGAAATTGAAATTATTCATATTAATGAGTTAGCAT 180

181 TAATATATACGCTGACATTACCAACCAATGTTCTGCTTTATGATAGTTCATAT 240

241 GTTGCACTTGATTATAGATACTATATAAACGTGGTTTATTTAAAAATCCGTACCAATAAC 300

301 AAAAGTGACCAAAACGATCCATGGTTTGTGTACTTTGTTGGTTAACGATAAT 360

361 ATGATTATGGAAGATTAAATCTTTACTAAATTATTAATAATTTGAAAAACAACCTTA 420

421 ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGAATAAATCGTGTATCTCACTTGA 480

481 CTAGAGTTGATATACATAAACAGTGATATTTTAACGACCGTACATAAACACATGTAT 540

Db 481 CTAGAGTTGATATACATAAACACGTGATATTTTACGACCGTACATTAACACATGTAT 540

3

661 TATGATTTCAGTTACGGAATTGATATTACATTACGAGTAGTACATACACATAATTTTT 720

721 TGTTTTGTTTTACCGATATAGAA TGAATGTGTCTTAAAAATATTGCTTTACTAA 780

781 AACTGTTTATGTTAACTATATATATGTCCTTCCGATGTAATTGGAACAAACTGTAA 840

841 TACAATTATGTGAAGCATTGCATTTAAAAATCCACGGGTAGTAAATCCTCAGAGAT 900

901 TATGTTAGCTACAAATTTCTCTTAGATTAGTAGTTGAGACAAATATGTATA 960

961 CTTGCAGGGGTATTAAGGTCACTGCATAGTCAGACTCAGCATGAAGCCAAAGATCGTC 1021

1021 TCTGTCTTAAGATATCTACAGCTGCTTCGCTGTGTAATAGAGAGAAATTGAATGATGA 108

1081 GAGATCCCATCTAGCGTTTCACGTTTGGCGTCTCCGTCGCACTTTGGCGGTGTGACT 114

1141 TTTTTCATGTGTTGTTGACTAATTTCTCAGAGTGAGTGTAATCAGAAACT 1201

Qy 1201 AATATTGAAAAGAAAAAAGGCAAGAAACTATTGTGCAAAAGACATTAATGAC 126

1261 ACTAAAATTGGATTATTAAAAATGCTATATATGTTGGTGGAAATTATATCATTACCA 132

1321 AATCAAAGAGAGAGAGGACCTCTTGCTTATGATTTCCCTCCTAAACAACGCT 1380

1381 CCCACTATCTTTTACTTCCACACAAATCATTCACACGAGAAATCTGTCTGATC 144

1441 ACCTTCAGCAAAATTAACTAAATTTTGGTATTTTGTCAAGTCTTGCTGTTTAAAG 1500

1501 TCGATTATTGGTAA TACTATATGTGTGGATATACATCCAGCTAATCATTAATGAT 1560

1561 CTCTTTCGCTTATCATAAATACACCACTTAGCTAATCAAGCTAATTAATACCA 1620

Db 1561 CTCCCTTCTGCTTATCATATAATTACACCATTAGCTATCAAGCTAATAATTACACCA 1620

QY	1621	CATTCTCTATCAATTTTATATGATATAATTAACAACCGACTATAGGCTACAGATT	1680
Db	1621	CATTCTCTATCAATTTTATATGATATAATTAACAACCGACTATAGGCTACAGATT	1680
QY	1681	GGTATTAAAGGATTAATGCCCTTCTAGTCGAAAGAAATTTTTTGTTATGATTAACACTCGTG	1740
Db	1681	GGTATTAAAGGATTAATGCCCTTCTAGTCGAAAGAAATTTTTTGTTATGATTAACACTCGTG	1740
QY	1741	GGAAAAAAATCCAGCCTTAATATGCTCATTTTAAAGATTAATGATTAAATGCTTAAATCA	1800
Db	1741	GGAAAAAAATCCAGCCTTAATATGCTCATTTTAAAGATTAATGATTAAATGCTTAAATCA	1800
QY	1801	TTAAATTAAGGTTTTTGGCTTTTAAAGGTTACAACGCGTTAATTCATCATTAAGAGAAAT	1860
Db	1801	TTAAATTAAGGTTTTTGGCTTTTAAAGGTTACAACGCGTTAATTCATCATTAAGAGAAAT	1860
QY	1861	ATTAACTTGAATCGAAATNTCCAAATATCTTTTAAACAATTAAGAAATTTTCAGATT	1920
Db	1861	ATTAACTTGAATCGAAATNTCCAAATATCTTTTAAACAATTAAGAAATTTTCAGATT	1920
QY	1921	TTAAATTAAGGGTACATTTATTTGGGTTCAATAAATATGTTTCCAGTAAAGTTTGAAGT	1980
Db	1921	TTAAATTAAGGGTACATTTATTTGGGTTCAATAAATATGTTTCCAGTAAAGTTTGAAGT	1980
QY	1981	TTAAACAATGATGTTTTTGTATTTAAAAAACAATPAATTTTCTAGTAATTAACAATT	2040
Db	1981	TTAAACAATGATGTTTTTGTATTTAAAAAACAATPAATTTTCTAGTAATTAACAATT	2040
QY	2041	TTTAAACGTCATCCAGATTTGTATTAAGTGAACAATCTGAAACAATTTTTTTTTTTCTTG	2100
Db	2041	TTTAAACGTCATCCAGATTTGTATTAAGTGAACAATCTGAAACAATTTTTTTTTTTCTTG	2100
QY	2101	AATCTGTGTTAAATTCCTCTGCTGCAATCTGCAAGGCAATTGACCAACGACTATACATA	2160
Db	2101	AATCTGTGTTAAATTCCTCTGCTGCAATCTGCAAGGCAATTGACCAACGACTATACATA	2160
QY	2161	TTGAAGCAAAATATCCACAGGAGATGATAGGGTTAATCCCAATTCATATCTTTTGT	2220
Db	2161	TTGAAGCAAAATATCCACAGGAGATGATAGGGTTAATCCCAATTCATATCTTTTGT	2220
QY	2221	CTTTGTTATTTATGAAAAACAATATTTATCAAGAAAAAAACGTTTCTCTCTAGTGTGA	2280
Db	2221	CTTTGTTATTTATGAAAAACAATATTTATCAAGAAAAAAACGTTTCTCTCTAGTGTGA	2280
QY	2281	TAAATATTAAGATTAATTAACAAATTTAATCTAGTTATGATTAATCTATCTTCAAACTT	2340
Db	2281	TAAATATTAAGATTAATTAACAAATTTAATCTAGTTATGATTAATCTATCTTCAAACTT	2340
QY	2341	ACCATCTCTCAACATTAATATTTGATTCATTTTATTTTTTTTACTTAAACATCTTCCACTA	2400
Db	2341	ACCATCTCTCAACATTAATATTTGATTCATTTTATTTTTTTTACTTAAACATCTTCCACTA	2400
QY	2401	AAAAAATGCCAAAGAGATATATTTTAAAGTCAAAATTAATTAAGTGAATGGGTGAT	2460
Db	2401	AAAAAATGCCAAAGAGATATATTTTAAAGTCAAAATTAATTAAGTGAATGGGTGAT	2460
QY	2461	TCTTCAGCAAAAACGCGCGCGTGAAGGTGTCTTATCTCATTTACAGCTGGGTGTGGCAG	2520
Db	2461	TCTTCAGCAAAAACGCGCGCGTGAAGGTGTCTTATCTCATTTACAGCTGGGTGTGGCAG	2520
QY	2521	ACATCATTAAGGCGCTACGTATATTTGAGCTTTACGTGACGTAAAGCTTTAACATATCTAGT	2580
Db	2521	ACATCATTAAGGCGCTACGTATATTTGAGCTTTACGTGACGTAAAGCTTTAACATATCTAGT	2580
QY	2581	TAGTTCTCATCTGATCAAAACAAATCCAAATTCGTAACATATTAACAATCTACTA	2640
Db	2581	TAGTTCTCATCTGATCAAAACAAATCCAAATTCGTAACATATTAACAATCTACTA	2640
QY	2641	GTACTAGATTAACGCTACGTATCATCGCTTTTTGCGAAATTTCTTAACTTAATCTATACAA	2700
Db	2641	GTACTAGATTAACGCTACGTATCATCGCTTTTTGCGAAATTTCTTAACTTAATCTATACAA	2700
QY	2701	CAAACTGTAATGTTGTTTTGTAAATTTATCTTAAACAAAGTTTTGAATGTGCAATGGG	2760

Db	2701	CAAACTGAATGGTTGTTGGTAATTAATCTTAAACCAAAAGTTTGAATTGTGCATTGGG	2760
Qy	2761	AGTACACACTAGTCCCTTTTCCCAAAATATCTCCTTACATGACCGGTTAAAGT	2820
Db	2761	AGCTACACTAGTCCCTTTTCCCAAAATATCTCCTTACATGACCGGTTAAAGT	2820
Qy	2821	ATTTAAACCAAAATTTAATTTGTTGCTGAAGGTAACAACATGTCACTATATAGAGA	2880
Db	2821	ATTTAAACCAAAATTTAATTTGTTGCTGAAGGTAACAACATGTCACTATATAGAGA	2880
Qy	2881	CAGACATGTTATCAATAATGTCAGATGTTATGGAATTCAAATTAATATCGAATTA	2940
Db	2881	CAGATGTTATCAATAATGTCAGATGTTATGGAATTCAAATTAATATCGAATTA	2940
Qy	2941	GCGACTCACTGGTTTAAATAGTTTGAAGATTAATGAATTAATAATGATTCAAAGATA	3000
Db	2941	GCGACTCACTGGTTTAAATAGTTTGAAGATTAATGAATTAATAATGATTCAAAGATA	3000
Qy	3001	CAGAGCTATATATGTCGGGTCACTTATAGACCGGTGACCAAAAGTTTGGTATTTCTAC	3060
Db	3001	CAGAGCTATATATGTCGGGTCACTTATAGACCGGTGACCAAAAGTTTGGTATTTCTAC	3060
Qy	3061	GGTGGCTATPAAGAAATTTTGGAACTTTCTCACCCCTTTATGAACTCTGATATAGTTT	3120
Db	3061	GGTGGCTATPAAGAAATTTTGGAACTTTCTCACCCCTTTATGAACTCTGATATAGTTT	3120
Qy	3121	TGTCGGATTAATATATTTGTAATTCGTATATTTTGTCTTAATATGATACGTAAATCA	3180
Db	3121	TGTCGGATTAATATATTTGTAATTCGTATATTTTGTCTTAATATGATACGTAAATCA	3180
Qy	3181	CGATPAAGAAAGACTCTCTTTTATTTAATTAATTTGATTTAAACCTTTGTTTGGAAATGACT	3240
Db	3181	CGATPAAGAAAGACTCTCTTTTATTTAATTAATTTGATTTAAACCTTTGTTTGGAAATGACT	3240
Qy	3241	CATACACAAGGTTAAAGTTGATACGTATCCAAATTAACAAAATCTTCGAGAGCGCTC	3300
Db	3241	CATACACAAGGTTAAAGTTGATACGTATCCAAATTAACAAAATCTTCGAGAGCGCTC	3300
Qy	3301	GAGTGTCTTACCAACATCGTACCAACTCGATGGGTTAATATAGTTTCTTTCTCTT	3360
Db	3301	GAGTGTCTTACCAACATCGTACCAACTCGATGGGTTAATATAGTTTCTTTCTCTT	3360
Qy	3361	TTTCCAAATGCTTTATATTAATGAACCACTCTAATTTCTTTTAAATAGGTTAAGAT	3420
Db	3361	TTTCCAAATGCTTTATATTAATGAACCACTCTAATTTCTTTTAAATAGGTTAAGAT	3420
Qy	3421	CTTGAATTTTCTGTGATTTTAAACCAAGGTTTCAATCTTCTTACCAAAAAAATAA	3480
Db	3421	CTTGAATTTTCTGTGATTTTAAACCAAGGTTTCAATCTTCTTACCAAAAAAATAA	3480
Qy	3481	AAAAGGTTTCAATTAATAAGATCTAAATTTTGTAGTCAAGAGTTTATGATAGCT	3540
Db	3481	AAAAGGTTTCAATTAATAAGATCTAAATTTTGTAGTCAAGAGTTTATGATAGCT	3540
Qy	3541	GAAGAGTTTATGATGATGCAAGTTTGCAACAGATGGTCGATGATCAATCAAAA	3600
Db	3541	GAAGAGTTTATGATGATGCAAGTTTGCAACAGATGGTCGATGATCAATCAAAA	3600
Qy	3601	CATGATCTAAATAATATTTCTGTCTTACGACAGAAACGATTAATAATCAACAAT	3660
Db	3601	CATGATCTAAATAATATTTCTGTCTTACGACAGAAACGATTAATAATCAACAAT	3660
Qy	3661	CGTTAACCACTTAAATCTTAGAATAATTTTGAGTGAATAATTTCTGTAAAGAGAGG	3720
Db	3661	CGTTAACCACTTAAATCTTAGAATAATTTTGAGTGAATAATTTCTGTAAAGAGAGG	3720
Qy	3721	TATCATATCTTACAAAAAAAGCTCAATTCAGATAAATAATATGTTGTCCATCGTTACA	3780
Db	3721	TATCATATCTTACAAAAAAAGCTCAATTCAGATAAATAATATGTTGTCCATCGTTACA	3780
Qy	3781	AGTATGTTTGTGCTGATCAAGTTGATTTGTAACCTCGTCTTTAGCCATATAGTTCTAAG	3840

Db 3781 AGATGTTTTTGGCTGATCAGTTGATGTAACTGCTCTTAGACATATAGTCTAAG 3840
Qy 3841 TTTTAAATGTTTCAAGACTTTACAAAATTAATAATTAAGGGAATTTGTAAGG 3900
Db 3841 TTTTAAATGTTTCAAGACTTTACAAAATTAATAATTAAGGGAATTTGTAAGG 3900
Qy 3901 CTTAAAGCGAAAAATTAATAATTAATAAGTAAGAAAGTCTTTCTCAATTAAGAAC 3960
Db 3901 CTTAAAGCGAAAAATTAATAATTAATAAGTAAGAAAGTCTTTCTCAATTAAGAAC 3960
Qy 3961 AGATCCCAACGATTCACAAACAGCAAAATTTGTCTTGTCTCTCTTAATATATC 4020
Db 3961 AGATCCCAACGATTCACAAACAGCAAAATTTGTCTTGTCTCTCTTAATATATC 4020
Qy 4021 CTTCAAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTCTGTTTCTCAACGCA 4080
Db 4021 CTTCAAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTCTGTTTCTCAACGCA 4080
Qy 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGTGTGTTCTGTGTAAACCAATGATGGT 4140
Db 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGTGTGTTCTGTGTAAACCAATGATGGT 4140
Qy 4141 TTTAGCTTACTCTTGAGAGATTATTAAGAAAGAGGAAATACATTATTAAGAA 4200
Db 4141 TTTAGCTTACTCTTGAGAGATTATTAAGAAAGAGGAAATACATTATTAAGAA 4200
Qy 4201 AGAGAGCAGAAACCAAAAAAGAACCC 4228
Db 4201 AGAGAGCAGAAACCAAAAAAGAACCC 4228

RESULT 2

US-10-059-911-3

/ Sequence 3, Application US/10059911
/ Publication No. US20030159180A1
/ GENERAL INFORMATION:
/ APPLICANT: Fischer, Robert L.
/ APPLICANT: Mizukami, Yukiko
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
/ FILE REFERENCE: 023070-090730US
/ CURRENT FILING DATE: 2002-06-17
/ NUMBER OF SEQ ID NOS: 42
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 4228
/ TYPE: DNA
/ ORGANISM: Arabidopsis thaliana
/ FEATURE:
/ OTHER INFORMATION: AINTEGUMENTA (ANT) promoter, 5'-upstream sequence
/ OTHER INFORMATION: of ANT gene
US-10-059-911-3

Query Match 93.1%; Score 3936; DB 6; Length 4228;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4226; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

Qy 1 GTGCACTTAGGCTTCACTGGCTTAATACGACTCACTAAGGAGCTCGAGATCCCTTA 60
Db 1 GTGCACTTAGGCTTCACTGGCTTAAATACGACTCACTAAGGAGCTCGAGATCCCTTA 60
Qy 61 GTTAGAAAAAATCTTCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Db 61 GTTAGAAAAAATCTTCTTGTAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy 121 ACATGTGATATCAATATATATATATGAATGGAATTTATTCATATTAATGAGTTAGCA 180
Db 121 ACATGTGATATCAATATATATATGAATGGAATTTATTCATATTAATGAGTTAGCA 180
Qy 181 TAATATATATAGCTGACATTAACCAACAAATGTTTCTGTTTATGATAGTTCTATAT 240
Db 181 TAATATATATAGCTGACATTAACCAACAAATGTTTCTGTTTATGATAGTTCTATAT 240

Qy 241 GTTGCACTTGAATATATGATATATATAAACTGGTTTATTTAAATCCGTACCATTAAC 300
Db 241 GTTGCACTTGAATATATGATATATATAAACTGGTTTATTTAAATCCGTACCATTAAC 300
Qy 301 AAAAGTGAACAAAACGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Db 301 AAAAGTGAACAAAACGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
Qy 361 ATGATATATGAGATTAATCTTTACTAATATTAATTAATTTGGAAAAACAACCTTA 420
Db 361 ATGATATATGAGATTAATCTTTACTAATATTAATTAATTTGGAAAAACAACCTTA 420
Qy 421 ATATGTTGAGTGTCTCAGTGTCTCACTGTTCAGAGATTAATCTGTGTATCTTACTTGA 480
Db 421 ATATGTTGAGTGTCTTCACTGTCTCACTGTTCAGAGATTAATCTGTGTATCTTACTTGA 480
Qy 481 CTGAAAGTTGATATACATTAACACGTGAATTTTAAAGACCGTACATTAACACATGTAT 540
Db 481 CTGAAAGTTGATATACATTAACACGTGAATTTTAAAGACCGTACATTAACACATGTAT 540
Qy 541 CGATCAAAATACAAATTTATGAGACTAGAAATCCAGATGAGATGACCTTACAGAAAT 600
Db 541 CGATCAAAATACAAATTTATGAGACTAGAAATCCAGATGAGATGACCTTACAGAAAT 600
Qy 601 TACACAGCTAAGAAATTTGACAAAGAGAGTGAAGAAATTAATCTAATCAATTTAAAAA 660
Db 601 TACACAGCTAAGAAATTTGACAAAGAGAGTGAAGAAATTAATCTAATCAATTTAAAAA 660
Qy 661 TATGATATTCAGTTACGATGATATTAATTAATTAATTAATTAATTAATTAATTAATTT 720
Db 661 TATGATATTCAGTTACGATGATATTAATTAATTAATTAATTAATTAATTAATTT 720
Qy 721 TGTGTTTGTGTTTACGATATATGAAATGAAATGTTGTGTTAAAAATTTGTTTACTTA 780
Db 721 TGTGTTTGTGTTTACGATATATGAAATGAAATGTTGTGTTAAAAATTTGTTTACTTA 780
Qy 781 AACTGTTTATGATTAATCTATATATATGTCCTTCCGATGAAATTTGAAACAAACCTGTA 840
Db 781 AACTGTTTATGATTAATCTATATATATGTCCTTCCGATGAAATTTGAAACAAACCTGTA 840
Qy 841 TACAAATTAATGTTAAAGCCATTCGAAATTAATAAATCAACGGGTATTAATCTCAGAAGAT 900
Db 841 TACAAATTAATGTTAAAGCCATTCGAAATTAATAAATCAACGGGTATTAATCTCAGAAGAT 900
Qy 901 TATGTTAATCTTCAAAATTTTCTCTTAATATGTAAGTTTGAACAAATTAATGTA 960
Db 901 TATGTTAATCTTCAAAATTTTCTCTTAATATGTAAGTTTGAACAAATTAATGTA 960
Qy 961 CCTGCAAGGGATTAAGGTCATGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 1020
Db 961 CCTGCAAGGGATTAAGGTCATGATGTCAGATGTCAGATGTCAGATGTCAGATGTCAGAT 1020
Qy 1021 TCTGTCTTAAAGATATCTAAGCTGCTTCCCTGTGAATTAAGAAATTTGAATGATGA 1080
Db 1021 TCTGTCTTAAAGATATCTAAGCTGCTTCCCTGTGAATTAAGAAATTTGAATGATGA 1080
Qy 1081 GAGATCCCATCTAGGCTTCACTGTTGCGTGTCCGTCCGAACTTTGGGGTTGTGACT 1140
Db 1081 GAGATCCCATCTAGGCTTCACTGTTGCGTGTCCGTCCGAACTTTGGGGTTGTGACT 1140
Qy 1141 TTTTCTTATATGCTGTTGTTTGAATTAATTTCTCAGAGTGAAGTGAATCAAGAAACT 1200
Db 1141 TTTTCTTATATGCTGTTGTTTGAATTAATTTCTCAGAGTGAAGTGAATCAAGAAACT 1200
Qy 1201 AATATTCGAAAGAAAGAAAGAAAGCAAGAAATCTATGTCGAAAGCAATAAATGAC 1260
Db 1201 AATATTCGAAAGAAAGAAAGAAAGCAAGAAATCTATGTCGAAAGCAATAAATGAC 1260
Qy 1261 ACTAAATATGATATTAATAATGATATATGTTTGTGGAATTTATATCTTACCA 1320
Db 1261 ACTAAATATGATATTAATAATGATATATGTTTGTGGAATTTATATCTTACCA 1320

QY 1321 AATCAAGAGAGAGAGGACCTTGGCTTATGATTTCCCTCTAAACAATGCT 1380
| | | | |
Db 1321 AATCAAGAGAGAGAGGACCTTGGCTTATGATTTCCCTCTAAACAATGCT 1380
QY 1381 CCCACTATCTTTTTCCTTCAACAATAATCATTCACAGAGAAATCTGTCTGTATC 1440
| | | | |
Db 1381 CCCACTATCTTTTTCCTTCAACAATAATCATTCACAGAGAAATCTGTCTGTATC 1440
QY 1441 ACTTTCATGCAAAATTAACATAATTTGGATTTTGTCAAGTTCTGTCTGTTTAA 1500
| | | | |
Db 1441 ACTTTCATGCAAAATTAACATAATTTGGATTTTGTCAAGTTCTGTCTGTTTAA 1500
QY 1501 TCGATTAATTTGGTAACTATATGATGAGATATACATCCAGCTATCAATAATGAT 1560
| | | | |
Db 1501 TCGATTAATTTGGTAACTATATGATGAGATATACATCCAGCTATCAATAATGAT 1560
QY 1561 CTCCTCTGCTTATCAATAATTAACACACATTAAGCTATCAAGCTAATAATTAACA 1620
| | | | |
Db 1561 CTCCTCTGCTTATCAATAATTAACACACATTAAGCTATCAAGCTAATAATTAACA 1620
QY 1621 CATCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGGCTACAGATT 1680
| | | | |
Db 1621 CATCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGGCTACAGATT 1680
QY 1681 GGTAATTAAGGATTAATGCTCTAGTGAAGAAATTTTGTATGATTAACACTGTG 1740
| | | | |
Db 1681 GGTAATTAAGGATTAATGCTCTAGTGAAGAAATTTTGTATGATTAACACTGTG 1740
QY 1741 GGAAGAAATTCAGACCTTAATATGCTCAATTAAGATTAATGATTAATGCTTAATCA 1800
| | | | |
Db 1741 GGAAGAAATTCAGACCTTAATATGCTCAATTAAGATTAATGATTAATGCTTAATCA 1800
QY 1801 TTAATAATTAAGGTTTGTCTTTTAAAGTTTCAACGCTTAATTCATTAAGAGAT 1860
| | | | |
Db 1801 TTAATAATTAAGGTTTGTCTTTTAAAGTTTCAACGCTTAATTCATTAAGAGAT 1860
QY 1861 ATTAACCTTGAATGCAAAATTCCTTTTAAAGCTTAAACATTAAGAGAT 1920
| | | | |
Db 1861 ATTAACCTTGAATGCAAAATTCCTTTTAAAGCTTAAACATTAAGAGAT 1920
QY 1921 TTAATAATTAAGGTTTGTCTTTTAAAGTTTCAACGCTTAATTCATTAAGAGAT 1980
| | | | |
Db 1921 TTAATAATTAAGGTTTGTCTTTTAAAGTTTCAACGCTTAATTCATTAAGAGAT 1980
QY 1981 TTAACAATGAATGTTTGTATTAATAAACAATTAATTTCTAGTAAATTAACAT 2040
| | | | |
Db 1981 TTAACAATGAATGTTTGTATTAATAAACAATTAATTTCTAGTAAATTAACAT 2040
QY 2041 TTTAAACGCTCATTCAGATTTGTAATTAAGTGAACAATCTGAACAATTTTCTTG 2100
| | | | |
Db 2041 TTTAAACGCTCATTCAGATTTGTAATTAAGTGAACAATCTGAACAATTTTCTTG 2100
QY 2101 AATCTGTTTAAATTTCTCTGCTGACACTTGTGACGCAATTTGCAACAATCTTTG 2160
| | | | |
Db 2101 AATCTGTTTAAATTTCTCTGCTGACACTTGTGACGCAATTTGCAACAATCTTTG 2160
QY 2161 TTGAAGAGAAATATCCACAGAGATGATAGGTTAGATCCCAATTCATTAATCTTTG 2220
| | | | |
Db 2161 TTGAAGAGAAATATCCACAGAGATGATAGGTTAGATCCCAATTCATTAATCTTTG 2220
QY 2221 CTTTGTATTTATGAAAAACAATTTTATCAGAAAAAAAGTTTCTTCTGTAGTGA 2280
| | | | |
Db 2221 CTTTGTATTTATGAAAAACAATTTTATCAGAAAAAAAGTTTCTTCTGTAGTGA 2280
QY 2281 TTAAGTATTAAGTATTAACAAATTTTATCTAGTTATGATTAATCAATCTTAACT 2340
| | | | |
Db 2281 TTAAGTATTAAGTATTAACAAATTTTATCTAGTTATGATTAATCAATCTTAACT 2340
QY 2341 ACCATCTTCAACATTAATTAATGATTAATTTTATTTTATCTTAACTTCACTA 2400
| | | | |
Db 2341 ACCATCTTCAACATTAATTAATGATTAATTTTATTTTATCTTAACTTCACTA 2400
QY 2401 AAAAAATGCAAAAGAGATATATTTAAGTCAAGATTAATAAGTGAATGAGTAT 2460
| | | | |

Db 2401 AAAAAATGCAAAAGAGATATATTTAAGTCAAGATTAATAAGTGAATGAGTAT 2460
| | | | |
QY 2461 TCTTACGAAAAAGGCGCGTAGAGTGTCTTATCTCAATTAACGCTGGGTGTGAG 2520
| | | | |
Db 2461 TCTTACGAAAAAGGCGCGTAGAGTGTCTTATCTCAATTAACGCTGGGTGTGAG 2520
QY 2521 ACATCATAGGCGCTATATTTAGCTTTACGTATGATTAAGCTTAACTATCTAGT 2580
| | | | |
Db 2521 ACATCATAGGCGCTATATTTAGCTTTACGTATGATTAAGCTTAACTATCTAGT 2580
QY 2581 TAGTTCTCATGTACAAACAACAATCCAATTCGTAAATCATATATACAAATCTACTA 2640
| | | | |
Db 2581 TAGTTCTCATGTACAAACAACAATCCAATTCGTAAATCATATATACAAATCTACTA 2640
QY 2641 GTACTAGATTAAGCTATGATATCATGCTTTTGGCAATTTCTAAATCTATACAA 2700
| | | | |
Db 2641 GTACTAGATTAAGCTATGATATCATGCTTTTGGCAATTTCTAAATCTATACAA 2700
QY 2701 CAACTTGAATGTTTGTATTTGTAATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
| | | | |
Db 2701 CAACTTGAATGTTTGTATTTGTAATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
QY 2761 AGCTACACTGATCCCTTTTCCCAAAATATCTCTTAATGACGCGTTAAAGT 2820
| | | | |
Db 2761 AGCTACACTGATCCCTTTTCCCAAAATATCTCTTAATGACGCGTTAAAGT 2820
QY 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGTACAAATGCTCATATATAGGA 2880
| | | | |
Db 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGTACAAATGCTCATATATAGGA 2880
QY 2881 CAGCATGTTTATTAACAATAATGTTGATGATTTGGAATCAATATTAATAGAAATTA 2940
| | | | |
Db 2881 CAGCATGTTTATTAACAATAATGTTGATGATTTGGAATCAATATTAATAGAAATTA 2940
QY 2941 GCGACTCACTGTTTAAATGTTTGAAGATTAATGAATAAATAATGAATGAATGAAT 2999
| | | | |
Db 2941 GCGACTCACTGTTTAAATGTTTGAAGATTAATGAATAAATAATGAATGAATGAAT 2999
QY 3000 ACAGAGCTATATATGCTGGGCTATTAAGAGCGGTACCAAAAGTTTGTGCTAAATTTCTA 3059
| | | | |
Db 3000 ACAGAGCTATATATGCTGGGCTATTAAGAGCGGTACCAAAAGTTTGTGCTAAATTTCTA 3059
QY 3060 CGGTGCTCATTAAGAAATTTTGACCTTTTCTCACCCCTTTATGAACTTCTGTATAGTT 3119
| | | | |
Db 3060 CGGTGCTCATTAAGAAATTTTGACCTTTTCTCACCCCTTTATGAACTTCTGTATAGTT 3119
QY 3120 TTTGCGAATTAATATTTGTAATGTAATTTTGTCTTAATTAATGATCGTAAATTC 3179
| | | | |
Db 3120 TTTGCGAATTAATATTTGTAATGTAATTTTGTCTTAATTAATGATCGTAAATTC 3179
QY 3180 ACGATTAAGAAAGACTCTTTTATTTATTTGATTAATAAATTTTGTGTTTGAATGAC 3239
| | | | |
Db 3180 ACGATTAAGAAAGACTCTTTTATTTATTTGATTAATAAATTTTGTGTTTGAATGAC 3239
QY 3240 TCATACACAAGGTTAAAGTTGATGATCCAAATTTCAAAAAAGTTTCGAGATGCGTT 3299
| | | | |
Db 3240 TCATACACAAGGTTAAAGTTGATGATCCAAATTTCAAAAAAGTTTCGAGATGCGTT 3299
QY 3300 CGAGTGTCTTACCAACATCGTACCAATCGTATGAGGTTTATTAATTAAGTTTCTTCT 3359
| | | | |
Db 3300 CGAGTGTCTTACCAACATCGTACCAATCGTATGAGGTTTATTAATTAAGTTTCTTCT 3359
QY 3360 TTTTCAATGTCTTATTAATTAAGAACACTTAAATTTCTTTTAAATTAAGTTAAGAA 3419
| | | | |
Db 3360 TTTTCAATGTCTTATTAATTAAGAACACTTAAATTTCTTTTAAATTAAGTTAAGAA 3419
QY 3420 TCTTGAATTTTGTGATATTTTAAACCAAGGTTTCAATCTTCTGACCAAAAAAAA 3479
| | | | |
Db 3420 TCTTGAATTTTGTGATATTTTAAACCAAGGTTTCAATCTTCTGACCAAAAAAAA 3479
QY 3480 AAAAAAGTTTCAATTAATTAAGAAATTTTGAATGCAAGGTTTAAATGATAGC 3539
| | | | |

Db	3480	AAAAAGTTTCAATTATTAAGAATCAAAATTTTTAGTTCAAGATTAAATGATGC	3539
Qy	3540	TGAAAAGTTATGATGATTCGACAGTTTGCAAACGATGCTGATGATGATCAATCAAAA	3599
Db	3540	TGAAAAGTTATGAAATGATTCGACAGTTTGCAAACGATGCTGATGATGATCAATCAAAA	3599
Qy	3600	ACATGCATCAAAATTAATATTCGCTTACGACAGAGAAACGATTGAAATTAACGAAACA	3655
Db	3600	ACATGCATCAAAATTAATATTCGCTTACGACAGAGAAACGATTGAAATTAACGAAACA	3655
Qy	3660	TCGTTAACCATTAATAAAATCTTAGAATATTTTGAGTATATTTCTGTAAAGAGAG	3719
Db	3660	TCGTTAACCATTAATAAAATCTTAGAATATTTTGAGTATATTTCTGTAAAGAGAG	3719
Qy	3720	GTATCATATCTTACAAAAAAAATCTCATTTCCAGATTAATAATGTTGCCAATGTTACC	3779
Db	3720	GTATCATATCTTACAAAAAAAATCTCATTTCCAGATTAATAATGTTGCCAATGTTACC	3779
Qy	3780	AAGTATGTTTTTGCCTGTCATCAGTTGTATTTGTAACTGCTCTTTAGCCATATAGTTCTAA	3839
Db	3780	AAGTATGTTTTTGCCTGTCATCAGTTGTATTTGTAACTGCTCTTTAGCCATATAGTTCTAA	3839
Qy	3840	GTTTTTAAATGTTTTCAAGACCTTACAAAAATTAATAATAGTGAATTTGTAGG	3899
Db	3840	GTTTTTAAATGTTTTCAAGACCTTACAAAAATTAATAATAGTGAATTTGTAGG	3899
Qy	3900	GCTTAAAGCGAAAAATTAATAATTAATAATGAAGAAAGCTCTTTCTCAATAGAACCA	3955
Db	3900	GCTTAAAGCGAAAAATTAATAATTAATAATGAAGAAAGCTCTTTCTCAATAGAACCA	3955
Qy	3960	CAGATCCCAAGGATTCAAACGCAAAATTTGCTTCTCTCTCTCTTATTTAAATAT	4019
Db	3960	CAGATCCCAAGGATTCAAACGCAAAATTTGCTTCTCTCTCTCTTATTTAAATAT	4019
Qy	4020	CCTCTCAAAAACCCCTCTCTATATCTCTCTTAAGCCCCCTTCTGTTTCTTACGGCA	4079
Db	4020	CCTCTCAAAAACCCCTCTCTATATCTCTCTTAAGCCCCCTTCTGTTTCTTACGGCA	4079
Qy	4080	ACAAAGAAAAACAATAGTTTGAGAAAAATGCTGTGTTCTGTGTACCAATGATTTGGG	4139
Db	4080	ACAAAGAAAAACAATAGTTTGAGAAAAATGCTGTGTTCTGTGTACCAATGATTTGGG	4139
Qy	4140	TTTTAGCTTACTACTTCGAGAGATTTATAGAAAGAAAGATGAGATACATTTATGAAAG	4199
Db	4140	TTTTAGCTTACTACTTCGAGAGATTTATAGAAAGAAAGATGAGATACATTTATGAAAG	4199
Qy	4200	AAGAGAGCAAAACCAAAAAAAGAAACC	4228
Db	4200	AAGAGAGCAAAACCAAAAAAAGAAACC	4228

```

RESULT 3
US-10-059-911-1
; Sequence 1, Application US/10059911
; Publication No. US20030159180A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
; FILE REFERENCE: 023070-090730US
; CURRENT APPLICATION NUMBER: US/10/059,911
; CURRENT FILING DATE: 2002-06-17
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2148
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AINTGUMENTA (ANT) cDNA
; FEATURE:
; NAME/KEY: CDS
;

```

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; LOCATION: (269) .. (1936)
; OTHER INFORMATION: Aradidopsis AINTEGUMENTA (ANT)
US-10-059-911-1

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Query Match	6.3%	Score 268;	DB 6;	Length 2148;
Best Local Similarity	100.0%	Pred. No. 5e-108;		
Matches 268; Conservative	0;	Mismatches	0;	Gaps 0;

3961 AGATCCCAACGATTCACAACAGCAATTGTGCTTGTCTCTCTATTATAATATC 4020

Db 1 AGATCCCAACGGATTCAAAACAGCAAATTGTGCTTGCTCTCTCTATTATAATATC 60

Qy 4021 CTTCAAAACCTCTCTATATCTCTAAAGCCCCCTCTGTGTTCTTACGGCAA 4080

DB 61 CTCACAAAAACCCCTCTCCTATATCCTCTAAACCCCCCTCTCTGTGTTCCTAACCGCAA 120

QY 4081 CAAGAAAAACAAGTTGAGAAAAATGTCGTTGCTGTTAACCAATGATTTGGGT 4140

DB 121 CAAAGAAAAACAAAAGTTTGAAAAATGGTGTCTGTAAGAACCAATCATGGC 180
OY 4141 TTAGCTACTACTTCGAGAGATTATAAGAAAAGAAGTAGAATACATTATAGAAAGA 4200

QY	4201	AGAGAGCAGAAACCAAAAAAAAAAGAAACC	4228
Db	241	AGAGAGCAGAAACCAAAAAAAAAAGAAACC	268

RESULT 4
US-10-623-477-1

```

; Publication No. US20050132445A1
;
; GENERAL INFORMATION:
;
; APPLICANT: Fischer, Robert L.

```

APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
TITLE OF INVENTION: And Enhancing Asexual Reproduction in Plants
FID NUMBER: 097070-000000

CURRENT APPLICATION NUMBER: US/10/623,477
 CURRENT FILING DATE: 2003-07-18
 PRIOR APPLICATION NUMBER: US/09/479,855
 PRIOR FILING DATE: 2000-01-07

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;
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2148

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;
; type: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS

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US-10-623-477-1
/ OTHER INFORMATION: AINTEGUMENTA (ANT)
/ LOCATION: 1257-1, 1258
/ OTHER INFORMATION: AINTEGUMENTA (ANT) CDNA
/

Query Match	6.3%	Score 268;	DB 9;	Length 2148;
Best Local Similarity	100.0%	Pred. No. 5e-108;		
Matches 268;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	3961	AGATTC	CACGGA	TTCAAA	CAGCAAT	TGTGCT	TTGCTCT	CTCTAT	TATATAT	ATATC	4020
Db	1	AGATTC <td>CACGGA <td>TTCAAA <td>CAGCAAT <td>TGTGCT <td>TTGCTCT <td>CTCTAT <td>TATATAT <td>ATATC</td> <td>60</td> </td></td></td></td></td></td></td>	CACGGA <td>TTCAAA <td>CAGCAAT <td>TGTGCT <td>TTGCTCT <td>CTCTAT <td>TATATAT <td>ATATC</td> <td>60</td> </td></td></td></td></td></td>	TTCAAA <td>CAGCAAT <td>TGTGCT <td>TTGCTCT <td>CTCTAT <td>TATATAT <td>ATATC</td> <td>60</td> </td></td></td></td></td>	CAGCAAT <td>TGTGCT <td>TTGCTCT <td>CTCTAT <td>TATATAT <td>ATATC</td> <td>60</td> </td></td></td></td>	TGTGCT <td>TTGCTCT <td>CTCTAT <td>TATATAT <td>ATATC</td> <td>60</td> </td></td></td>	TTGCTCT <td>CTCTAT <td>TATATAT <td>ATATC</td> <td>60</td> </td></td>	CTCTAT <td>TATATAT <td>ATATC</td> <td>60</td> </td>	TATATAT <td>ATATC</td> <td>60</td>	ATATC	60

QY 4021 CTCACAAAACCCCTCTCTATATCTCGTAAAGCCCCCTCTGTCTCTACCGCA 4088
Db 61 CTCACAAAACCCCTCTCTATATCTCTAAAGCCCCCTCTGTGTCTACCGCA 120

QY	4081	CAAGAAAAA	CAAAAGTTG	AGAAAAAT	TGTGTGTT	CGTGTA	CCAATGAT	TTGGT	4148
Db	121	CAAGAAAAA	CAAAAGTTG	AGAAAAAT	TGTGTGTT	CGTGTA	CCAATGAT	TTGGT	180

SEQUENCE DESCRIPTION: SEQ ID NO: 26;
US-09-988-462-26

Query Match 0.6%; Score 32; DB 3; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.004;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCTATATAGACTCACTATAGGAGCTCGA 50
DB 4162 TGGCTATATAGACTCACTATAGGAGCTCGA 4131

RESULT 7

US-10-431-252-17/c
; Sequence 17, Application US/10431252
; Publication No. US20030226166A1
; GENERAL INFORMATION:
; APPLICANT: Li, Zhongqun
; APPLICANT: Falco, S. Carl
; TITLE OF INVENTION: S-ADENOSYL-L-METHIONINE SYNTHETASE PROMOTER AND
; TITLE OF INVENTION: ITS USE IN EXPRESSION OF TRANSGENIC GENES IN PLANTS
; FILE REFERENCE: BB1205 US CIP
; CURRENT APPLICATION NUMBER: US/10/431,252
; CURRENT FILING DATE: 2003-05-07
; PRIOR APPLICATION NUMBER: US 60/113,045
; PRIOR FILING DATE: 1998-12-21
; PRIOR APPLICATION NUMBER: US 09/464,528
; PRIOR FILING DATE: 1999-12-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 17
; LENGTH: 6975
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid
; NAME/KEY: unsure
; LOCATION: (3367)
; OTHER INFORMATION: n = a, c, g or t
US-10-431-252-17

Query Match 0.6%; Score 27; DB 6; Length 6975;
Best Local Similarity 100.0%; Pred. No. 0.69;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCACTATAGGAGCTCG 49
DB 4123 CTATACGACTCACTATAGGAGCTCG 4097

RESULT 8

US-09-925-065A-275529
; Sequence 275529, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086

SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275529
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-275529

Query Match 0.6%; Score 26; DB 4; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAATTAATAATTAATAAGTAAA 3935
DB 161 AAAAATTAATAATTAATAAGTAAA 186

RESULT 9

US-09-925-065A-275530
; Sequence 275530, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275530
; LENGTH: 625
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-275530

Query Match 0.6%; Score 26; DB 4; Length 625;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAATTAATAATTAATAAGTAAA 3935
DB 161 AAAAATTAATAATTAATAAGTAAA 186

RESULT 10

US-10-223-646-58
; Sequence 58, Application US/10223646
; Publication No. US20030140372A1
; GENERAL INFORMATION:
; APPLICANT: Shen, Jennie B.
; TITLE OF INVENTION: GENES FOR DESATURASES TO ALTER LIPID PROFILES IN CORN
; FILE REFERENCE: BB-1137
; CURRENT APPLICATION NUMBER: US/10/223,646
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US/09/326,285
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: 60/088,987
; PRIOR FILING DATE: JUNE 11, 1998
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 58
; LENGTH: 6337

TYPE: DNA
ORGANISM: Zea mays
US-10-223-646-58

Query Match 0.6%; Score 26; DB 6; Length 6337;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAGCTC 48
DB 6312 CTAATACGACTCACTATAGGAGCTC 6337

RESULT 11
US-10-087-192-2011/c
Sequence 2011, Application US/10087192
Publication No. US20020182586A1
GENERAL INFORMATION:
APPLICANT: Morrie, David W.
TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
FILE REFERENCE: 52945200122
CURRENT APPLICATION NUMBER: US/10/087,192
PRIOR FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/747,377
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/798,586
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 2059
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 2011
LENGTH: 96499
TYPE: DNA
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(96499)
OTHER INFORMATION: n = A,T,C or G
US-10-087-192-2011

Query Match 0.6%; Score 26; DB 5; Length 96499;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3914 ATAAATATAATATAAGTAAAGAA 3939
DB 1233 ATAAATATAATATAAGTAAAGAA 1208

RESULT 12
US-10-322-281-456/c
Sequence 456, Application US/10322281
Publication No. US20040126762A1
GENERAL INFORMATION:
APPLICANT: David W. Morris
APPLICANT: Marc S. Malandro
TITLE OF INVENTION: Novel Compositions and Methods in Cancer
FILE REFERENCE: 529452001000
CURRENT APPLICATION NUMBER: US/10/322,281
PRIOR FILING DATE: 2002-12-17
NUMBER OF SEQ ID NOS: 866
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 456
LENGTH: 301477
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(301477)
OTHER INFORMATION: n = A,T,C or G
US-10-322-281-456

Query Match 0.6%; Score 26; DB 7; Length 301477;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAAATATAATATAAGTAAA 3935
DB 105296 AAAAAATATAATATAAGTAAA 105271

RESULT 13
US-10-223-666-11/c
Sequence 11, Application US/10223666
Publication No. US20030180744A1
GENERAL INFORMATION:
APPLICANT: LARRY GOLD et al.
TITLE OF INVENTION: HIGH AFFINITY OLIGONUCLEOTIDE
TITLE OF INVENTION: LIGANDS TO GROWTH
TITLE OF INVENTION: FACTORS
NUMBER OF SEQUENCES: 304
CORRESPONDENCE ADDRESS:
ADDRESSER: Swanson & Bratechun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/223,666
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/973,124
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/08014
FILING DATE: 30-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,423
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,424
FILING DATE: 02-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,594
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,591
FILING DATE: 05-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,725
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/479,783
FILING DATE: 07-JUNE-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/618,693
FILING DATE: 20-MARCH-1996
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-10-223-666-11

Query Match 0.6%; Score 25; DB 6; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 33 TAATAGACTCACTATAGGAGCTC 9

RESULT 14
US-09-449-204-16
Sequence 16, Application US/09449204A
Patent No. US20020051974A1
GENERAL INFORMATION:
APPLICANT: Sincropl, Dominick V.
APPLICANT: Williams, P. Mickey
APPLICANT: Meng, Yu-Ju G. H.
APPLICANT: Dodge, Anthony H.
APPLICANT: Sims, Paul W.
APPLICANT: Wong, Wei Lee Tan
TITLE OF INVENTION: PCR ASSAY
FILE REFERENCE: P1543R1
CURRENT APPLICATION NUMBER: US/09/449,204A
CURRENT FILING DATE: 1999-11-24
EARLIER APPLICATION NUMBER: US 60/110,259
EARLIER FILING DATE: 1998-11-30
NUMBER OF SEQ ID NOS: 32
SEQ ID NO 16
LENGTH: 48
TYPE: DNA
ORGANISM: artificial sequence
FEATURE:
OTHER INFORMATION: Sequence source: synthetic primer
US-09-449-204-16

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 15
US-09-860-474-2
Sequence 2, Application US/09860474
Publication No. US20030032785A1
GENERAL INFORMATION:
APPLICANT: GOLD, L. and JANJIC, N.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TO VASCULAR ENDOTHELIAL GROWTH
FACTOR (VEGF)
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado
COUNTRY: USA
ZIP: 80129
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/860,474

FILING DATE: 18-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/156,824
FILING DATE: 18-SEPTEMBER-1998
APPLICATION NUMBER: 08/447,169
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX14/CIP-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-860-474-2

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 16
US-10-037-986-37
Sequence 37, Application US/10037986
Publication No. US20030157467A1
GENERAL INFORMATION:
APPLICANT: Larry Gold
CRAIG Tuerk
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995

APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX01/C7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-037-986-37

Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TAATACGACTCATTAGGAGCTC 48
Db 9 TAATACGACTCATTAGGAGCTC 33

RESULT 17
US-10-409-565-2
Sequence 2, Application US/10409565
Publication No. US20030176680A1
GENERAL INFORMATION:
APPLICANT: GOLD, L. and JANJIC, N.
TITLE OF INVENTION: HIGH-AFFINITY OLIGONUCLEOTIDE LIGANDS
TO VASCULAR ENDOTHELIAL GROWTH
FACTOR (VEGF)
NUMBER OF SEQUENCES: 242
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 1745 Shea Center Drive, Suite 330
CITY: Highlands Ranch
STATE: Colorado
COUNTRY: USA
ZIP: 80129
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/409,565
FILING DATE: 07-Apr-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/860,474
FILING DATE: 18-May-2001
APPLICATION NUMBER: 09/156,824
FILING DATE: 18-SEPTEMBER-1998
APPLICATION NUMBER: 08/447,169
FILING DATE: 19-MAY-1995
APPLICATION NUMBER: 08/233,012
FILING DATE: 25-APRIL-1994
APPLICATION NUMBER: 08/205,515
FILING DATE: 03-MARCH-1994
APPLICATION NUMBER: 07/964,624
FILING DATE: 21-OCTOBER-1992
APPLICATION NUMBER: 07/714,131

FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX14/CIP-CON
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-409-565-2

Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TAATACGACTCATTAGGAGCTC 48
Db 9 TAATACGACTCATTAGGAGCTC 33

RESULT 18
US-10-085-37
Sequence 37, Application US/10408085
Publication No. US20030198989A1
GENERAL INFORMATION:
APPLICANT: Larry Gold
TITLE OF INVENTION: Nucleic Acid Ligands
NUMBER OF SEQUENCES: 374
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/408,085
FILING DATE: 03-Apr-2003
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10/037,986
FILING DATE: 18-Oct-2001
APPLICATION NUMBER: 09/143,190
FILING DATE: August 27, 1998
APPLICATION NUMBER: 08/469,609
FILING DATE: June 6, 1995
APPLICATION NUMBER: 08/428,964
FILING DATE: April 25, 1995
APPLICATION NUMBER: 08/412,110
FILING DATE: March 27, 1995
APPLICATION NUMBER: 08/409,442
FILING DATE: March 24, 1995
APPLICATION NUMBER: 07/714,131
FILING DATE: June 10, 1991
APPLICATION NUMBER: 07/536,428
FILING DATE: June 11, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33, 215
REFERENCE/DOCKET NUMBER: NEX01/C7

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 48 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 37:
US-10-408-085-37

Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 19
US-10-885-403-2
Sequence 2, Application US/10885403
Publication No. US20050043265A1
GENERAL INFORMATION:
APPLICANT: Gold, Larry
TITLE OF INVENTION: High-Affinity RNA Ligands of Basic
Fibroblast Growth Factors
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Prentice Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MG storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/885,403
FILING DATE: 06-Jul-2004
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/442,423
FILING DATE: 16-MAY-1995
APPLICATION NUMBER: 08/195,005
FILING DATE: 10-FEBRUARY-1994
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEX07/D2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:
LENGTH: 48 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-885-403-2

Query Match 0.6%; Score 25; DB 8; Length 48;

Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 20
US-09-816-089A-7
Sequence 7, Application US/09816089A
Publication No. US20020086299A1
GENERAL INFORMATION:
APPLICANT: OBOKATA, Junichi et al.
TITLE OF INVENTION: Methods of Screening Potential
TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
FILE REFERENCE: 10235/9
CURRENT APPLICATION NUMBER: US/09/816,089A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2000-291084
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 59
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-816-089A-7

Query Match 0.6%; Score 25; DB 3; Length 59;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATAGCACTCACTATAGGGA 44
DB 4 GGCCTAATAGCACTCACTATAGGGA 28

RESULT 21
US-09-816-089A-3
Sequence 3, Application US/09816089A
Publication No. US20020086299A1
GENERAL INFORMATION:
APPLICANT: OBOKATA, Junichi et al.
TITLE OF INVENTION: Methods of Screening Potential
TITLE OF INVENTION: Translational Regulatory Elements of Messenger RNA
FILE REFERENCE: 10235/9
CURRENT APPLICATION NUMBER: US/09/816,089A
CURRENT FILING DATE: 2001-03-26
PRIOR APPLICATION NUMBER: JP 2000-291084
PRIOR FILING DATE: 2000-09-25
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 63
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-816-089A-3

Query Match 0.6%; Score 25; DB 3; Length 63;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 GGCCTAATAGCACTCACTATAGGGA 44
DB 9 GGCCTAATAGCACTCACTATAGGGA 33

RESULT 22

```
US-09-976-800-109
; Sequence 109, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
US-09-976-800-109

Query Match      0.6%; Score 24; DB 3; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTAATAGGAG 45
Db      5 CCTAATAGACTCACTAATAGGAG 28

RESULT 23
US-10-138-838-109
; Sequence 109, Application US/10138838
; Publication No. US2003004982A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,838
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
US-10-138-838-109

Query Match      0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTAATAGGAG 45
Db      5 CCTAATAGACTCACTAATAGGAG 28

Query Match      0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTAATAGGAG 45
Db      5 CCTAATAGACTCACTAATAGGAG 28
```

```
QY      22 CCTAATAGACTCACTAATAGGAG 45
Db      5 CCTAATAGACTCACTAATAGGAG 28

RESULT 24
US-10-139-031-109
; Sequence 109, Application US/10139031
; Publication No. US2003004982A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
US-10-139-031-109

Query Match      0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATAGACTCACTAATAGGAG 45
Db      5 CCTAATAGACTCACTAATAGGAG 28

RESULT 25
US-10-138-905-109
; Sequence 109, Application US/10138905
; Publication No. US2003006880A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,905
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
```

LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-138-905-109

Query Match 0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATCGACTCACTATAGGAG 45
DB 5 CCTAATCGACTCACTATAGGAG 28

RESULT 26
US-10-138-916-109

Sequence 109, Application US/10138916
Publication No. US20030073220A1

GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,916
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: 09/976,800
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/302,602
PRIOR FILING DATE: 1999-04-30
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-138-916-109

Query Match 0.6%; Score 24; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATCGACTCACTATAGGAG 45
DB 5 CCTAATCGACTCACTATAGGAG 28

RESULT 27
US-10-139-296-109

Sequence 109, Application US/10139296
Publication No. US20030148486A1

GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE

TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,296
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-139-296-109

Query Match 0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATCGACTCACTATAGGAG 45
DB 5 CCTAATCGACTCACTATAGGAG 28

RESULT 28
US-10-139-218-109

Sequence 109, Application US/10139218
Publication No. US20030153060A1

GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Eshoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 109
LENGTH: 29
TYPE: DNA
ORGANISM: Bacteriophage T7
US-10-139-218-109

Query Match 0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATCGACTCACTATAGGAG 45
DB 5 CCTAATCGACTCACTATAGGAG 28

RESULT 29
US-10-405-660-109

Sequence 109, Application US/10405660
Publication No. US20030186411A1

GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley

```

; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; PRIOR APPLICATION NUMBER: 2003-04-02
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
; US-10-405-660-109

```

```

Query March          0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy      22 CCTAATAGCACTCACTAATAGGAG 45
      |||||
Db      5 CCTAATAGCACTCACTAATAGGAG 28

```

```

RESULT 30
; Sequence 109, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Behoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; PRIOR APPLICATION NUMBER: 2002-05-03
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 109
; LENGTH: 29
; TYPE: DNA
; ORGANISM: Bacteriophage T7
; US-10-138-898-109

```

```

Query March          0.6%; Score 24; DB 6; Length 29;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Cy      22 CCTAATAGCACTCACTAATAGGAG 45
      |||||
Db      5 CCTAATAGCACTCACTAATAGGAG 28

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RESULT 31
; US-10-294-055-6
; Sequence 6, Application US/10294055
; Publication No. US20030095968A1
; GENERAL INFORMATION:
; APPLICANT: Spriggs, Melanie
; TITLE OF INVENTION: VIRAL ENCODED SEMAPHORIN PROTEIN
; RECEPTOR DNA AND POLYPEPTIDES
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Janis C. Henry
; STREET: 51 University St.
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: MS-DOS/Windows 95
; SOFTWARE: Word for Windows 95, 7.0a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/294,055
; FILING DATE: 13-NO. US20030095968A1-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/958,598
; FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2631
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)470-4189
; TELEFAX: (206)233-0644
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 43 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: primer
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
; US-10-294-055-6

```

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Query March          0.6%; Score 24; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy      22 CCTAATAGCACTCACTAATAGGAG 45
      |||||
Db      5 CCTAATAGCACTCACTAATAGGAG 28

```

```

RESULT 32
; US-10-983-198-33
; Sequence 33, Application US/10983198
; Publication No. US20050130203A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Qingyun
; APPLICANT: McDonald, Terrence
; APPLICANT: Bonner, Timothy P.
; APPLICANT: Ng, Gordon
; APPLICANT: Kolakowski, Lee F., Jr.
; APPLICANT: Clark, Janet
; APPLICANT: Bonner, Tom I.
; TITLE OF INVENTION: NOVEL GABAB RECEPTOR DNA SEQUENCES
; FILE REFERENCE: 20052YP
; CURRENT APPLICATION NUMBER: US/10/983,198
; CURRENT FILING DATE: 2004-11-04
; PRIOR APPLICATION NUMBER: US/09/601,582

```

;; PRIOR FILING DATE: 2000-12-04
;; PRIOR APPLICATION NUMBER: PCT/US99/02361
;; PRIOR FILING DATE: 1999-02-03
;; PRIOR APPLICATION NUMBER: 60/073,767
;; PRIOR FILING DATE: 1998-02-05
;; NUMBER OF SEQ ID NOS: 46
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 33
;; LENGTH: 43
;; TYPE: DNA
;; ORGANISM: Homo Sapiens
US-10-983-198-33

Query Match 0.6%; Score 24; DB 9; Length 43;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCCTATAGGAGCT 47
DB 6 TAATACGACTCCTATAGGAGCT 29

RESULT 33
US-10-740-773-6
;; Sequence 6, Application US/10740773
;; Publication No. US20040180825A1
;; GENERAL INFORMATION:
;; APPLICANT: Sprigge, Melanie K.
;; TITLE OF INVENTION: NOVEL SEMAPHORIN POLYPEPTIDES
;; FILE REFERENCE: 2634-US
;; CURRENT APPLICATION NUMBER: US/10/740,773
;; CURRENT FILING DATE: 2003-12-19
;; PRIOR APPLICATION NUMBER: US/09/689,012
;; PRIOR FILING DATE: 2000-10-12
;; PRIOR APPLICATION NUMBER: PCT/US99/09831
;; PRIOR FILING DATE: 1999-05-05
;; PRIOR APPLICATION NUMBER: US 60/085,497
;; PRIOR FILING DATE: 1998-05-14
;; NUMBER OF SEQ ID NOS: 10
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 6
;; LENGTH: 44
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: PRIMER
US-10-740-773-6

Query Match 0.6%; Score 24; DB 8; Length 44;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 6 CCTAATACGACTCCTATAGGAG 29

RESULT 34
US-10-154-801-6
;; Sequence 6, Application US/10154801
;; Publication No. US20020151014A1
;; GENERAL INFORMATION:
;; APPLICANT: CAMPBELL, ANTHONY KEITH
;; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
;; FILE REFERENCE: 09/225,302
;; CURRENT APPLICATION NUMBER: US/10/154,801
;; CURRENT FILING DATE: 2002-05-28
;; PRIOR APPLICATION NUMBER: 08/957,135
;; PRIOR FILING DATE: 1998-09-14
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 6
;; LENGTH: 45

;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-154-801-6

Query Match 0.6%; Score 24; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 3 CCTAATACGACTCCTATAGGAG 26

RESULT 35
US-10-154-801-9
;; Sequence 9, Application US/10154801
;; Publication No. US20020151014A1
;; GENERAL INFORMATION:
;; APPLICANT: CAMPBELL, ANTHONY KEITH
;; TITLE OF INVENTION: MODIFIED BIOLUMINESCENT PROTEINS AND THEIR USE
;; FILE REFERENCE: 09/225,302
;; CURRENT APPLICATION NUMBER: US/10/154,801
;; CURRENT FILING DATE: 2002-05-28
;; PRIOR APPLICATION NUMBER: 08/957,135
;; PRIOR FILING DATE: 1998-09-14
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 9
;; LENGTH: 45
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-154-801-9

Query Match 0.6%; Score 24; DB 5; Length 45;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCCTATAGGAG 45
DB 3 CCTAATACGACTCCTATAGGAG 26

RESULT 36
US-09-816-089A-6
;; Sequence 6, Application US/09816089A
;; Publication No. US20020086299A1
;; GENERAL INFORMATION:
;; APPLICANT: OBOKATA, Junichi et al.
;; TITLE OF INVENTION: Methods of Screening Potential
;; FILE REFERENCE: 10235/9
;; CURRENT APPLICATION NUMBER: US/09/816,089A
;; CURRENT FILING DATE: 2001-03-26
;; PRIOR APPLICATION NUMBER: JP 2000-291084
;; PRIOR FILING DATE: 2000-09-25
;; NUMBER OF SEQ ID NOS: 28
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 6
;; LENGTH: 48
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Primer
US-09-816-089A-6

Query Match 0.6%; Score 24; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 GGCTAATAGACTCACTATAGG 43
Db 4 GGCTAATAGACTCACTATAGG 27

RESULT 37

US-10-094-507-32
; Sequence 32, Application US/10094507
; Publication No. US2003014353A1
; GENERAL INFORMATION:
; APPLICANT: Sommer, Steve S.
; TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION WITH DIRECT SEQUENCING
; FILE REFERENCE: 27709-42A4
; CURRENT APPLICATION NUMBER: US/10/094,507
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 32
; LENGTH: 48
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Replication segment
US-10-094-507-32

Query Match 0.6%; Score 24; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 CCTAATAGACTCACTATAGGAG 45

Db 5 CCTAATAGACTCACTATAGGAG 28

RESULT 38

US-09-976-800-59
; Sequence 59, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. GLUTAMICUM
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-59

Query Match 0.6%; Score 24; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 CCTAATAGACTCACTATAGGAG 45

Db 5 CCTAATAGACTCACTATAGGAG 28

RESULT 39
US-09-976-800-71
; Sequence 71, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. GLUTAMICUM
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-71

Query Match 0.6%; Score 24; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 CCTAATAGACTCACTATAGGAG 45

Db 5 CCTAATAGACTCACTATAGGAG 28

RESULT 40

US-09-976-800-75
; Sequence 75, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C. GLUTAMICUM
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-75

Query Match 0.6%; Score 24; DB 3; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 CCTAATAGACTCACTATAGGAG 45

Db 5 CCTAATAGACTCACTATAGGAG 28

Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 41

US-10-138-838-59
; Sequence 59, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Behoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Bremner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-838-59

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 42

US-10-138-838-71
; Sequence 71, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Behoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Bremner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03

PRIOR APPLICATION NUMBER: US/09/976,800

PRIOR FILING DATE: 2001-10-12

NUMBER OF SEQ ID NOS: 118

SOFTWARE: PatentIn version 3.1

SEQ ID NO 71

LENGTH: 49

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Primer

US-10-138-838-71

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 43

US-10-138-838-75
; Sequence 75, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Behoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Bremner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/138,838
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-838-75

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
|||||
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 44

US-10-139-031-59
; Sequence 59, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:

APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Behoo, Mark

```

; APPLICANT: Madduri, Kriehna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-59

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28

RESULT 45
US-10-139-031-71
; Sequence 71, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Esheo, Mark
; APPLICANT: Madduri, Kriehna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-71

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28
```

```

; APPLICANT: Madduri, Kriehna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; PRIOR FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-59

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28

RESULT 46
US-10-139-031-75
; Sequence 75, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Esheo, Mark
; APPLICANT: Madduri, Kriehna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-75

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28

RESULT 47
US-10-138-905-59
; Sequence 59, Application US/10138905
; Publication No. US20030068800A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Esheo, Mark
; APPLICANT: Madduri, Kriehna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,905
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-59

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      22 CCTAATAGACTCACTATAGGAG 45
Db      5 CCTAATAGACTCACTATAGGAG 28
```

/ SEQ ID NO 59
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-59

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 48
US-10-138-905-71
/ Sequence 71, Application US/10138905
/ Publication No. US20030068800A1
/ GENERAL INFORMATION:
/ APPLICANT: Wilson, Ron C.
/ APPLICANT: Craft, David L.
/ APPLICANT: Birch, Dudley
/ APPLICANT: Bahoo, Mark
/ APPLICANT: Madduri, Krishna M.
/ APPLICANT: Cornett, Cathy A.
/ APPLICANT: Brenner, Alfred A.
/ APPLICANT: Tang, Maria
/ APPLICANT: Loper, John C.
/ APPLICANT: Gleeson, Martin
/ TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
/ TITLE OF INVENTION: P450 OXIDOREDUCTASE
/ TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
/ TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
/ FILE REFERENCE: 1010-16
/ CURRENT APPLICATION NUMBER: US/10/138,905
/ CURRENT FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US/09/976,800
/ PRIOR FILING DATE: 2001-10-12
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 71
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-71

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 49
US-10-138-905-75
/ Sequence 75, Application US/10138905
/ Publication No. US20030068800A1
/ GENERAL INFORMATION:
/ APPLICANT: Wilson, Ron C.
/ APPLICANT: Craft, David L.
/ APPLICANT: Birch, Dudley
/ APPLICANT: Bahoo, Mark
/ APPLICANT: Madduri, Krishna M.
/ APPLICANT: Cornett, Cathy A.
/ APPLICANT: Brenner, Alfred A.
/ APPLICANT: Tang, Maria

/ APPLICANT: Loper, John C.
/ APPLICANT: Gleeson, Martin
/ TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
/ TITLE OF INVENTION: P450 OXIDOREDUCTASE
/ TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
/ TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
/ FILE REFERENCE: 1010-16
/ CURRENT APPLICATION NUMBER: US/10/138,905
/ CURRENT FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: US/09/976,800
/ PRIOR FILING DATE: 2001-10-12
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 75
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-75

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

RESULT 50
US-10-138-916-59
/ Sequence 59, Application US/10138916
/ Publication No. US20030073220A1
/ GENERAL INFORMATION:
/ APPLICANT: Wilson, Ron C.
/ APPLICANT: Craft, David L.
/ APPLICANT: Birch, Dudley
/ APPLICANT: Bahoo, Mark
/ APPLICANT: Madduri, Krishna M.
/ APPLICANT: Cornett, Cathy A.
/ APPLICANT: Brenner, Alfred A.
/ APPLICANT: Tang, Maria
/ APPLICANT: Loper, John C.
/ APPLICANT: Gleeson, Martin
/ TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDU
/ TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
/ TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
/ FILE REFERENCE: 1010-16
/ CURRENT APPLICATION NUMBER: US/10/138,916
/ CURRENT FILING DATE: 2002-05-03
/ PRIOR APPLICATION NUMBER: 09/976,800
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US/09/302,602
/ PRIOR FILING DATE: 1999-04-30
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 59
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-916-59

Query Match 0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
DB 5 CCTAATACGACTCATTATAGGAG 28

```
RESULT 51
US-10-138-916-71
; Sequence 71, Application US/10138916
; Publication No. US20030073220A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Elrich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYP1B1
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,916
; PRIORITY FILING DATE: 2002-05-03
; PRIORITY APPLICATION NUMBER: 09/976,800
; PRIORITY FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: US 09/302,602
; PRIORITY FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-916-71

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28

RESULT 52
US-10-138-916-75
; Sequence 75, Application US/10138916
; Publication No. US20030073220A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Elrich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYP1B1
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,916
; PRIORITY FILING DATE: 2002-05-03
; PRIORITY APPLICATION NUMBER: 09/976,800
; PRIORITY FILING DATE: 2001-10-12
; PRIORITY APPLICATION NUMBER: US 09/302,602
; PRIORITY FILING DATE: 1999-04-30
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
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; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-916-75

Query Match      0.6%; Score 24; DB 5; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28

RESULT 53
US-10-139-296-59
; Sequence 59, Application US/10139296
; Publication No. US20030148486A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Elrich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF CYP1B1
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,296
; PRIORITY FILING DATE: 2002-05-03
; PRIORITY APPLICATION NUMBER: 09/976,800
; PRIORITY FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-296-59

Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28

RESULT 54
US-10-139-296-71
; Sequence 71, Application US/10139296
; Publication No. US20030148486A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Elrich, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
```

APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,296
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-296-71

Query Match 0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTGACTATAGGAG 45
DB 5 CCTAATACGACTGACTATAGGAG 28

RESULT 55
US-10-139-296-75
Sequence 75, Application US/10139296
Publication No. US20030148486A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,296
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 75
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-296-75

Query Match 0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTGACTATAGGAG 45
DB 5 CCTAATACGACTGACTATAGGAG 28

RESULT 56

US-10-139-218-59
Sequence 59, Application US/10139218
Publication No. US20030153060A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-218-59

Query Match 0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTGACTATAGGAG 45
DB 5 CCTAATACGACTGACTATAGGAG 28

RESULT 57
US-10-139-218-71
Sequence 71, Application US/10139218
Publication No. US20030153060A1
GENERAL INFORMATION:
APPLICANT: Wilson, Ron C.
APPLICANT: Craft, David L.
APPLICANT: Birch, Dudley
APPLICANT: Bahoo, Mark
APPLICANT: Madduri, Krishna M.
APPLICANT: Cornett, Cathy A.
APPLICANT: Brenner, Alfred A.
APPLICANT: Tang, Maria
APPLICANT: Loper, John C.
APPLICANT: Gleeson, Martin
TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
TITLE OF INVENTION: P450 OXIDOREDUCTASE
TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF
TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
FILE REFERENCE: 1010-16
CURRENT APPLICATION NUMBER: US/10/139,218
CURRENT FILING DATE: 2002-05-03
PRIOR APPLICATION NUMBER: US/09/976,800
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 118
SOFTWARE: PatentIn version 3.1
SEQ ID NO 71
LENGTH: 49
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:

```

; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-218-71
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATACGACTCACTATAGGAG 45
      |||||
      5 CCTAATACGACTCACTATAGGAG 28

RESULT 58
US-10-139-218-75
; Sequence 75, Application US/10139218
; Publication No. US20030153060A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139, 218
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-218-75
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATACGACTCACTATAGGAG 45
      |||||
      5 CCTAATACGACTCACTATAGGAG 28

RESULT 59
US-10-405-660-59
; Sequence 59, Application US/10405660
; Publication No. US20030186411A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDU
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
```

```

; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-405-660-59
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATACGACTCACTATAGGAG 45
      |||||
      5 CCTAATACGACTCACTATAGGAG 28

RESULT 60
US-10-405-660-71
; Sequence 71, Application US/10405660
; Publication No. US20030186411A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDU
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-405-660-71
Query Match      0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 CCTAATACGACTCACTATAGGAG 45
      |||||
      5 CCTAATACGACTCACTATAGGAG 28

RESULT 61
US-10-405-660-75
; Sequence 75, Application US/10405660
; Publication No. US20030186411A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
```

```

; APPLICANT: Birch, Dudley
; APPLICANT: Bahoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/405,660
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 75
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-405-660-75
```

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Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      22 CCTAATACGACTCCTATTAGGAG 45
Db      5 CCTAATACGACTCCTATTAGGAG 28
```

```

RESULT 62
US-10-138-898-59
; Sequence 59, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Bahoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 59
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-898-59
```

```

Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy      22 CCTAATACGACTCCTATTAGGAG 45
Db      5 CCTAATACGACTCCTATTAGGAG 28
```

```

RESULT 63
US-10-138-898-71
; Sequence 71, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Bahoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 71
; LENGTH: 49
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-898-71
```

```

Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      22 CCTAATACGACTCCTATTAGGAG 45
Db      5 CCTAATACGACTCCTATTAGGAG 28
```

```

RESULT 64
US-10-138-898-75
; Sequence 75, Application US/10138898
; Publication No. US20030212946A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Bahoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,898
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
```



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/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 75
/ LENGTH: 49
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-898-75
```

```
Query Match          0.6%; Score 24; DB 6; Length 49;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 65

```
US-10-212-476-16
/ Sequence 16, Application US/10212476
/ Publication No. US20030157509A1
/ GENERAL INFORMATION:
/ APPLICANT: MIRZABEKOV, ANDREI
/ APPLICANT: GUSCHIN, DMITRY Y.
/ APPLICANT: SHIK, VALENTINE
/ APPLICANT: DROBYSHEV, ALEKSEI
/ APPLICANT: POTIN, ALEXANDER
/ APPLICANT: YERSHOV, GENNADIY
/ APPLICANT: LYSOV, YU
/ TITLE OF INVENTION: CUSTOMIZED OLIGONUCLEOTIDE MICROCHIPS THAT CONVERT
/ TITLE OF INVENTION: MULTIPLE GENETIC INFORMATION TO SIMPLE PATTERNS, ARE
/ FILE REFERENCE: 21416/90184
/ CURRENT APPLICATION NUMBER: US/10/212,476
/ CURRENT FILING DATE: 2002-08-08
/ PRIOR APPLICATION NUMBER: US/09/261,115
/ PRIOR FILING DATE: 1999-03-03
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 50
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Reverse primer
US-10-212-476-16
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```
Query Match          0.6%; Score 24; DB 6; Length 50;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      7 CCTAATACGACTCACTATAGGAG 30
```

```
RESULT 66
US-10-094-507-1
/ Sequence 1, Application US/10094507
/ Publication No. US20030143553A1
/ GENERAL INFORMATION:
/ APPLICANT: Sommer, Steve S.
/ TITLE OF INVENTION: NUCLEIC ACID AMPLIFICATION WITH DIRECT SEQUENCING
/ FILE REFERENCE: 27709-A2A
/ CURRENT APPLICATION NUMBER: US/10/094,507
/ CURRENT FILING DATE: 2002-03-07
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 1
/ LENGTH: 51
/ TYPE: DNA
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```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Replication segment
US-10-094-507-1
```

```
Query Match          0.6%; Score 24; DB 6; Length 51;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 67

```
US-09-760-285-1
/ Sequence 1, Application US/09760285
/ Publication No. US20030091997A1
/ GENERAL INFORMATION:
/ APPLICANT: Nicolaidis, Nicholas C
/ APPLICANT: Grasso, Luigi
/ APPLICANT: Sasse, Philip M
/ TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
/ FILE REFERENCE: MOR-0017
/ CURRENT APPLICATION NUMBER: US/09/760,285
/ CURRENT FILING DATE: 2001-01-15
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 52
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: oligonucleotide
US-09-760-285-1
```

```
Query Match          0.6%; Score 24; DB 3; Length 52;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
DB      5 CCTAATACGACTCACTATAGGAG 28
```

```
RESULT 68
US-10-079-429-65
/ Sequence 65, Application US/10079429
/ Publication No. US20030027177A1
/ GENERAL INFORMATION:
/ APPLICANT: Haselcine et al.
/ TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
/ FILE REFERENCE: P106P3D1
/ CURRENT APPLICATION NUMBER: US/10/079,429
/ CURRENT FILING DATE: 2002-02-22
/ PRIOR APPLICATION NUMBER: PCT/US95/01035
/ PRIOR FILING DATE: 1995-01-25
/ PRIOR APPLICATION NUMBER: 08/468,024
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: 08/465,769
/ PRIOR FILING DATE: 1995-06-06
/ PRIOR APPLICATION NUMBER: 08/294,312
/ PRIOR FILING DATE: 1994-08-23
/ PRIOR APPLICATION NUMBER: 08/210,143
/ PRIOR FILING DATE: 1994-03-16
/ PRIOR APPLICATION NUMBER: 08/187,757
/ PRIOR FILING DATE: 1994-01-27
/ NUMBER OF SEQ ID NOS: 78
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 65
/ LENGTH: 52
/ TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer useful for amplifying codons 1 to 863 hmlh3
US-10-079-429-65
```

```
Query Match          0.6%; Score 24; DB 5; Length 52;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 69

```
US-10-369-845-1
; Sequence 1, Application US/10369845
; Publication No. US20030186441A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: METHODS FOR ISOLATING NOVEL ANTIMICROBIAL AGENTS FROM
; FILE REFERENCE: MOR-0005
; CURRENT APPLICATION NUMBER: US/10/369,845
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: US/09/708,200
; PRIOR FILING DATE: 2000-11-07
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 52
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-10-369-845-1
```

```
Query Match          0.6%; Score 24; DB 6; Length 52;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 70

```
US-09-976-800-69
; Sequence 69, Application US/09976800
; Publication No. US2003007795A1
; GENERAL INFORMATION:
; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Birch, Dudley
; APPLICANT: Eshoo, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/09/976,800
; CURRENT FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
```

```
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-09-976-800-69
```

```
Query Match          0.6%; Score 24; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 71

```
US-09-760-285-3
; Sequence 3, Application US/09760285
; Publication No. US20030091997A1
; GENERAL INFORMATION:
; APPLICANT: Nicolaides, Nicholas C
; APPLICANT: Grasso, Luigi
; APPLICANT: Sasse, Philip M
; TITLE OF INVENTION: CHEMICAL INHIBITORS OF MISMATCH REPAIR
; FILE REFERENCE: MOR-0017
; CURRENT APPLICATION NUMBER: US/09/760,285
; CURRENT FILING DATE: 2001-01-15
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:oligonucleotide
US-09-760-285-3
```

```
Query Match          0.6%; Score 24; DB 3; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 72

```
US-10-079-429-56
; Sequence 56, Application US/10079429
; Publication No. US20030027177A1
; GENERAL INFORMATION:
; APPLICANT: Haefliger et al.
; TITLE OF INVENTION: Human DNA Mismatch Repair Proteins
; FILE REFERENCE: P106P3D1
; CURRENT APPLICATION NUMBER: US/10/079,429
; CURRENT FILING DATE: 2002-02-22
; PRIOR APPLICATION NUMBER: PCT/US95/01035
; PRIOR FILING DATE: 1995-01-25
; PRIOR APPLICATION NUMBER: 08/468,024
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/465,769
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/294,312
; PRIOR FILING DATE: 1994-08-23
; PRIOR APPLICATION NUMBER: 08/210,143
; PRIOR FILING DATE: 1994-03-16
; PRIOR APPLICATION NUMBER: 08/187,757
; PRIOR FILING DATE: 1994-01-27
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
```

```

; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: primer useful for amplifying codons 1 to 500 of hmlh2
US-10-079-429-56
```

```
Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 73

```
US-10-138-838-69
; Sequence 69, Application US/10138838
; Publication No. US20030049821A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoco, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,838
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-838-69
```

```
Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 74

```
US-10-139-031-69
; Sequence 69, Application US/10139031
; Publication No. US20030049822A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoco, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
```

```

; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/139,031
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-139-031-69
```

```
Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

RESULT 75

```
US-10-138-905-69
; Sequence 69, Application US/10138905
; Publication No. US20030068800A1
; GENERAL INFORMATION:
```

```

; APPLICANT: Wilson, Ron C.
; APPLICANT: Craft, David L.
; APPLICANT: Ertich, Dudley
; APPLICANT: Esnoco, Mark
; APPLICANT: Madduri, Krishna M.
; APPLICANT: Cornett, Cathy A.
; APPLICANT: Brenner, Alfred A.
; APPLICANT: Tang, Maria
; APPLICANT: Loper, John C.
; APPLICANT: Gleeson, Martin
; TITLE OF INVENTION: CYTOCHROME P450 MONOOXYGENASE AND NADPH CYTOCHROME
; TITLE OF INVENTION: P450 OXIDOREDUCTASE
; TITLE OF INVENTION: GENES AND PROTEINS RELATED TO THE OMEGA HYDROXYLASE COMPLEX OF C
; TITLE OF INVENTION: TROPICALIS AND METHODS RELATING THERETO
; FILE REFERENCE: 1010-16
; CURRENT APPLICATION NUMBER: US/10/138,905
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/976,800
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 69
; LENGTH: 53
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer
US-10-138-905-69
```

```
Query Match          0.6%; Score 24; DB 5; Length 53;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      22 CCTAATACGACTCACTATAGGAG 45
Db      5 CCTAATACGACTCACTATAGGAG 28
```

Search completed: February 28, 2006, 02:31:37

Job time : 3141 secs

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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 20:09:32 ; Search time 1581 Seconds

(without alignments)
17823.100 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgactctcgcctcactg.....agaaaccaaaaaagaacc 4228

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 100 summaries

Database :

1: Genesegq19808:*
2: Genesegq19908:*
3: Genesegq20006:*
4: Genesegq2001as:*
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12: Genesegq2004as:*
13: Genesegq2004as:*
14: Genesegq2005as:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4228	100.0	4228	10	ADG25137 Thalecres
2	4228	100.0	4228	14	AEAL17182 A. thalia
3	4107	97.1	4227	3	AAAS9221 Promoter
4	3936	93.1	4228	10	ADG88432 Arabidops
5	268	6.3	2148	3	AAAS9220 Aas59220 cDNA enco
6	268	6.3	2148	8	ABX13437 A. thalia
7	268	6.3	2148	10	ADG25135 Thalecres
8	268	6.3	2148	10	ADG88430 Arabidops
9	268	6.3	2148	14	AEAL17180 A. thalia
10	55	1.3	1421	12	ADMA42796 DNA encod
11	55	1.3	1421	14	ADY55721 Mouse odo
12	55	1.3	1421	14	AEBS6275 Arab56275 Event seq
13	55	1.3	2408	2	AAT30737 Rat ctyp
14	55	1.3	3049	6	ABN81284 Beet prom
15	55	1.3	3869	8	ABZ82143 Arabidops
16	55	1.3	11630	4	AAO2362 Galactosy
17	55	1.3	16905	12	ADOS9305 Mouse kan
18	55	1.3	27048	4	AAO2354 Porcine G
19	46	1.1	4026	4	AAO2355 Porcine G

20	37	0.9	1905	12	ADG61538 AdG61538 Transcrip
21	28	0.7	3484	2	AAV34987 Arabidops
22	27	0.6	1205	3	AAV94303 EGM3 gene
23	27	0.6	6975	3	AAAS1053 Plasmid p
24	27	0.6	7038	3	AAAS5633 2-hybrid
25	27	0.6	8815	3	AAAS5630 Desinat
26	27	0.6	11240	14	AEAG62089 Replicat
27	27	0.6	21178	13	ADU81180 Thale cre
28	27	0.6	22635	13	ADU81181 Thale cre
29	26	0.6	38	3	AAAC60777 Candidate
30	26	0.6	40	2	AAAH88214 Oligonuc
31	26	0.6	43	14	AEBO0576 Drosophi
32	26	0.6	239	3	AAT36342 Human imm
33	26	0.6	6337	3	AAZ35182 Corn del
34	26	0.6	6337	10	AAAD64515 Plasmid p
35	26	0.6	96499	11	ACN45188 Mouse gen
36	26	0.6	301477	13	ABD33362 Human can
37	25	0.6	45	10	ADCG4226 Identific
38	25	0.6	47	2	AAV45614 Primer fo
39	25	0.6	47	3	AAZ44303 M. tuberc
40	25	0.6	47	4	AAV77539 M. tuberc
41	25	0.6	48	2	AAO52391 PCR prime
42	25	0.6	48	2	AAO62710 Primer fo
43	25	0.6	48	2	AAO63026 Primer us
44	25	0.6	48	2	AAO63022 Primer us
45	25	0.6	48	2	AAT06077 Substance
46	25	0.6	48	2	AAT73197 HIV-1 int
47	25	0.6	48	2	AAQ98306 SELEX pri
48	25	0.6	48	2	AAO89173 VEGF RNA
49	25	0.6	48	2	AAO89176 VEGF RNA
50	25	0.6	48	2	AAT07688 Amplifica
51	25	0.6	48	2	AAT84603 RNA ligas
52	25	0.6	48	2	AAT79124 3' primer
53	25	0.6	48	2	AAT87307 SELEX PCR
54	25	0.6	48	2	AAV00777 PCR prime
55	25	0.6	48	2	AAV14558 Primer fo
56	25	0.6	48	2	AAV79637 HSV-1 DNA
57	25	0.6	48	3	AAAS2737 HSV-1 DNA
58	25	0.6	48	4	AAAF70540 SELEX exp
59	25	0.6	48	6	AAAD4075 PCR prime
60	25	0.6	48	6	ABK61113 SELEX pro
61	25	0.6	48	10	ADPF67501 SELEX cDN
62	25	0.6	48	12	ADG39049 cDNA prim
63	25	0.6	59	6	ABL86785 HIV-1 rev
64	25	0.6	59	6	ABL41041 GUS mRNA
65	25	0.6	63	6	ABL41037 GUS mRNA
66	25	0.6	123	12	ADN14395 PCR prime
67	25	0.6	136	2	AAO23256 Plasmid p
68	25	0.6	243934	14	ADZ13446 Human can
69	24	0.6	29	2	AAK00218 T7 RNA po
70	24	0.6	29	6	ABK31899 Bacteriop
71	24	0.6	29	10	ADC44990 T7 promot
72	24	0.6	29	10	ADC45560 T7 promot
73	24	0.6	29	10	ADG52071 T7 promot
74	24	0.6	29	10	ADP72378 Bacteriop
75	24	0.6	29	10	ADP11818 T7 promot
76	24	0.6	29	10	ADP11700 T7 promot
77	24	0.6	29	12	ADBE64235 T7 promot
78	24	0.6	29	12	ADJ26617 Bacteriop
79	24	0.6	29	12	ADQ76186 Chemokine
80	24	0.6	38	2	AAQ12513 Portion o
81	24	0.6	41	2	AAT69676 Upstteam
82	24	0.6	43	2	AAZ06993 Murine GA
83	24	0.6	43	2	AAAS5564 VESPR DNA
84	24	0.6	43	3	AAAC63725 Human VES
85	24	0.6	43	3	AAZ29445 PCR prime
86	24	0.6	43	4	AAAF76949 Human EST
87	24	0.6	43	5	AAAF25253 PCR prime
88	24	0.6	43	5	AAAL57778 PCR prime
89	24	0.6	44	3	AAAT90930 Primer fo
90	24	0.6	44	3	AAZ40171 PCR prime
91	24	0.6	46	12	ADT60084 Oligonuc
92	24	0.6	47	2	AAT34362 TDH conta

C	93	24	0.6	47	2	AA134350	AA134350	TDH	conta
94	24	0.6	47	2	AA191751	AA191751	Primer	BB	
95	24	0.6	47	2	AA283938	AA283938	Primer	BB	
96	24	0.6	47	2	AA87786	AA87786	T7	promot	
97	24	0.6	47	2	AA25623	AA25623	Staphyloc		
98	24	0.6	47	2	AA58766	AA58766	Oligonuct		
99	24	0.6	48	2	AAV07636	AAV07636	Human	Leu	
100	24	0.6	48	3	AA289013	AA289013	Human	Fac	

ALIGNMENTS

RESULT 1	
ID	ADG25137
XX	ADG25137 standard; DNA; 4228 BP.
XX	
XX	ADG25137;
XX	
DT	26-FEB-2004 (first entry)
DE	Thalecress Aintegumenta, ANT, gene promoter.
XX	
KW	Thalecress; ds; promoter; Aintegumenta; ANT; AP2 domain; plant;
KW	seed mass; asexual reproduction; reduced fertility.
XX	
OS	Arabidopsis thaliana.
XX	
FN	US6639128-B1.
XX	
PD	28-OCT-2003.
XX	
PF	07-JAN-2000; 2000US-00479855.
XX	
PR	08-JAN-1999; 99US-00227421.
XX	
PA	(NASC-) NAT SCI FOUND.
XX	
PI	Flascher RL, Mizukami Y,
XX	
DR	WPI; 2003-842795/78.
XX	
PT	New nucleic acid, useful in conferring desired traits on plants, such as
PT	increased seed mass, asexual reproduction or reduced fertility.
XX	
PS	Disclosure; SEQ ID NO 3; 25bp; English.
XX	
CC	The invention relates to an isolated nucleic acid comprising a
CC	polynucleotide encoding a polypeptide having at least 90% identity with
CC	Canola Aintegumenta, ANT, (appearing as ADG25139) as determined using a
CC	BLAST algorithm and comprising two AP2 domains. Also included are an
CC	expression cassette comprising a plant promoter operably linked to a
CC	heterologous polynucleotide encoding the polypeptide, a vector comprising
CC	the expression cassette, a plant comprising the plant promoter operably
CC	linked to the heterologous polynucleotide, a method of asexually
CC	reproducing a plant and a method of reducing fertility in a plant. The
CC	nucleic acid is useful in conferring desired traits on plants, such as
CC	increased seed mass, asexual reproduction or reduced fertility. The
CC	present sequence is the promoter region of teh Thalecress Aintegumenta,
CC	ANT, gene.
XX	
XX	
SQ	Sequence 4228 BP; 1489 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;
Query March	100.0%; Score 4228; DB 10; Length 4228;
Best Local Similarity	100.0%; Pred. NO. 0;
Matches 4228;	Conservative 0; Mismatches 0; Indels 0; Gaps 0
QY	1 GTGCAGCTTAGGCGCTCACTGCGCTTATACGACTCACTATAGGAGCTCGAGATCCTTTA 60
DB	1 GTGCAGCTTAGGCGCTCACTGCGCTTATACGACTCACTATAGGAGCTCGAGATCCTTTA 60
QY	61 GTTGAAGAAAACTTTCTTTGTGACGTGTGTGTGTGTTTAAAGTTCAATTATACAGTC 120

Db	61	GTTAGAAAAAACTTTCTTTGTAAGCTGTGTGTGCTTTTAAGTTCAATTATTAACCTAGTC	120
Qy	121	ACATCGATGATCACAAATATATATATATGAAATTTGAAATTTATCATATTAATGATGATGACAT	180
Db	121	ACATCGATGATCACAAATATATATATATGAAATTTGAAATTTATCATATTAATGATGATGACAT	180
Qy	181	TAAATATATATACGCTGACATTAACCAACAAATGTTTCGCTTTATNGATAGTCTTATAT	240
Db	181	TAAATATATATACGCTGACATTAACCAACAAATGTTTCGCTTTATNGATAGTCTTATAT	240
Qy	241	GTTGCACTGATTTATAGATATGATATTAATAACCGGGTTATTTAAATCCGATCCGATAC	300
Db	241	GTTGCACTGATTTATAGATATGATATTAATAACCGGGTTATTTAAATCCGATCCGATAC	300
Qy	301	AAAAGTGAACCAAAACGAGATCCATGCTTTTGTTTACTTTGTTGTTTAAACCAATAT	360
Db	301	AAAAGTGAACCAAAACGAGATCCATGCTTTTGTTTACTTTGTTGTTTAAACCAATAT	360
Qy	361	ATGATTTATGGAAGATTAATCTTTATCTATAATTATTAATATTTGGAAAAACCACTTAA	420
Db	361	ATGATTTATGGAAGATTAATCTTTATCTATAATTATTAATATTTGGAAAAACCACTTAA	420
Qy	421	ATATGTGAGTGTCTTCAAGTCTACGCTCAAGTAATCTCGGTATCTCTACTTTGAA	480
Db	421	ATATGTGAGTGTCTTCAAGTCTACGCTCAAGTAATCTCGGTATCTCTACTTTGAA	480
Qy	481	CTAGAAGTGAATATACATTAACACGTGAATATTTTAAACGACCGTATCATTAACACATGTAT	540
Db	481	CTAGAAGTGAATATACATTAACACGTGAATATTTTAAACGACCGTATCATTAACACATGTAT	540
Qy	541	CGATCAAAATACAAATTATTTATGACACTAGAAATCCAAAGTGAAGATGACTTAGCAGAAATA	600
Db	541	CGATCAAAATACAAATTATTTATGACACTAGAAATCCAAAGTGAAGATGACTTAGCAGAAATA	600
Qy	601	TACACAGCTGAAGAAATTTGTACAGAAGGCTGAAAAATGATTTCTAATCAATTTAAAAAAGA	660
Db	601	TACACAGCTGAAGAAATTTGTACAGAAGGCTGAAAAATGATTTCTAATCAATTTAAAAAAGA	660
Qy	661	TATGATTTTCAGTTACCGATGATTAATCACTTACGCAAGTATGATACATACATATATTTT	720
Db	661	TATGATTTTCAGTTACCGATGATTAATCACTTACGCAAGTATGATACATACATATATTTT	720
Qy	721	TGTTTTTGTTTTACCGAATATGAAATGTTGTGTATAAAAATATGTTTTTACTAA	780
Db	721	TGTTTTTGTTTTACCGAATATGAAATGTTGTGTATAAAAATATGTTTTTACTAA	780
Qy	781	AACCTGTTTATNGTAACATATATATATGCTTCCGCAATGTAATTTGAAACAAACCTGTAA	840
Db	781	AACCTGTTTATNGTAACATATATATATGCTTCCGCAATGTAATTTGAAACAAACCTGTAA	840
Qy	841	TACAAATATATGTAAGCATTGCAATTTAAAAATTCACGCGGTAGTAATCTCTCAGAAGAT	900
Db	841	TACAAATATATGTAAGCATTGCAATTTAAAAATTCACGCGGTAGTAATCTCTCAGAAGAT	900
Qy	901	TATGTTAAGTCTACAAATTTTCTCTTTAGATTAGTAAGGTTTGAACAAATATATGTATA	960
Db	901	TATGTTAAGTCTACAAATTTTCTCTTTAGATTAGTAAGGTTTGAACAAATATATGTATA	960
Qy	961	CCTTGACAGGGGTATTAAGGTGACATGCAATGTCACACTCAGATATGAAGCCAAAGGCTGCTC	1020
Db	961	CCTTGACAGGGGTATTAAGGTGACATGCAATGTCACACTCAGATATGAAGCCAAAGGCTGCTC	1020
Qy	1021	TCTGTCCTAAGAATATCTACAGCTGCTTCGCTGTGAATAGAGAAGAAATTTGAATGATGA	1080
Db	1021	TCTGTCCTAAGAATATCTACAGCTGCTTCGCTGTGAATAGAGAAGAAATTTGAATGATGA	1080
Qy	1081	GAGATCCCATCTACAGCTTTCAGTTTGCGTTCTCCGTGCGCAACTTTGGCGGTTGTGACT	1140
Db	1081	GAGATCCCATCTACAGCTTTCAGTTTGCGTTCTCCGTGCGCAACTTTGGCGGTTGTGACT	1140
Qy	1141	TTTTTTCTTATAGTGTGTTTGAATTTTCTCAAGTGAAGATGTATCAAGAAACT	1200
Db	1141	TTTTTTCTTATAGTGTGTTTGAATTTTCTCAAGTGAAGATGTATCAAGAAACT	1200

QY	1201	AAATTTGGAAAAGAAAAGAAAAAAGGCAAAAAAGTAAGTCGAAAAAGCATTAATAGAC	1260
Db	1201	AAATTTGGAAAAGAAAAGAAAAAAGGCAAAAAAGTAATGTCGAAAAAGCATTAATAGAC	1260
QY	1261	ACTAAAAATGGATTAATTAATAAATGGTAATATGTTGGTGGAATTTAATCATTAACCA	1320
Db	1261	ACTAAAAATGGATTAATTAATAAATGGTAATATGTTGGTGGAATTTAATCATTAACCA	1320
QY	1321	AATCAAAAGAAAGAGAGAGGAGCCTCTTCGTCCTTAATTTCCCTCCTAAACAATGCT	1380
Db	1321	AATCAAAAGAAAGAGAGAGGAGCCTCTTCGTCCTTAATTTCCCTCCTAAACAATGCT	1380
QY	1381	CCCACTAATCCTTTTAACTTCCAACAAAATCATTTCAACAGAAAAATCTGTCTGTATC	1440
Db	1381	CCCACTAATCCTTTTAACTTCCAACAAAATCATTTCAACAGAAAAATCTGTCTGTATC	1440
QY	1441	ACTTTCATGCAAAATTAACCTAAATTTTGTATTTTGTCAAGTCTCTGCTGTTTTAG	1500
Db	1441	ACTTTCATGCAAAATTAACCTAAATTTTGTATTTTGTCAAGTCTCTGCTGTTTTAG	1500
QY	1501	TCGATTAATTTGGTAATCTATATATGGGGAATATCAACATCCAGCTAATCAATAATGAT	1560
Db	1501	TCGATTAATTTGGTAATCTATATATGGGGAATATCAACATCCAGCTAATCAATAATGAT	1560
QY	1561	CTCCCTCTGCTTAATCAATAAAATTAACACACATTAAGCTAATCAAGCTAATAATTAACA	1620
Db	1561	CTCCCTCTGCTTAATCAATAAAATTAACACACATTAAGCTAATCAAGCTAATAATTAACA	1620
QY	1621	CATTCTCTTAATCAATTTTATATATGGTAATTAATAACAACGACTATATAGCTACAGATT	1680
Db	1621	CATTCTCTTAATCAATTTTATATATGGTAATTAATAACAACGACTATATAGCTACAGATT	1680
QY	1681	GGATTAAGGCAATTAATGCTCTTCTAGTGAAGAAATTTTGTATGATTAACAATCTGTG	1740
Db	1681	GGATTAAGGCAATTAATGCTCTTCTAGTGAAGAAATTTTGTATGATTAACAATCTGTG	1740
QY	1741	GGAAAAAATCAGCGCTAATATAGCTCATTTAAGGATATGATTTAATGCTTTAATCA	1800
Db	1741	GGAAAAAATCAGCGCTAATATAGCTCATTTAAGGATATGATTTAATGCTTTAATCA	1800
QY	1801	TTAAATTAAGGTTTTGCTTTTAAAGGTTACACGCGCTTAATTCATCATTAAGAGAT	1860
Db	1801	TTAAATTAAGGTTTTGCTTTTAAAGGTTACACGCGCTTAATTCATCATTAAGAGAT	1860
QY	1861	ATTAACTTGAATCGAAATTCGAAATACTTTTTPAACACATTAAGAAATTTTCAGCAATT	1920
Db	1861	ATTAACTTGAATCGAAATTCGAAATACTTTTTPAACACATTAAGAAATTTTCAGCAATT	1920
QY	1921	TTAAATTAAGGTAATTTATTTGGGTTCAATTAATATGTTCACAGTAAGTTGGAGGT	1980
Db	1921	TTAAATTAAGGTAATTTATTTGGGTTCAATTAATATGTTCACAGTAAGTTGGAGGT	1980
QY	1981	TTAACCAATGAATGTTTTTGTATTAATAAACAATTAATTTTCTAGTAATTAACAATT	2040
Db	1981	TTAACCAATGAATGTTTTTGTATTAATAAACAATTAATTTTCTAGTAATTAACAATT	2040
QY	2041	TTTAAACGTCATCCAGATTTGAATTAAGTGAACAATCTGAANAACATTTTTTTTCTTG	2100
Db	2041	TTTAAACGTCATCCAGATTTGAATTAAGTGAACAATCTGAANAACATTTTTTTTCTTG	2100
QY	2101	AATCTGTTTAAATTTCTCTCTGCTGCAATCTTGACAGGATTTGACAAACGATCTTTTGT	2160
Db	2101	AATCTGTTTAAATTTCTCTCTGCTGCAATCTTGACAGGATTTGACAAACGATCTTTTGT	2160
QY	2161	TTGAAGCAAAATATCCACAGAGGATGATAGGGTTAGATCCCACTTCAATATCTTTTGT	2220
Db	2161	TTGAAGCAAAATATCCACAGAGGATGATAGGGTTAGATCCCACTTCAATATCTTTTGT	2220
QY	2221	CTTTGTTATTTATGAAAAACAATTTTATCAAGAAAAAAACGTTTCTTCTATAGTGTA	2280
Db	2221	CTTTGTTATTTATGAAAAACAATTTTATCAAGAAAAAAACGTTTCTTCTATAGTGTA	2280

QY	2281		PAGTATPAGTATATACAAAATTTATACGTGGTTAAAGATTTATCATCTTCAAACTT	2340
Db	2281		TAACTATPAGTATATACAAAATTTATACGTGGTTAAAGATTTATCATCTTCAAACTT	2340
QY	2341		ACCAATCCTTCAACATTAATATATGATCAATTTTATTTTAACTAACTACTTCCACTA	2400
Db	2341		ACCAATCCTTCAACATTAATATGATCAATTTTATTTTAACTAACTACTTCCACTA	2400
QY	2401		AAAAATGCAAAAGAAAGATATATATTTAAGTCAAAAGTAAATTAAGATGGATGGTGAT	2460
Db	2401		AAAAATGCAAAAGAAAGATATATATTTAAGTCAAAAGTAAATTAAGATGGATGGTGAT	2460
QY	2461		TCTTCACGAAACGGCCCGTAGAGGGTGCTTAATCCATCACTTAAGCTGGGTTGGCAG	2520
Db	2461		TCTTCACGAAACGGCCCGTAGAGGGTGCTTAATCCATCACTTAAGCTGGGTTGGCAG	2520
QY	2521		ACATCATPAGGCCCTACGATATATTTGACCTTTACGTGACGTAAAGCTTTAACATATCTAGT	2580
Db	2521		ACATCATPAGGCCCTACGATATATTTGACCTTTACGTGACGTAAAGCTTTAACATATCTAGT	2580
QY	2581		TAGTTCTCACTGTAACAAACAAAACAAAATCCAAATTCGTAATATATPACAAATCTACTA	2640
Db	2581		TAGTTCTCACTGTAACAAACAAAACAAAATCCAAATTCGTAATATATPACAAATCTACTA	2640
QY	2641		GTACTAATATPACGTACGTATACATCCGCTTTTGGCAAAATTTCTAACTAATCTATCAAA	2700
Db	2641		GTACTAATATPACGTACGTATACATCCGCTTTTGGCAAAATTTCTAACTAATCTATCAAA	2700
QY	2701		CAAACTTGAATGTTTGTGTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTTGGG	2760
Db	2701		CAAACTTGAATGTTTGTGTTGTATTTATCTTAAACCAAGTTTGAATGTGTGCATTTGGG	2760
QY	2761		AGCTACACTAGTACCCCTTTTTCGCCCAAAATATCTCCTTAATGACGCGGTAAAGT	2820
Db	2761		AGCTACACTAGTACCCCTTTTTCGCCCAAAATATCTCCTTAATGACGCGGTAAAGT	2820
QY	2821		ATTTAAACCAACAAATTTTATTTGTTGTGCTGAAGGTACAAACATGTCACATATATAGAA	2880
Db	2821		ATTTAAACCAACAAATTTTATTTGTTGTGCTGAAGGTACAAACATGTCACATATATAGAA	2880
QY	2881		CAGCATGTTTATACAAATATATGTTGCATATTTGGAATCAATATPAAATACGAATTA	2940
Db	2881		CAGCATGTTTATACAAATATATGTTGCATATTTGGAATCAATATPAAATACGAATTA	2940
QY	2941		GCGACTCACTGGTTTAAATAGTTTGGAAAGATATGAATATAAAATGAATTCAAAGATA	3000
Db	2941		GCGACTCACTGGTTTAAATAGTTTGGAAAGATATGAATATAAAATGAATTCAAAGATA	3000
QY	3001		CAGAGCTATATATGTGGGTCATTTAGAGCCGTGACCAAAAGTTTGGTATTTTCTAC	3060
Db	3001		CAGAGCTATATATGTGGGTCATTTAGAGCCGTGACCAAAAGTTTGGTATTTTCTAC	3060
QY	3061		GGTGGCTATPAGAAATTTTGGACCTTTCTCACCCCTTTATGAACTTCTGTATAGTTTTT	3120
Db	3061		GGTGGCTATPAGAAATTTTGGACCTTTCTCACCCCTTTATGAACTTCTGTATAGTTTTT	3120
QY	3121		TGTGCGATTAATATTTGTGATTCGTATATTTTGTCTTAATATGATACGTAAATTCGA	3180
Db	3121		TGTGCGATTAATATTTGTGATTCGTATATTTTGTCTTAATATGATACGTAAATTCGA	3180
QY	3181		CGATPAGAAAGACTTCTTTTATATTTAATTTGATTTAAACCTTTGTTTGGAAATGACT	3240
Db	3181		CGATPAGAAAGACTTCTTTTATATTTAATTTGATTTAAACCTTTGTTTGGAAATGACT	3240
QY	3241		CATACACAAAGTTTAAAGTTTGAATGATCCAAATTTACAAAAGTTTTCGAGAGCGCTTC	3300
Db	3241		CATACACAAAGTTTAAAGTTTGAATGATCCAAATTTACAAAAGTTTTCGAGAGCGCTTC	3300
QY	3301		GAGTGTCTTACCAACATCTGTACCAACTCGATPAGGGTTTATATATAGGTTTTTTCTTCTT	3360
Db	3301		GAGTGTCTTACCAACATCTGTACCAACTCGATPAGGGTTTATATATAGGTTTTTTCTTCTT	3360
QY	3361		TTTTCAATGTCTTATATATGAAACACTGTAAATTTCTTTTATTTAAATAGGTTAAGAT	3420

Db	3361	TTTCATATGCTTTATATATTAACCACTCTAAATTTCTTTTATTAATTAGGTTAAGAT	3420
Qy	3421	CTTGAAATTTCTGTGATTTTAAACCAAGTTTCAATCTCTCTAGCACAAAAAAAAA	3480
Db	3421	CTTGAAATTTCTGTGATTTTAAACCAAGTTTCAATCTCTCTAGCACAAAAAAAAA	3480
Qy	3481	AAAAAGTTTCAATTAATTAAGAATCTAAATTTTTCAGTTCAGAGTTTATGATGCT	3540
Db	3481	AAAAAGTTTCAATTAATTAAGAATCTAAATTTTTCAGTTCAGAGTTTATGATGCT	3540
Qy	3541	GAAAAGTTATGAATGATTGCAAGTTTGCAAGATGGTGCATGATGATACATCAAAA	3600
Db	3541	GAAAAGTTATGAATGATTGCAAGTTTGCAAGATGGTGCATGATGATACATCAAAA	3600
Qy	3601	CATGCATCAAAATTAATATTCGTGCTTAGCAAGAGAAACGATTAATAAACAACAAT	3660
Db	3601	CATGCATCAAAATTAATATTCGTGCTTAGCAAGAGAAACGATTAATAAACAACAAT	3660
Qy	3661	CGTTAACCCTTAATAAATCTTAAGAATAATTTTGTAAGTAATTTCTGTAAAGAGAG	3720
Db	3661	CGTTAACCCTTAATAAATCTTAAGAATAATTTTGTAAGTAATTTCTGTAAAGAGAG	3720
Qy	3721	TATCATATCTTAACAAAAAAACATTCATTCAGATTAATAATATGTTGTCATCGTTACA	3780
Db	3721	TATCATATCTTAACAAAAAAACATTCATTCAGATTAATAATATGTTGTCATCGTTACA	3780
Qy	3781	AGTATGTTTTGCTGTCATCAGTTGATTTGTACTCGTCTGTAGCCATATAGTCTAAG	3840
Db	3781	AGTATGTTTTGCTGTCATCAGTTGATTTGTACTCGTCTGTAGCCATATAGTCTAAG	3840
Qy	3841	TTTTTAATGTTTTCAAGACCTTTACAAATAATTAATAATTAAGTGGAAATTTGTAGG	3900
Db	3841	TTTTTAATGTTTTCAAGACCTTTACAAATAATTAATAATTAAGTGGAAATTTGTAGG	3900
Qy	3901	CTAAAGCGSAAAAATAAAAATAAAAATAAAAATGAAGAAGCGCTTCTCATTAAGAAC	3960
Db	3901	CTAAAGCGSAAAAATAAAAATAAAAATAAAAATGAAGAAGCGCTTCTCATTAAGAAC	3960
Qy	3961	AGATCCCAACGGAATTCAAACAGCAAAATTTGTGCTTGTCTCTCTCTATTAATATATC	4020
Db	3961	AGATCCCAACGGAATTCAAACAGCAAAATTTGTGCTTGTCTCTCTCTATTAATATATC	4020
Qy	4021	CTCTCAAAAAACCCCTCTCTATATCTCTTAAGCCGCCCTCTCTGTTTCTCTACCCGA	4080
Db	4021	CTCTCAAAAAACCCCTCTCTATATCTCTTAAGCCGCCCTCTCTGTTTCTCTACCCGA	4080
Qy	4081	CAAGAAAAAACAAGGTTTGAGAAAAATGGTGTGTTGCTGTGTAAACCAATGATGGGT	4140
Db	4081	CAAGAAAAAACAAGGTTTGAGAAAAATGGTGTGTTGCTGTGTAAACCAATGATGGGT	4140
Qy	4141	TTTAGCTTACTACTTCGAGAGATTATAGAAAGAAAGAGTGAAGATACATTATAGAAAGA	4200
Db	4141	TTTAGCTTACTACTTCGAGAGATTATAGAAAGAAAGAGTGAAGATACATTATAGAAAGA	4200
Qy	4201	AGAGAGCAGAAACCAAAAAAAGAAC	4228
Db	4201	AGAGAGCAGAAACCAAAAAAAGAAC	4228

RESULT 2
AEA17182
ID AEA17182 standard; cDNA; 4228 BP.
XX
XX AEA17182;
AC
XX
DT 25-AUG-2005 (first entry)
XX
XX
DE A. thaliana aintegumenta (ANT) 5' promoter, seq id 3.
XX
XX Plant engineering; growth; cell proliferation; organ mass; fertility;
KW asexual reproduction; aintegumenta; ANT; plant; promoter; ds.
XX

OS	Ardidicopsis thaliana.
XX	US2005132445-A1.
PN	16-JUN-2005.
XX	18-JUL-2003; 2003US-00623477.
PP	07-JAN-2000; 2000US-00479855.
XX	(REGC) UNIV CALIFORNIA.
XX	Fischer RU, Mizukami Y;
PI	WPI; 2005-424635/43.
XX	Modulating growth and cell proliferation in a plant, useful in plant genetic engineering, comprises modulating aineugenta (ANT) gene activity and selecting plants with altered cell number.
PT	Claim 52, SEQ ID NO 3; 27pp; English.
PS	The invention relates to modulating growth and cell proliferation in a plant comprising modulating aineugenta (ANT) gene activity and selecting plants with altered cell number. Further disclosed is a method for directing expression of a heterologous nucleic acid in meristematic cells of a plant. The method is useful in plant genetic engineering, specifically for altering organ mass, controlling fertility and enhancing axsexual reproduction in plants. The current sequence represents the A. thaliana ANT promoter sequence..
CC	Sequence 4228 BP; 1489 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;
SQ	Query Match 100.0%; Score 4228; DB 14; Length 4228; Best Local Similarity 100.0%; Pred. No. 0; Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GTGACCTCTAGGGCTCACTGGCCCTAATACGACTCACTTAGGGAGCTCGAGATCCTTTA 60
DB	1 GTGCACCTTAAAGGCTCACGTGCTTAATACGACTCACTTAGGGAGCTCGAGATCCTTTA 60
OY	61 GTTAGAAAAAACTTCCTTTGTACGCTGTGTGTGTGTATTAACTTAAGTTCAATTAACTAGTC 120
DB	61 GTTAGAAAAAACTTCCTTTGTACGCTGTGTGTGTGTATTAAAGTTCAATTAACTAGTC 120
OY	121 ACATGTGATATCACAATATATATATTTTGAAATTGAATTATTCATTTAATAGTTAGCAT 180
DB	121 ACATGTGATATCACAATATATATATTTTGAAATTGAATTATTCATTTAATAGTTAGCAT 180
OY	181 TAATATATATATCGCTGACATTAACAACCAATGTTTTGCTTTATATAGATAGTTCTATAT 240
DB	181 TAATATATATATCGCTGACATTAACAACCAATGTTTTGCTTTATATAGATAGTTCTATAT 240
OY	241 GTTGACCTGTGATTATAGATCTATATATAAACTGGGTTTATTATAAATCGTAGCCATAAC 300
DB	241 GTTGACCTGTGATTATAGATCTATATATAAACTGGGTTTATTATAAATCGTAGCCATAAC 300
OY	301 AAAAGTGAACCAAACGATACCATGTTTTGTCTTACTTTGTGTTAACCAATAT 360
DB	301 AAAAGTGAACCAAACGATACCATGTTTTGTCTTACTTTGTGTTAACCAATAT 360
OY	361 ATGATTTATGMAAGATTAAATCTTTACTAATAATTAATTTGAATAAAACAATCTTA 420
DB	361 ATGATTTATGMAAGATTAAATCTTTACTAATAATTAATTTGAATAAAACAATCTTA 420
OY	421 ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGAATATATCTCGTTATCTTAATTGAA 480
DB	421 ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGAATATATCTCGTTATCTTAATTGAA 480
OY	481 CTAAAGTGTATATATCACTAAACAGCTGAATTTTAAACGACCGTATCAATAACAGTAT 540
DB	481 CTAAAGTGTATATATCACTAAACAGCTGAATTTTAAACGACCGTATCAATAACAGTAT 540

SQ Sequence 4228 BP; 1489 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;

Query Match	100.0%	Score 4228;	DB 14;	Length 4228;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 4228; Conservative	0;	Mismatches	0;	Gaps 0

Oy	1	GTGCACCTCTAGGCTCTACCTGGCTCTAAATACGACTCACTATAGGAGCTTCGAGATCTCTTA	60
Db	1	GTGCACCTCTAGGCTCTACCTGGCTCTAAATACGACTCACTATAGGAGCTTCGAGATCTCTTA	60
Oy	61	GTTGAAAAAACTTCTTTGACGCTGCTGCTGCTTTAAAGTCAATTTAACTAGTC	120
Db	61	GTTGAAAAAACTTCTTTGACGCTGCTGCTGCTTTAAAGTCAATTTAACTAGTC	120
Oy	121	ACATGTGATACACAATATATATATTGAAATGGAAATTAATCATATTAATGATTAGAT	180
Db	121	ACATGTGATACACAATATATATATTGAAATGGAAATTAATCATATTAATGATTAGAT	180
Oy	181	TAAATATATATACGCTGACATTACCAACCAATGTTTCTGCTTTATGAGTACGTTATAT	240
Db	181	TAAATATATATACGCTGACATTACCAACCAATGTTTCTGCTTTATGAGTACGTTATAT	240
Oy	241	GTTGCACCTGATTTATAGTACTATATATAACCTGGGTTATTTAAATCCGATCCCATAC	300
Db	241	GTTGCACCTGATTTATAGTACTATATATAACCTGGGTTATTTAAATCCGATCCCATAC	300
Oy	301	AAAAGTGAACCAAAACGAGATCCATGCTTTGTGTTTACTTTGTGTTGCTTAAACGATAT	360
Db	301	AAAAGTGAACCAAAACGAGATCCATGCTTTGTGTTTACTTTGTGTTGCTTAAACGATAT	360
Oy	361	ATGATTTATGGAAGATTAAATCTTTACTAAATTAATAAATTAATTTGAAAAACAACTTAA	420
Db	361	ATGATTTATGGAAGATTAAATCTTTACTAAATTAATAAATTAATTTGAAAAACAACTTAA	420
Oy	421	ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGATATCTCGTGTATCTCACTTGA	480
Db	421	ATATGTTGAGTGTCTTCACTGCTCACTGTTCAAGATATCTCGTGTATCTCACTTGA	480
Oy	481	CTAACAAGTTGATACATPAAACAGGTGAATTTTAAACGACCGTACATPAAACACATGAT	540
Db	481	CTAACAAGTTGATACATPAAACAGGTGAATTTTAAACGACCGTACATPAAACACATGAT	540


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Qy 541 CGATCAATACAAATTATAGACTAGAAATCCAGATGAGATGACTCAGAGAAATA 600
Db 541 CGATCAATAACAAATTATATAGACTAGAAATCCAGATGAGATGACTCAGAGAAATA 600
Qy 601 TACACAGCTAAGATTTGTACAGAGAGTCCGAAAAATAGATTCTATATCAATTTAAAAAGA 660
Db 601 TACACAGCTAAGATTTGTACAGAGAGTCCGAAAAATAGATTCTATATCAATTTAAAAAGA 660
Qy 661 TATGGAATTCAGTTACGGAATGATATTAACATTAACGAGTAGTACATACATAATTTTT 720
Db 661 TATGGAATTCAGTTACGGAATGATATTAACATTAACGAGTAGTACATACATAATTTTT 720
Qy 721 TGTTTTGTTTTACCAGATAAGAAATGTTGCTTAAAAATATGGTTTTACTTA 780
Db 721 TGTTTTGTTTTACCAGATAAGAAATGTTGCTTAAAAATATGGTTTTACTTA 780
Qy 781 AACTGTTTTATGTTAACTATATATGCTTCCGCAATGTAATTGAAACAAACGTGTA 840
Db 781 AACTGTTTTATGTTAACTATATATGCTTCCGCAATGTAATTGAAACAAACGTGTA 840
Qy 841 TACAAATTAATGTTAAGCCATTGCAATTAATAAAATCCAGGGTAGTAATCCTCAGAAAT 900
Db 841 TACAAATTAATGTTAAGCCATTGCAATTAATAAAATCCAGGGTAGTAATCCTCAGAAAT 900
Qy 901 TATGTTAAGTCTACAAATTTTCTCTTATAGATTAGTAAAGTTTGAACAAATTAATGTA 960
Db 901 TATGTTAAGTCTACAAATTTTCTCTTATAGATTAGTAAAGTTTGAACAAATTAATGTA 960
Qy 961 CCTTGACGGGGTATTAAGSTCACTGCAATGTCAGACTCAGCATGAGCCAAAGAGTGTG 1020
Db 961 CCTTGACGGGGTATTAAGSTCACTGCAATGTCAGACTCAGCATGAGCCAAAGAGTGTG 1020
Qy 1021 TCTGTCCTAAAGATATCTACAGCTGCTCCGCTGTGTAATAGAGAAATGAATGATGA 1080
Db 1021 TCTGTCCTAAAGATATCTACAGCTGCTCCGCTGTGTAATAGAGAAATGAATGATGA 1080
Qy 1081 GAGAATCCCATCTAGCCGTTTCACTGTTGCGTCTCCGTCGCAACTTTGGCGGTTGTACT 1140
Db 1081 GAGAATCCCATCTAGCCGTTTCACTGTTGCGTCTCCGTCGCAACTTTGGCGGTTGTACT 1140
Qy 1141 TTTTTCTTATGTCGTTGTTGACTAAATTTTCTCAGAGTGAAGTGTATCAAGAAACT 1200
Db 1141 TTTTTCTTATGTCGTTGTTGACTAAATTTTCTCAGAGTGAAGTGTATCAAGAAACT 1200
Qy 1201 AATATTCGAAAAAGAAAGAAAAAGGCAAGAAAACTATGTGCAAAAAGACATTAATGAC 1260
Db 1201 AATATTCGAAAAAGAAAGAAAAAGGCAAGAAAACTATGTGCAAAAAGACATTAATGAC 1260
Qy 1261 ACTTAAATTTGATATTAATAAATGATATATGTTGGTGAATTTATATCATTTACCAA 1320
Db 1261 ACTTAAATTTGATATTAATAAATGATATATGTTGGTGAATTTATATCATTTACCAA 1320
Qy 1321 AATCAAAAGAGAGAGAGGAGCTCTTCGTCCTATGATTTCCCTCTAAACAACTGCT 1380
Db 1321 AATCAAAAGAGAGAGAGGAGCTCTTCGTCCTATGATTTCCCTCTAAACAACTGCT 1380
Qy 1381 CCCAGCTATCCTTTTTTATCTTCCAAACAAATCATTCACAGAGAAATCTGTCTGTATC 1440
Db 1381 CCCAGCTATCCTTTTTTATCTTCCAAACAAATCATTCACAGAGAAATCTGTCTGTATC 1440
Qy 1441 ACTTTCAATGCAAAATTAACATAATTTTGGTATTTTGTCAAGTTCTGTCTGTTTTAG 1500
Db 1441 ACTTTCAATGCAAAATTAACATAATTTTGGTATTTTGTCAAGTTCTGTCTGTTTTAG 1500
Qy 1501 TCGATTTATTTGGTAACTATATGTTGATATACATCCAGCTATTCATATATGAT 1560
Db 1501 TCGATTTATTTGGTAACTATATGTTGATATACATCCAGCTATTCATATATGAT 1560
Qy 1561 CTCCTTGTCTTATCAATAATTAACACACATAGCTATCAAGCTATATTAATTAACCA 1620
Db 1561 CTCCTTGTCTTATCAATAATTAACACACATAGCTATCAAGCTATATTAATTAACCA 1620
Qy 1621 CATTCCTTATCAATTTTATATAGTATTAATAAAACAACGACTATATAGGCTACAGATT 1680
Db 1621 CATTCCTTATCAATTTTATATAGTATTAATAAAACAACGACTATATAGGCTACAGATT 1680

Qy 1621 CATTCCTTATCAATTTTATATAGTATTAATAAAACAACGACTATATAGGCTACAGATT 1680
Db 1621 CATTCCTTATCAATTTTATATAGTATTAATAAAACAACGACTATATAGGCTACAGATT 1680
Qy 1681 GGTATTAAGGCTATATGCTTCTAGTCAAGAGATTTTGTATGATTAACACTGTG 1740
Db 1681 GGTATTAAGGCTATATGCTTCTAGTCAAGAGATTTTGTATGATTAACACTGTG 1740
Qy 1741 GGAATAAAATTCAGCTTAATATGCTCATTTAAAGATTAATGATTAAATGCTTAATCA 1800
Db 1741 GGAATAAAATTCAGCTTAATATGCTCATTTAAAGATTAATGATTAAATGCTTAATCA 1800
Qy 1801 TTAATAAAGGTTTTGCTTTTAAAGTTACACCGCTTAATTCATATAGAGAT 1860
Db 1801 TTAATAAAGGTTTTGCTTTTAAAGTTACACCGCTTAATTCATATAGAGAT 1860
Qy 1861 ATTAACCTTGATCCAAATTCCAAATATCTTTTAAACATTAAGAAATTTTCAGCATTT 1920
Db 1861 ATTAACCTTGATCCAAATTCCAAATATCTTTTAAACATTAAGAAATTTTCAGCATTT 1920
Qy 1921 TTAATAAAGGTTACATTTATGCGTCAATAATATGTTTCCAGTAAAGTTTGAGGT 1980
Db 1921 TTAATAAAGGTTACATTTATGCGTCAATAATATGTTTCCAGTAAAGTTTGAGGT 1980
Qy 1981 TTAACCAATGAATTTTTTGAATTTAAAAACAATTAATTTCTGTAATTAACAATT 2040
Db 1981 TTAACCAATGAATTTTTTGAATTTAAAAACAATTAATTTCTGTAATTAACAATT 2040
Qy 2041 TTTAACCGTCCATCCAGATGTAATTAAGTGAACAATCTGAAACATTTTTTTTTCTTG 2100
Db 2041 TTTAACCGTCCATCCAGATGTAATTAAGTGAACAATCTGAAACATTTTTTTTTCTTG 2100
Qy 2101 AATCTGTTTAAATTCCTCTGCTGCAATCTTGCAAGCATTTGACAAACGATTAACATA 2160
Db 2101 AATCTGTTTAAATTCCTCTGCTGCAATCTTGCAAGCATTTGACAAACGATTAACATA 2160
Qy 2161 TTGAAAGCAAAATTAACAACAGGAGTAGTAGGGTTAGATCCCAATCAATCTTTTGT 2220
Db 2161 TTGAAAGCAAAATTAACAACAGGAGTAGTAGGGTTAGATCCCAATCAATCTTTTGT 2220
Qy 2221 CTTTGTATTTATGAAAAACAATATTTATCAGAAAAAAACGTTCTTCTAGTGTGA 2280
Db 2221 CTTTGTATTTATGAAAAACAATATTTATCAGAAAAAAACGTTCTTCTAGTGTGA 2280
Qy 2281 TAAATTAAGATTAATTAACAAATTTAATTAATTAATTAATTAATTAATTAATTAATTA 2340
Db 2281 TAAATTAAGATTAATTAACAAATTTAATTAATTAATTAATTAATTAATTAATTAATTA 2340
Qy 2341 ACCATCCTTCAACATTAATTAATTAATTAATTTTATTTTACTAATAACTTCCAATA 2400
Db 2341 ACCATCCTTCAACATTAATTAATTAATTAATTTTATTTTACTAATAACTTCCAATA 2400
Qy 2401 AAAAAATGCAAAAGAGAGATATATTTTAAGTCAAGTAATTAAGATGAGGTGAT 2460
Db 2401 AAAAAATGCAAAAGAGAGATATATTTTAAGTCAAGTAATTAAGATGAGGTGAT 2460
Qy 2461 TCTTCAACAAACGCGCGGTAGAGGTCTTAATCTTACATTAACAGCTGGGTTGTGAG 2520
Db 2461 TCTTCAACAAACGCGCGGTAGAGGTCTTAATCTTACATTAACAGCTGGGTTGTGAG 2520
Qy 2521 ACATCATAGGCGCTACATTAATTTGAGCTTTACGTATACGTAAAGCTTTAACAATCTAGT 2580
Db 2521 ACATCATAGGCGCTACATTAATTTGAGCTTTACGTATACGTAAAGCTTTAACAATCTAGT 2580
Qy 2581 TAGTTCTCATCTGTAACAACAAACAAATCAATTCGTAACATATATACAAATCTACTA 2640
Db 2581 TAGTTCTCATCTGTAACAACAAACAAATCAATTCGTAACATATATACAAATCTACTA 2640
Qy 2641 GTAATGATTAAGCTATGATTAATCAATCGTTTTTGCAAATTTCTAAATCTATACAA 2700
Db 2641 GTAATGATTAAGCTATGATTAATCAATCGTTTTTGCAAATTTCTAAATCTATACAA 2700
Qy 2701 CAAACTGAATGTTTGTGTTGTAATTAATCTTAAACAAAGTTTGAATGTGATGGG 2760
Db 2701 CAAACTGAATGTTTGTGTTGTAATTAATCTTAAACAAAGTTTGAATGTGATGGG 2760
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Db      2701 CAAACTGAAATGTTGTTTGTAAATTAATCTAAACCAAGTTTGAATTCATTCGGG 2760
Qy      2761 AGCTACCTGAGCCCTTTTCCCAAAATATCTCCTACATCGACCGGTAAAGT 2820
Db      2761 AGCTACCTGAGCCCTTTTCCCAAAATATCTCCTACATCGACCGGTAAAGT 2820
Qy      2821 ATTTAAACCAACAAATTTTAATTTGTTGTCGAAGGTACAAACATGTCATATATAGAGA 2880
Db      2821 ATTTAAACCAACAAATTTTAATTTGTTGTCGAAGGTACAAACATGTCATATATAGAGA 2880
Qy      2881 CAGCATGCTTAAATCAAAATATGTTGATGTTATGGAATCAATATTAATACGAATTA 2940
Db      2881 CAGCATGCTTAAATCAAAATATGTTGATGTTATGGAATCAATATTAATACGAATTA 2940
Qy      2941 GGCACCTACTGGTTTAATGTTTGAAGATTAATGAATTAATGAATTCAGAGATA 3000
Db      2941 GGCACCTACTGGTTTAATGTTTGAAGATTAATGAATTAATGAATTCAGAGATA 3000
Qy      3001 CAGAGCTATATATGTCGGGTCAATTAAGACCGTGACCAAAAGTTTCTGCTAAATTTCTAC 3060
Db      3001 CAGAGCTATATATGTCGGGTCAATTAAGACCGTGACCAAAAGTTTCTGCTAAATTTCTAC 3060
Qy      3061 GGTGCGTCATAGAAATTTGGAATTTCTTCAACCTTTATGAACTTCTGTATAGTTT 3120
Db      3061 GGTGCGTCATAGAAATTTGGAATTTCTTCAACCTTTATGAACTTCTGTATAGTTT 3120
Qy      3121 TGTGCGATTAATATTTGTAATTTGTAATTTTGTCTTAATTAAGATACGAATTC 3180
Db      3121 TGTGCGATTAATATTTGTAATTTGTAATTTTGTCTTAATTAAGATACGAATTC 3180
Qy      3181 CGATTAAGAAAGACTCTCTTTTAAATTTAAATTTGATTTAAACCTTTGTTTGAAGTACT 3240
Db      3181 CGATTAAGAAAGACTCTCTTTTAAATTTAAATTTGATTTAAACCTTTGTTTGAAGTACT 3240
Qy      3241 CATACACAGGTTAAAGTTGATGATATCCAAATTTACAAAATGTTTGAAGTGGTTC 3300
Db      3241 CATACACAGGTTAAAGTTGATGATATCCAAATTTACAAAATGTTTGAAGTGGTTC 3300
Qy      3301 GAGTGTCTTACCAACATCGTACCAACATCGTATGGGTTATTAATGTTTCTTCTT 3360
Db      3301 GAGTGTCTTACCAACATCGTACCAACATCGTATGGGTTATTAATGTTTCTTCTT 3360
Qy      3361 TTTCCATGCTTTATTAATTTGAACCACTAAATTTCTTTTAAATTTAGTTAAGAAAT 3420
Db      3361 TTTCCATGCTTTATTAATTTGAACCACTAAATTTCTTTTAAATTTAGTTAAGAAAT 3420
Qy      3421 CTGGAATTTCTGTGATTTTAAACCAAGGTTTCAATCTTCTTACCAAAAAAAA 3480
Db      3421 CTGGAATTTCTGTGATTTTAAACCAAGGTTTCAATCTTCTTACCAAAAAAAA 3480
Qy      3481 AAAAGGTTTCAATTTAAAGATCAATTTTGAAGTTCAAGTTTAAGATAGCT 3540
Db      3481 AAAAGGTTTCAATTTAAAGATCAATTTTGAAGTTCAAGTTTAAGATAGCT 3540
Qy      3541 GAAAAGTTAATGATTTGCAAGTTTGCAACAGATGATGATATATCAAAA 3600
Db      3541 GAAAAGTTAATGATTTGCAAGTTTGCAACAGATGATGATATATCAAAA 3600
Qy      3601 CATGCAATCAAAATTAATTTCTGCTTACAGAGAAACGATGAATTAACGAACAAT 3660
Db      3601 CATGCAATCAAAATTAATTTCTGCTTACAGAGAAACGATGAATTAACGAACAAT 3660
Qy      3661 CAGTCAATCAAAATTAATTTCTGCTTACAGAGAAACGATGAATTAACGAACAAT 3720
Db      3661 CAGTCAATCAAAATTAATTTCTGCTTACAGAGAAACGATGAATTAACGAACAAT 3720
Qy      3721 TATCATATCTTACAAAAAACTCATTTGATTAATTAATGTTGCTCATGCTTACCA 3780
Db      3721 TATCATATCTTACAAAAAACTCATTTGATTAATTAATGTTGCTCATGCTTACCA 3780
Qy      3781 AGTATGTTTGTGCTCATGATGTTGATGTAATCTGCTCTTACCATATAGTTCTAAG 3840
Db      3781 AGTATGTTTGTGCTCATGATGTTGATGTAATCTGCTCTTACCATATAGTTCTAAG 3840

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Qy      3841 TTTTAAATGTTTCAAGAATTACAAAAATAAATTAATTAAGGTGAATTTGTAGGG 3900
Db      3841 TTTTAAATGTTTCAAGAATTACAAAAATAAATTAATTAAGGTGAATTTGTAGGG 3900
Qy      3901 CTAAAAACGAAAAATTAATAATTAATAATTAATAAGTAAAGAAAGTCTTCTCAATAGAAC 3960
Db      3901 CTAAAAACGAAAAATTAATAATTAATAATTAATAAGTAAAGAAAGTCTTCTCAATAGAAC 3960
Qy      3961 AGATCCCAACGAAATTAACCAAGCAATTTGTGTTGCTTCTTCTTATTAATATC 4020
Db      3961 AGATCCCAACGAAATTAACCAAGCAATTTGTGTTGCTTCTTCTTATTAATATC 4020
Qy      4021 CTCTCAAAAAACCTCTCTATATCTCTTAAGACCCCTTCTCTGTTTCTTACGCGAA 4080
Db      4021 CTCTCAAAAAACCTCTCTATATCTCTTAAGACCCCTTCTCTGTTTCTTACGCGAA 4080
Qy      4081 CAAAGAAAAACAAAGTTTGAAGAAAAATGTTGTTGCTTGTGTAACCAATGATGGGT 4140
Db      4081 CAAAGAAAAACAAAGTTTGAAGAAAAATGTTGTTGCTTGTGTAACCAATGATGGGT 4140
Qy      4141 TTTAGCTTACTTCTGAGAGATTAATAGAAAAAGTGAAGATTCATTAATAGAAAGA 4200
Db      4141 TTTAGCTTACTTCTGAGAGATTAATAGAAAAAGTGAAGATTCATTAATAGAAAGA 4200
Qy      4201 AGAGAGCAGAAACCAAAAAAGAAACC 4228
Db      4201 AGAGAGCAGAAACCAAAAAAGAAACC 4228

RESULT 3
ID      AAAS9221
AAAS9221 standard; cDNA; 4227 BP.
XX
XX      AAAS9221;
XX
XX      07-NOV-2000 (first entry)
XX
XX      Promoter sequence of the Arabidopsis aintegumenta (ANT) gene.
XX
XX      Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;
XX      asexual reproduction; plant; male sterile plant; female sterile plant;
XX      early flowering; promoter; ss.
XX
XX      Arabidopsis sp.
XX
XX      WO200040694-A2.
XX
XX      13-JUL-2000.
XX
XX      07-JAN-2000; 2000WC-US000465.
XX
XX      08-JAN-1999; 99US-00227421.
XX
XX      (REGC ) UNIV CALIFORNIA.
XX
XX      Fischer RL, Mizukami Y;
XX
XX      WPI; 2000-465969/40.
XX
XX      Modulating growth and cell proliferation in a plant used to alter organ
XX      mass, control fertility and enhance asexual reproduction in plants
XX      comprises modulating ANT activity and selecting plants with altered cell
XX      number.
XX
XX      Claim 4; Page 41-43; 54p; English.
XX
XX      The present sequence represents a promoter of an aintegumenta (ANT) gene.
XX      The ANT gene is expressed and functions not only in developing ovaries but
XX      also in various developing organs. Growth and cell proliferation in plant
XX      can be modulated by modulating ANT activity. Modulation of ANT activity
XX      is used to alter organ mass, control fertility and enhance asexual
XX      reproduction in plants. Increased ANT activity can be used to produce

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CC male or female sterile plants. Inhibition of AMT activity can be used to
CC truncate vegetative growth, resulting in early flowering

XX Sequence 4227 BP; 1488 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;

Query Match 97.1%; Score 4107; DB 3; Length 4227;

Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Indels 1; Gaps 1;
Matches 4227; Conservative 0;

QY 1 GTGACTCTAGGCTCACTGGCCCTAATACGACTCATAATGAGAGCTGAGATCTTTA 60
DB 1 GTGACTCTAGGCTCACTGGCCCTAATACGACTCATAATGAGAGCTGAGATCTTTA 60
QY 61 GTTAGAAAAAATCTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 GTTAGAAAAAATCTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ACATGATATCAATCAAT 180
DB 121 ACATGATATCAATCAAT 180
QY 181 TAATATATATACGTGACATTAACCAACCAATGTTCTGTTTATGATAGTCTATAT 240
DB 181 TAATATATATACGTGACATTAACCAACCAATGTTCTGTTTATGATAGTCTATAT 240
QY 241 GTTGCACTGAT 300
DB 241 GTTGCACTGAT 300
QY 301 AAAAGTGAACCAAAAGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 AAAAGTGAACCAAAAGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 ATGATATATGAAAGATTAATCTTACTAAATATATATATATATATATATATATATAT 420
DB 361 ATGATATATGAAAGATTAATCTTACTAAATATATATATATATATATATATATATAT 420
QY 421 ATATGTTGAGTCTTCACTGCTCACTGTTCAAGATATATCTGTTTATCTTACTTGA 480
DB 421 ATATGTTGAGTCTTCACTGCTCACTGTTCAAGATATATCTGTTTATCTTACTTGA 480
QY 481 CTGAGATGAT 540
DB 481 CTGAGATGAT 540
QY 541 CGATCAAAATCAAAATTTATATATATATATATATATATATATATATATATATATAT 600
DB 541 CGATCAAAATCAAAATTTATATATATATATATATATATATATATATATATATATAT 600
QY 601 TACAAGCTAAGATTTTGAACAAGAGTGGAAAAATATATATATATATATATATATAT 660
DB 601 TACAAGCTAAGATTTTGAACAAGAGTGGAAAAATATATATATATATATATATATAT 660
QY 661 TATGATTTTGAATGAGATTTGATATATATATATATATATATATATATATATATAT 720
DB 661 TATGATTTTGAATGAGATTTGATATATATATATATATATATATATATATATATAT 720
QY 721 TGTGTTTGTGTTTCCGAT 780
DB 721 TGTGTTTGTGTTTCCGAT 780
QY 781 AACTCGTTTATGTTAAT 840
DB 781 AACTCGTTTATGTTAAT 840
QY 841 TACAAATTAATGTTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAG 900
DB 841 TACAAATTAATGTTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAGCAATTAAG 900
QY 901 TATGTTAAGTCAAT 960
DB 901 TATGTTAAGTCAAT 960

QY 961 CTTTGAGGGGATATTAAGGTCACTGATAGTCAAGCTCAGCATGAAAGCAAGAGTGTG 1020
DB 961 CTTTGAGGGGATATTAAGGTCACTGATAGTCAAGCTCAGCATGAAAGCAAGAGTGTG 1020
QY 1021 TCTGTCTTAAGATATATCAAGCTGTGCTGCTGTGATATAGAAAGAAATTTGATATGA 1080
DB 1021 TCTGTCTTAAGATATATCAAGCTGTGCTGCTGTGATATAGAAAGAAATTTGATATGA 1080
QY 1081 GAGATCCCATATAGCGTTTCAAGTTTGCCTTCTGCTGCAACTTTGGCGTGTGACT 1140
DB 1081 GAGATCCCATATAGCGTTTCAAGTTTGCCTTCTGCTGCAACTTTGGCGTGTGACT 1140
QY 1141 TTTTCTTATATGCTGT 1200
DB 1141 TTTTCTTATATGCTGT 1200
QY 1201 AATATTCGAAAAAGAAAGAAAAAGCAAGAAACATATGCGAAAGACATTAATGAC 1260
DB 1201 AATATTCGAAAAAGAAAGAAAAAGCAAGAAACATATGCGAAAGACATTAATGAC 1260
QY 1261 ACTTAAATGATATATTAATTAATGATATATATATATATATATATATATATATAT 1320
DB 1261 ACTTAAATGATATATTAATTAATGATATATATATATATATATATATATATATAT 1320
QY 1321 AATCAAGAAAGAGAGAGGACCTCTGCTGCTATATATATATATATATATATATATAT 1380
DB 1321 AATCAAGAAAGAGAGAGGACCTCTGCTGCTATATATATATATATATATATATATAT 1380
QY 1381 CCCGATCTCTTTTACTTCAACAAATCATTCACAGAGAAATCTGCTGATG 1440
DB 1381 CCCGATCTCTTTTACTTCAACAAATCATTCACAGAGAAATCTGCTGATG 1440
QY 1441 ACTTCATGCAAAATTAATTAATTTGTGATATATATATATATATATATATATATAT 1500
DB 1441 ACTTCATGCAAAATTAATTAATTTGTGATATATATATATATATATATATATATAT 1500
QY 1501 TCGATTTATTTGAT 1560
DB 1501 TCGATTTATTTGAT 1560
QY 1561 CTCCTGCTGTTATCAATTAATTAATCAACACATTAAGTATCAAGCTATTAATTAACCA 1620
DB 1561 CTCCTGCTGTTATCAATTAATTAATCAACACATTAAGTATCAAGCTATTAATTAACCA 1620
QY 1621 CATCTCTTATCAATTTTAT 1680
DB 1621 CATCTCTTATCAATTTTAT 1680
QY 1681 GGTATTAAGCATTTATGCTCTTATGCTGAGAGAAATTTTGTATATATATATATAT 1740
DB 1681 GGTATTAAGCATTTATGCTCTTATGCTGAGAGAAATTTTGTATATATATATATAT 1740
QY 1741 GGAAGAAAAATCAAGCTTATATATATATATATATATATATATATATATATATATAT 1800
DB 1741 GGAAGAAAAATCAAGCTTATATATATATATATATATATATATATATATATATATAT 1800
QY 1801 TTAATAATTAAGGTTTGTCTTTTAAAGTTTAAAGCAAGCTTAAATCAATTAAGAGAT 1860
DB 1801 TTAATAATTAAGGTTTGTCTTTTAAAGTTTAAAGCAAGCTTAAATCAATTAAGAGAT 1860
QY 1861 ATTAACCTTATGATGAATTTCCAAATATCTTTTAAACATTAAGAAATTTTTCAGCAT 1920
DB 1861 ATTAACCTTATGATGAATTTCCAAATATCTTTTAAACATTAAGAAATTTTTCAGCAT 1920
QY 1921 TTAATAATTAAGGTTTAT 1980
DB 1921 TTAATAATTAAGGTTTAT 1980
QY 1981 TTAACACATGAATGTTTAT 2040
DB 1981 TTAACACATGAATGTTTAT 2040
QY 2041 TTTAACCGTCAATCAGATTTGATATATATATATATATATATATATATATATATATAT 2100

Db 2041 TTTTACGCTCCACAGATGTATTAAGTACAAATCGAAAACTTTTTTTTTCTTG 2100
Qy 2101 AATCTGTTAAATTCCTGCTGCATCTACTGACGCACTTTCACCAAGACATATACATA 2160
Db 2101 AATCTGTTT-AAATCTCTGCTGCATCTTGGACGCAATTCGACCAACACATACATA 2159
Qy 2161 TTGAAAGCAAAATATCCACGAGGATGATAGGTTAGATCCCACTCAATATCTTTGT 2220
Db 2160 TTGAAAGCAAAATATCCACGAGGATGATAGGTTAGATCCCACTCAATATCTTTGT 2219
Qy 2221 CTTTGTATTATGAAAAAATAATTTATCAGAAAAAAACGTTCTCTAGTGTGA 2280
Db 2220 CTTTGTATTATGAAAAAATAATTTATCAGAAAAAAACGTTCTCTAGTGTGA 2279
Qy 2281 TAAGTATTAAGTAAATAAATAATTTAACTAGTTAAATGTAATTTACTATCTTCAACT 2340
Db 2280 TAAGTATTAAGTAAATAAATAATTTAACTAGTTAAATGTAATTTACTATCTTCAACT 2339
Qy 2341 ACCATCCTTCAACATTAATATTTGATCAATTTTTTATTTTTTACTAACTACTCCACTA 2400
Db 2340 ACCATCCTTCAACATTAATATTTGATCAATTTTTTATTTTTTACTAACTACTCCACTA 2399
Qy 2401 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAATTAATTAAGATGATGGGTGAT 2460
Db 2400 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAATTAATTAAGATGATGGGTGAT 2459
Qy 2461 TCTTCAGCAAAAGGGCGGTAGAGGTCTTATCCCACTTACAGTGGGTGTGCAG 2520
Db 2460 TCTTCAGCAAAAGGGCGGTAGAGGTGTCTTATCCCACTTACAGTGGGTGTGCAG 2519
Qy 2521 ACATCATAGGGCTTACGTATATTTGAGCTTTACTGTACGTAAAGCTTTACATATCTAGT 2580
Db 2520 ACATCATAGGGCTTACGTATATTTGAGCTTTACTGTACGTAAAGCTTTACATATCTAGT 2579
Qy 2581 TAGTTCTACTGTACAAACAAACAAATCGAATTCGTAATATATACAAATACACTA 2640
Db 2580 TAGTTCTACTGTACAAACAAACAAATCGAATTCGTAATATATACAAATACACTA 2639
Qy 2641 GATCTAGATTAGGCTACGTATACATGCTTTTCGCAAAATTTCTAACTATCTATACAA 2700
Db 2640 GATCTAGATTAGGCTACGTATACATGCTTTTCGCAAAATTTCTAACTATCTATACAA 2699
Qy 2701 CAAACTGGAATGTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTGGG 2760
Db 2700 CAAACTGGAATGTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTGGG 2759
Qy 2761 AGCTACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATCGACCGGTTAAAGT 2820
Db 2760 AGCTACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATCGACCGGTTAAAGT 2819
Qy 2821 AATTTAAACCAACAAATTTTAAATTTGTCGGAAGTACAAACATGTCACTATATAGAGA 2880
Db 2820 AATTTAAACCAACAAATTTTAAATTTGTCGGAAGTACAAACATGTCACTATATAGAGA 2879
Qy 2881 CAGCATCGTTTATACAAATGATGTCGATGTTTGAAGATCAAAATTAATTCGAATTA 2940
Db 2880 CAGCATCGTTTATACAAATGATGTCGATGTTTGAAGATCAAAATTAATTCGAATTA 2939
Qy 2941 GCGACTCACTGGTTTAAATAGTTTGAAGATTAATGAAATGAAATTCAAAGAGATA 3000
Db 2940 GCGACTCACTGGTTTAAATAGTTTGAAGATTAATGAAATGAAATTCAAAGAGATA 2999
Qy 3001 CAGAGCTATATAGTGGGCTCATTTAGAGCGGTGACCAAAAGTTTGGTGTATATTTCTAC 3060
Db 3000 CAGAGCTATATAGTGGGCTCATTTAGAGCGGTGACCAAAAGTTTGGTGTATATTTCTAC 3059
Qy 3061 GGTGCGTCAATAGAAATTTTGAATTTCTTCAACCTTTATGAACTTCGTATAGTTT 3120
Db 3060 GGTGCGTCAATAGAAATTTTGAATTTCTTCAACCTTTTATGAACTTCGTATAGTTT 3119
Qy 3121 TGTGGAATTAATATATTTGTAATTCGTATATTTTGTCTAATATGATACGTAAATTC 3180

Db 3120 TGTGGAATTAATATATTTGTAATTCGTATATTTTGTCTAATATGATACGTAAATTC 3179
Qy 3181 CGATTAAGAAAGACTTCCTTTTATTTATTTGATTTTAAACCTTTGTTTGGAAATGACT 3240
Db 3180 CGATTAAGAAAGACTTCCTTTTATTTATTTGATTTTAAACCTTTTGTGGAATGACT 3239
Qy 3241 CATACACAAGGTTAAAGTTGATGATCCAAATTTTACAAAAATGTTTCGAGTGCCTTC 3300
Db 3240 CATACACAAGGTTAAAGTTTGAATGTATCCAAATTTTCAAAAAATGTTTCGAGTGCCTTC 3299
Qy 3301 GAGTGTCTTACCAACCATCGTACCACTCGTATGGGTTATATTTAGGTTTCTTCTT 3360
Db 3300 GAGTGTCTTACCAACCATCGTACCACTCGTATGGGTTATATTTAGGTTTCTTCTT 3359
Qy 3361 TTTCCAAATGCTTTATATATGAAACAATCTAAATCTTTTAAATGATGTTAAGAT 3420
Db 3360 TTTCCAAATGCTTTATATATGAAACAATCTAAATCTTTTAAATGATGTTAAGAT 3419
Qy 3421 CTTGAAATTTCTGTTGATTTTAAACCAAGTTTTCATCTCTTACCAAAAAAATA 3480
Db 3420 CTTGAAATTTCTGTTGATTTTAAACCAAGTTTTCATCTCTTACCAAAAAAATA 3479
Qy 3481 AAAAGTTTCAATTTATTAAGATCTAAATTTTGTAGTTCAAGATTATGATAGCT 3540
Db 3480 AAAAGTTTCAATTTATTAAGATCTAAATTTTGTAGTTCAAGATTATGATAGCT 3539
Qy 3541 GAAAGTTTAAATGATGATGCAAGTTTGCAACGAATGTTGATGATATATCAATA 3600
Db 3540 GAAAGTTTAAATGATGATGCAAGTTTGCAACGAATGTTGATGATATATCAATA 3599
Qy 3601 CATGATCAAAATTAATAATTCGTCTTACGAGAGAAACGATTTGAAATTAACAGAACAT 3660
Db 3600 CATGATCAAAATTAATAATTCGTCTTACGAGAGAGAACGATTTGAAATTAACAGAACAT 3659
Qy 3661 CGTTAACCTTAAATCTTAAATATTTTGTAGTATATTTTCTGTAAGAGAGG 3720
Db 3660 CGTTAACCTTAAATCTTAAATATTTTGTAGTATATTTTCTGTAAGAGAGG 3719
Qy 3721 TATCATATCTTACAAAAAAACCTCAATTCAGATAAAATATGTTGCCAATGTTACCA 3780
Db 3720 TATCATATCTTACAAAAAAACCTCAATTCAGATAAAATATGTTGCCAATGTTACCA 3779
Qy 3781 AGTATGTTTTGTGTCATCAGTTGTATGTAATCTGTCCTTACGCATATAGTTCTAAG 3840
Db 3780 AGTATGTTTTGTGTCATCAGTTGTATGTAATCTGTCCTTACGCATATAGTTCTAAG 3839
Qy 3841 TTTTAAATGTTTCAAAAGCTTTCAAAAAATTAATATATATAGGTGAAATTTGAGGG 3900
Db 3840 TTTTAAATGTTTCAAAAGCTTTCAAAAAATTAATATATATAGGTGAAATTTGAGGG 3899
Qy 3901 CTAAAGCGAAAAATTAATAATAATAAAGTAAAGAAACGCTTCTCAATTAAGAAC 3960
Db 3900 CTAAAGCGAAAAATTAATAATAATAAAGTAAAGAAACGCTTCTCAATTAAGAAC 3959
Qy 3961 AGATCCCAACGATTCAAACAGCAAAATTTGTGCTTCTCTCTTATTAATATC 4020
Db 3960 AGATCCCAACGATTCAAACAGCAAAATTTGTGCTTCTCTCTTATTAATATC 4019
Qy 4021 CTCTCAAAAAACCTCTCTATATCTCTTAAAGCCCCCTCTCTGTTTCTTACCGCAA 4080
Db 4020 CTCTCAAAAAACCTCTCTATATCTCTTAAAGCCCCCTCTCTGTTTCTTACCGCAA 4079
Qy 4081 CAAAGAAAAACAAAGTTTGAAGAAATGAGTGTCTGTTGTGTAACCAATATGGGGT 4140
Db 4080 CAAAGAAAAACAAAGTTTGAAGAAATGAGTGTGTGTTGTGTAACCAATATGGGGT 4139
Qy 4141 TTTAGCTTACTCTTGAAGAGATTATAGAAAGAAAGAGTGAAGATCATATAGAAAGA 4200
Db 4140 TTTAGCTTACTCTTGAAGAGATTATAGAAAGAAAGAGTGAAGATCATATAGAAAGA 4199
Qy 4201 AGAGAAAGCAAAACCAAAAAAGAAAC 4228
Db 4200 AGAGAAAGCAAAACCAAAAAAGAAAC 4227

RESULT 4
ADG88432
ID ADG88432 standard; DNA; 4228 BP.
XX
AC ADG88432;
XX
DT 11-MAR-2004 (first entry)
XX
DE Arabidopsis thaliana aintegumenta (ANT) promoter DNA.
XX
KM Plant; genetic engineering; cell proliferation; aintegumenta; ANT;
KM transgenic; transgenic plant; organ mass alteration; fertility;
KM asexual reproduction; ds.
XX
OS Arabidopsis thaliana.
XX
PN US2003159180-A1.
XX
PD 21-AUG-2003.
XX
PF 28-JAN-2002; 2002US-00059911.
XX
PR 28-JAN-2002; 2002US-00059911.
XX
PA (REGC) UNIV CALIFORNIA OFFICE TECHNOLOGY.
XX
PI Fischer RL, Mizukami Y;
XX
PS WPI; 2003-787370/74.
XX
PT Increasing cell proliferation in a plant by introducing into the plant an
PT expression cassette containing a plant promoter operably linked to a
PT nucleic acid encoding a modified ANT polypeptide and selecting plants
PT with increased mass.
XX
PS Disclosure, SEQ ID NO 3; 51pp; English.
XX
CC The present invention relates to plant genetic engineering. The invention
CC particularly relates to a method of increasing cell proliferation in a
CC plant. The method involves introducing into the plant an expression
CC cassette containing a plant promoter operably linked to a nucleic acid
CC encoding a modified aintegumenta (ANT) polypeptide comprising an ANT AP2
CC domain and selecting plants the with increased size or mass. The
CC invention is useful to generate transgenic plants. The method is useful
CC for increasing cell proliferation in a plant for altering organ mass,
CC controlling fertility or enhancing asexual reproduction. The present
CC sequence is Arabidopsis thaliana ANT promoter DNA.
XX
SQ Sequence 4228 BP; 1488 A; 651 C; 643 G; 1446 T; 0 U; 0 Other;
Query Match 93.1%; Score 3936; DB 10; Length 4228;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 1; Indels 2; Gaps 2;
Matches 4228; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
QY 1 GTGACCTCTAGGCTCTGAGCTTAATGACATCACTATAGGAGCTGAGATCTTTA 60
DB 1 GTGACCTCTAGGCTCTGAGCTTAATGACATCACTATAGGAGCTGAGATCTTTA 60
QY 61 GTTAGAAAAAATTCTTTGAGCTGTGTGTGTTTAAAGTTCAATTATTAACCTAGTC 120
DB 61 GTTAGAAAAAATTCTTTGAGCTGTGTGTGTTTAAAGTTCAATTATTAACCTAGTC 120
QY 121 ACATGATATATCAATATATATATGAAATTGAAATTAATCATTAATGAGTTAGCAT 180
DB 121 ACATGATATATCAATATATATATGAAATTGAAATTAATCATTAATGAGTTAGCAT 180
QY 181 TAATATATATACGCTGACATTAACCAACCAATGTTTCTGCTTTATGATAGTTCTATAT 240
DB 181 TAATATATATACGCTGACATTAACCAACCAATGTTTCTGCTTTATGATAGTTCTATAT 240
QY 241 GTTGCACTGATTTATAGACTATATATAAACTGGGTTTATTTAAATCCGATACCAATAC 300

DB 241 GTTGCACTGATTTATAGACTATATATAAACTGGGTTTATTTAAATCCGATACCAATAC 300
QY 301 AAAAGTGACCAAAAAGAGATCCATGGTTTGTGTTTACTTTGTTGTTAAACGATATAT 360
DB 301 AAAAGTGACCAAAAAGAGATCCATGGTTTGTGTTTACTTTGTTGTTAAACGATATAT 360
QY 361 ATGATTTATGAAAGTTAAATCTTTATCAATATTAATAATTTGAAAAACAACCTTAA 420
DB 361 ATGATTTATGAAAGTTAAATCTTTATCAATATTAATAATTTGAAAAACAACCTTAA 420
QY 421 ATATGTTAGAGTGTCTTCACTGCTCACTGTTCAAGATATATCTCGTTTATCCCTACTGAA 480
DB 421 ATATGTTAGAGTGTCTTCACTGCTCACTGTTCAAGATATATCTCGTTTATCCCTACTGAA 480
QY 481 CTAGAAAGTTGATATACATTAACAGCTGAATATTTTAAAGACCGTATCAATTAACATGTTAT 540
DB 481 CTAGAAAGTTGATATACATTAACAGCTGAATATTTTAAAGACCGTATCAATTAACATGTTAT 540
QY 541 CGATCAAAATACAAATTTATATGAGACTAGAAATCCAGATGAGATGACTCTAGCAAGATA 600
DB 541 CGATCAAAATACAAATTTATATGAGACTAGAAATCCAGATGAGATGACTCTAGCAAGATA 600
QY 601 TACACAGCTAAGAAATTTGTACAAGAGAGTGAAGAAATATGATTTCAATCATTTAAAGAAAGA 660
DB 601 TACACAGCTAAGAAATTTGTACAAGAGAGTGAAGAAATATGATTTCAATCATTTAAAGAAAGA 660
QY 661 TATGATTTTCACTAGCTAGATGATATTAATCAATTAACGATAGTATCATATCAATATTTT 720
DB 661 TATGATTTTCACTAGCTAGATGATATTAATCAATTAACGATAGTATCATATCAATATTTT 720
QY 721 TGTGTTTGTGTTTACCGATTAATAGAAATGTTGTGTTTAAATATTTGTTTACTTAA 780
DB 721 TGTGTTTGTGTTTACCGATTAATAGAAATGTTGTGTTTAAATATTTGTTTACTTAA 780
QY 781 AACTCGTTTATGTTAATCTATATATATGATGCTTCCGATGTTAAATGAAACAAACCTGTA 840
DB 781 AACTCGTTTATGTTAATCTATATATATGATGCTTCCGATGTTAAATGAAACAAACCTGTA 840
QY 841 TACAAATTAATGTTAAGCATTTGCAATTAATAAATCCAGGGTATGTAATCTCAGAAAT 900
DB 841 TACAAATTAATGTTAAGCATTTGCAATTAATAAATCCAGGGTATGTAATCTCAGAAAT 900
QY 901 TATGTTAAGCTTACAAATTTTCTTTTATGATATGATAGTTTGAACAAATTAATGTTA 960
DB 901 TATGTTAAGCTTACAAATTTTCTTTTATGATATGATAGTTTGAACAAATTAATGTTA 960
QY 961 CCTTGACAGGGGTATTAAGGTCACTGACATGTCAGATCAGCATGAACCAAGAGTGTGC 1020
DB 961 CCTTGACAGGGGTATTAAGGTCACTGACATGTCAGATCAGCATGAACCAAGAGTGTGC 1020
QY 1021 TCTGTCTTAAAGATATCTACAGCTGCTTCCCTGTGATAGAGAAATTTGAATGATGA 1080
DB 1021 TCTGTCTTAAAGATATCTACAGCTGCTTCCCTGTGATAGAGAAATTTGAATGATGA 1080
QY 1081 GAGATCCCATCTAGCGTTTCAAGTTTCCGTTCCGTCGCAACTTGGCGGTTGTGACT 1140
DB 1081 GAGATCCCATCTAGCGTTTCAAGTTTCCGTTCCGTCGCAACTTGGCGGTTGTGACT 1140
QY 1141 TTTTCTTATATGCTGTTGTTTGAATATTTTCTCAAGTGAAGATGTAATCAAAAACT 1200
DB 1141 TTTTCTTATATGCTGTTGTTTGAATATTTTCTCAAGTGAAGATGTAATCAAAAACT 1200
QY 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATCTATTGTCGAAAGACATTAATGAC 1260
DB 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATCTATTGTCGAAAGACATTAATGAC 1260
QY 1261 ACTTAAATTTGATTTATTAATATATATATATATATATATATATATATATATATATAT 1320
DB 1261 ACTTAAATTTGATTTATTAAT 1320
QY 1321 AATCAAG 1380

Dp	1321	AATCAAGGAAGAGAGAGGGAGCTCTTCGTCGTTATGATTTCCCTCTTAACAACCTGCT	1380
Qy	1381	CCCACTATCCCTTTTATTACTTCCAACAAAATGATTCAACAAGAAATCTGCTCGTATC	1440
Dp	1381	CCCACTATCCCTTTTATTACTTCCAACAAAATGATTCAACAAGAAATCTGCTCGTATC	1440
Qy	1441	ACTTCATGCAAAATTAAACTTAAATTTTGGTATTTTGTCAAGTCTTGCTGTTTAAg	1500
Dp	1441	ACTTCATGCAAAATTAAACTTAAATTTTGGTATTTTGTCAAGTCTTGCTGTTTAAg	1500
Qy	1501	TGCAATTATGATTACTATATATGAGGATATACATATCAAGCTATCAATTAATGAT	1560
Dp	1501	TGCAATTATGATTACTATATATGAGGATATACATATCAAGCTATCAATTAATGAT	1560
Qy	1561	CTCCTCTGCTTATCAATAAATTACACAACATTAAGCTATCAAGCTATAAATACACA	1620
Dp	1561	CTCCTCTGCTTATCAATAAATTACACAACATTAAGCTATCAAGCTATAAATGAT	1620
Qy	1621	CATTCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGGCTACAGATT	1680
Dp	1621	CATTCTCTTATCAATTTTATATGATTAATAAACAACGACTATAGGCTACAGATT	1680
Qy	1681	GGTATTAAGGATATATGCGCTTACAGTGAAGAAATTTTGTATGATATACCTGCTg	1740
Dp	1681	GGTATTAAGGATATATGCGCTTACAGTGAAGAAATTTTGTATGATATACCTGCTg	1740
Qy	1741	GGAAAAAAATCAGCGCTTAATATGCTCATTTTAAAGATTAATGATTTAAATGCTTTAATCA	1800
Dp	1741	GGAAAAAAATCAGCGCTTAATATGCTCATTTTAAAGATTAATGATTTAAATGCTTTAATCA	1800
Qy	1801	TTAAATTAAGTTTTTGTCTTTTAAAGGTTACACGCTTAATCATATTAAGGAAT	1860
Dp	1801	TTAAATTAAGTTTTTGTCTTTTAAAGGTTACACGCTTAATCATATTAAGGAAT	1860
Qy	1861	ATTAACCTTGAATCGAAATTCGAAATACCTTTTAAACAATAAGAAATTTTCAGCATTT	1920
Dp	1861	ATTAACCTTGAATCGAAATTCGAAATACCTTTTAAACAATAAGAAATTTTTCAGCATTT	1920
Qy	1921	TTAATATAAGGGTACATTTATTTGGGTTCAATAATATATGTTCCAGTAAAGTTGGAAGT	1980
Dp	1921	TTAATATAAGGGTACATTTATTTGGGTTCAATAATATATGTTCCAGTAAAGTTGGAAGT	1980
Qy	1981	TTAAACAATGATTTTTTGAATTTAAAAACAATAAATTTTCTAGTATTAACAATT	2040
Dp	1981	TTAAACAATGATTTTTTGAATTTAAAAACAATAAATTTTCTAGTATTAACAATT	2040
Qy	2041	TTTAAACGTCATCCAGATTTGTATTAAGTGAACAATCTGAAACAATTTTTTTTTCTTG	2100
Dp	2041	TTTAAACGTCATCCAGATTTGTATTAAGTGAACAATCTGAAACAATTTTTTTTTCTTG	2100
Qy	2101	AATCTGTGTTAAATTCCTCTGCTGCAATCTGCAAGGATTTGACCAACGACTATACATA	2160
Dp	2101	AATCTGTGTTAAATTCCTCTGCTGCAATCTGCAAGGATTTGACCAACGACTATACATA	2160
Qy	2161	TTGAAGCAAAATATCCACAAGGATGATAGGTTAAGTCCACATTCATATCTTTTGT	2220
Dp	2161	TTGAAGCAAAATATCCACAAGGATGATAGGTTAAGTCCACATTCATATCTTTTGT	2220
Qy	2221	CTTTGTTATTTATGAAAAACAATTTTATCAGAAAAAAACGTTTCTTCTATAGTGTA	2280
Dp	2221	CTTTGTTATTTATGAAAAACAATTTTATCAGAAAAAAACGTTTCTTCTATAGTGTA	2280
Qy	2281	TAACTATTAAGTAAATAAATAAATTTAATCTAGTATGATTTTACATCTTCAAACTT	2340
Dp	2281	TAACTATTAAGTAAATAAATAAATTTAATCTAGTATGATTTTACATCTTCAAACTT	2340
Qy	2341	ACCATCTTCAACATTAATATTTGATTCATTTTTTTTTTTTAACTAATCTTCCACTA	2400
Dp	2341	ACCATCTTCAACATTAATATTTGATTCATTTTTTTTTTTTAACTAATCTTCCACTA	2400
Qy	2401	AAAAATGCAAAAGAGATATATATTTAAAGTCAAAAGTAAATTAAGATGAGTGGTAT	2460
Dp	2401	AAAAATGCAAAAGAGATATATATTTAAAGTCAAAAGTAAATTAAGATGAGTGGTAT	2460

QY	2461	TCCTCAGCAAAA	CGGCGCCCGTGAAGAGTGCTCTTAATCCATCAATTACAGCTGGGTGTGGCAG	2522
Dp	2461	TCCTCAGCAAAA	CGGCGCCCGTGAAGAGTGCTCTTAATCCATCAATTACAGCTGGGTGTGGCAG	2522
QY	2521	ACATCATAGGGCC	CTACGTAATATTGAGCTTACTGTACGTAAAGCTTAAACATATCTAGT	2580
Dp	2521	ACATCATAGGGCC	CTACGTAATATTGAGCTTACTGTACGTAAAGCTTAAACATATCTAGT	2580
QY	2581	TAGTTCCTCACTGTA	CAAAACAACAAATCCAAATTCGTATCATATATACAATACTACTA	2640
Dp	2581	TAGTTCCTCACTGTA	CAAAACAACAAATCCAAATTCGTATCATATATACAATACTACTA	2640
QY	2641	GTACTAGATTACGCT	AGTAATACATCGCTTTTGGCAAAATTTCTAACTATATAGCA	2700
Dp	2641	GTACTAGATTACGCT	AGTAATACATCGCTTTTGGCAAAATTTCTAACTATATAGCA	2700
QY	2701	CAAACTGAATGTTG	TTTTGTATTTATCTTAAACCAAGTTTGAATTGGCATTTGGG	2766
Dp	2701	CAAACTGAATGTTG	TTTTGTATTTATCTTAAACCAAGTTTGAATTGGCATTTGGG	2766
QY	2761	AGCTACACTCTAGT	CCCCCTTTTTTCCCCCAAAATATATCTCTTACATCGACCGGTAAAGT	2822
Dp	2761	AGCTACACTCTAGT	CCCCCTTTTTTCCCCCAAAATATATCTCTTACATCGACCGGTAAAGT	2822
QY	2821	ATTTTAAACCAACA	ATTTTAAATTTTATTTGTGTCGAAGGTACAAACATGTCCATATATAGAGA	2880
Dp	2821	ATTTTAAACCAACA	ATTTTAAATTTTATTTGTGTCGAAGGTACAAACATGTCCATATATAGAGA	2880
QY	2881	CAGCATGTTTATAT	CAATATATGTTGCATGTATTTGGAAATCAAAATATTAATAGCAATTA	2940
Dp	2881	CAGCATGTTTATAT	CAATATATGTTGCATGTATTTGGAAATCAAAATATTAATAGCAATTA	2940
QY	2941	GCGACTCACTGGT	TATATAGTTTGAAGATTAATGAATAAATAA - ATGAATTCAAAGAT	2999
Dp	2940	GCGACTCACTGGT	TATATAGTTTGAAGATTAATGAATAAATAAATAA - ATGAATTCAAAGAT	2999
QY	3000	ACAGAGCTATATAT	ATGTCGGGTCAATTAGAGCCGTACCAAAAGTTTCGTCTGTAAATTTCTA	3055
Dp	3000	ACAGAGCTATATAT	ATGTCGGGTCAATTAGAGCCGTACCAAAAGTTTCGTCTGTAAATTTCTA	3055
QY	3060	CGGTCCGCTCAT	TAAGAAATTTTGGACTTTTCTTCACCCCTTTTAATGAATTCGTGTATAGTT	3119
Dp	3060	CGGTCCGCTCAT	TAAGAAATTTTGGACTTTTCTTCACCCCTTTTAATGAATTCGTGTATAGTT	3119
QY	3120	TTGTGCGATTAT	ATATTTTGTATTCGTAAATATATATGATCGATAATTC	3179
Dp	3120	TTGTGCGATTAT	ATATTTTGTATTCGTAAATATATATGATCGATAATTC	3179
QY	3180	ACGATTAAGAAAG	ACTTCTTTTATTTATTTGATTTAAACTTTTGTTTTTGGAAATGAC	3239
Dp	3180	ACGATTAAGAAAG	ACTTCTTTTATTTATTTGATTTAAACTTTTGTTTTTGGAAATGAC	3239
QY	3240	TCATACACAAAG	TTAAAGTTTGAATGATCAATTTCAAAAAAGTTTCGAGAGTGCCTT	3299
Dp	3240	TCATACACAAAG	TTAAAGTTTGAATGATCAATTTCAAAAAAGTTTCGAGAGTGCCTT	3299
QY	3300	CGAGTGTCCATAC	CAACATCGCAATCGATGGGTTTATATATAGGTTTTTTTCTTCT	3359
Dp	3300	CGAGTGTCCATAC	CAACATCGCAATCGATGGGTTTATATATAGGTTTTTTTCTTCT	3359
QY	3360	TTTTCCAAATGCT	TTTAAATTTGAACCACTCTAAATTTCTTTTAAATTAATAGTTAAGAA	3419
Dp	3360	TTTTCCAAATGCT	TTTAAATTTGAACCACTCTAAATTTCTTTTAAATTAATAGTTAAGAA	3419
QY	3420	TCCTTGAATTTCT	GTGATTTTAAACCAAGTTTTCATTTCTTCTAGCACAAAAAAAA	3479
Dp	3420	TCCTTGAATTTCT	GTGATTTTAAACCAAGTTTTCATTTCTTCTAGCACAAAAAAAA	3479
QY	3480	AAAAAGTTTCAAT	TTTAAAGATCTAAATTTTGTGAGTTCAAGGTTTAAATATGATGAC	3539
Dp	3480	AAAAAGTTTCAAT	TTTAAAGATCTAAATTTTGTGAGTTCAAGGTTTAAATATGATGAC	3539

QY	3540	GGAAAGTTAAGATGATGCAAGATTTGCAACGAATGCTGAGTATACATTAACAA	3539
Ds	3540	TGAAAAGTTAAGATGATGCAAGATTTGCAACGAATGCTGAGTATACATTAACAA	3539
QY	3600	ACATGCATCAAAATTAATATTCGTCTAGCAAGAAACGATTGAATTAACGACAA	3659
Ds	3600	ACATGCATCAAAATTAATATTCGTCTAGCAAGAAACGATTGAATTAACGACAA	3659
QY	3660	TCGTTAACCACTTAAAAATCTTAGAATATTTGTAGTAAATTTCTGTAAAGAGAG	3719
Ds	3660	TCGTTAACCACTTAAAAATCTTAGAATATTTGTAGTAAATTTCTGTAAAGAGAG	3719
QY	3720	GTATCATATCTTACAAAAAAACATTCAGATTAATTAATATGTGTCCATCGTTACC	3779
Ds	3720	GTATCATATCTTACAAAAAAACATTCAGATTAATTAATATGTGTCCATCGTTACC	3779
QY	3780	AAGATATGTTTTGCGTCATCAGTTGATTTGTAATCGTCTTACGCAATATAGTTCTAA	3839
Ds	3780	AAGATATGTTTTGCGTCATCAGTTGATTTGTAATCGTCTCTTACGCAATATAGTTCTAA	3839
QY	3840	GTTTTAAATGTTTTCAAGACTTTACAAAAATAAATATAAAGTGAATTTGTAGG	3899
Ds	3840	GTTTTAAATGTTTTCAAGACTTTACAAAAATAAATATAAAGTGAATTTGTAGG	3899
QY	3900	GCTAAAGCGAAAAATTAATTAATTAAGTAAGAAAGCTCTTTCTCATTAAGAAC	3959
Ds	3900	GCTAAAGCGAAAAATTAATTAATTAAGTAAGAAAGCTCTTTCTCATTAAGAAC	3959
QY	3960	CAGATCCCAAGGATTCAAACAGCAAAATTTGTGCTTGTCTCTCTTATTAATAAT	4019
Ds	3960	CAGATCCCAAGGATTCAAACAGCAAAATTTGTGCTTGTCTCTCTTATTAATAAT	4019
QY	4020	CCTCTCAAAAAACCTCTCCTATATCTCCTTAAAGCCCCCTTCTCTTCTTACACGA	4079
Ds	4020	CCTCTCAAAAAACCTCTCCTATATCTCCTTAAAGCCCCCTTCTCTTCTTACACGA	4079
QY	4080	ACAAAGAAAAACAAAGTTTGAGAAAAATGGTGTGTTGTTGTGTAAACAAATATTTGGG	4139
Ds	4080	ACAAAGAAAAACAAAGTTTGAGAAAAATGGTGTGTTGTTGTGTAAACAAATATTTGGG	4139
QY	4140	TTTTAGCTTACTACTTGCAGAGATTATTAAGAAAGAAAGTGAGATACATTAATTAAG	4199
Ds	4140	TTTTAGCTTACTACTTGCAGAGATTATTAAGAAAGAAAGTGAGATACATTAATTAAG	4199
QY	4200	AAAGAAAGCAAAACCAAAAAAGAAAC	4228
Ds	4200	AAAGAAAGCAAAACCAAAAAAGAAAC	4228

	RESULT 5
XX	AAA59220
ID	AAA59220 standard; cDNA; 2148 BP.
XX	
AC	AAA59220;
XX	
DT	07-NOV-2000 (first entry)
XX	
DE	cDNA encoding an Arabidopsis aintegumenta (ANT) polypeptide.
XX	
KM	Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;
KW	asexual reproduction; plant; male sterile plant; female sterile plant;
XX	early flowering; sb.
XX	
OS	Arabidopsis sp.
XX	
FH	Key Location/Qualifiers
FT	CDS
FT	269..1936
FT	/+tag= a
XX	/product= "aintegumenta polypeptide"
PN	WO200040694-A2.
XX	
XX	
PD	13-JUL-2000.

XX 07-JAN-2000; 2000WO-US000465.
PP
XX
PR 08-JAN-1999; 99US-00227421.
XX
PA (REGC) UNIV CALIFORNIA.
XX
PI Fischer RL, Mizukami Y;
XX WPI: 2000-465969/40.
DR P-PADB; AAB07724.
XX
PT Modulating growth and cell proliferation in a plant used to alter organ mass, control fertility and enhance asexual reproduction in plants
PT comprises modulating ANT activity and selecting plants with altered cell number.
PT
XX
PS Claim 9; Page 40-41; 54pp; English.
XX

The present sequence encodes an aineugmenta (ANT) polypeptide. The ANT gene is expressed and functions not only in developing ovules but also in various developing organs. Growth and cell proliferation in plant can be modulated by modulating ANT activity. Modulation of ANT activity is used to alter organ mass, control fertility and enhance asexual reproduction in plants. Increased ANT activity can be used to produce male or female sterile plants. Inhibition of ANT activity can be used to truncate vegetative growth, resulting in early flowering

Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;

Query Match	6.3%;	Score 268;	DB 3;	Length 2148;
Best Local Similarity	100.0%;	Pred. No. 1,1e-97;		
Matches 268;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	3961	AGATCCCAACGAGATTCAACAGCAAAATTGTGCTTTGCTCTCTCTCTTAATTAATATTC	4020
Db	1	AGATCCCAACGAGATTCAACAGCAAAATTGTGCTTTGCTCTCTCTCTTAATTAATATTC	60
Qy	4021	CTTCGAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCCTGTTCCTTAACGGCAA	4080
Db	61	CTTCGAAAAACCCCTCTCTATATCTCTAAAGCCCCCTTCCTGTTCCTTAACGGCAA	120
Qy	4081	CAAGAAAAAACAATAATTGAGAAAAATGGTGTGTTGCTGTGTAACAATGATTTGGGT	4140
Db	121	CAAGAAAAAACAATAATTGAGAAAAATGGTGTGTTGCTGTGTAACAATGATTTGGGT	180
Qy	4141	TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGATGAAGATACATTATTAAGAAAG	4200
Db	181	TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGATGAAGATACATTATTAAGAAAG	240
Qy	4201	AGAGAAAGCAAGAAACCAAAAAAAGAAACC	4228
Db	241	AGAGAAAGCAAGAAACCAAAAAAAGAAACC	268

RESULT 6
ABX13437
ID ABX13437 standard; DNA; 2148 BP.
XX AC ABX13437;
XX AC
XX
DE 04-JUN-2003 (first entry)
XX
XX A. thaliana AINTEGUMENTA DNA corresponding to Genbank U40256.
XX
KM Expression cassette; transgenic; promoter; LOX5; plant; food production;
KM animal feed; seed; stress resistance; disease resistance; starch content;
KM lipid content; dormancy; fibre content; pharmaceutical production;
KM fine chemical production; sterile plant; vitamin; flavouring; perfume;
KM dye; cotyledon; embryonic tissue; stress factor; LOX; ds.
XX
XX Arabidopsis thaliana.
XX

PN DE10127882-A1.
XX 12-DEC-2002.
XX
XX 11-JUN-2001; 2001DE-01027882.
XX
XX 11-JUN-2001; 2001DE-01027882.
XX
XX (BADI) BASF PLANT SCI GMBH.
XX
XX Bischoff P, Feussner I, Loyal LP;
XX WPI; 2003-279966/28.
XX
XX Cassette for expressing transgene, useful e.g. in production of
PT pharmaceuticals and fine chemicals, contains promoter from the LoxS gene
PT of Arabidopsis, provides cotyledon-specific expression.
XX
XX Claim 5; Page; 28pp; German.
XX
XX This invention describes a novel cassette for the transgenic expression
CC of nucleic acid containing the promoter of the LoxS gene from Arabidopsis
CC thaliana or deletion variants of the LoxS promoter which are functionally
CC linked to the nucleic acid of the invention. The cassette is used to
CC prepare transgenic organisms, especially plants, for production of foods,
CC animal feeds, seeds (including those with increased resistance to stresses
CC and disease, altered starch/lipid contents or dormancy, or altered fibre
CC content), pharmaceuticals (especially antibodies, vaccines, enzymes and
CC pharmaceutical proteins) and fine chemicals (especially enzymes,
CC vitamins, amino acids, sugars, (un)saturated fatty acids, flavourings,
CC perfumes and dyes), also to produce sterile plants. The LoxS promoter
CC provides strong and specific expression in cotyledons and/or other early
CC embryonic tissues, so can degrade, or protect against, stress factors to
CC which these tissues are particularly sensitive. Since cotyledons are the
CC main storage organs of seeds, expressing transgenes in them produces
CC targeted increases/modifications in nutritional value. Expression in the
CC cotyledons is homogeneous, there are no side effects on other plant
CC organs (pollen) and the promoter is functional in a wide variety of
CC plants (ornamentals or crops). This sequence represents a nucleic acid
CC sequence associated with the Arabidopsis thaliana Lox gene described in
CC the disclosure of the invention
XX
XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
SQ
Query Match 6.3%; Score 268; DB 8; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.1e-97; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3961 AGATCCCAACGAGATTCAACAGCAAAATTTGCTTTCCTCTCTCTTATTATATATC 4020
DB 1 AGATCCCAACGAGATTCAACAGCAAAATTTGCTTTCCTCTCTCTTATTATATATC 60
QY 4021 CTCTCAAAAACCTCTCTCTATATCTCTTAAGCCCCCTTCTTGTTCCTTAACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTCTATCTCTTAAGCCCCCTTCTTGTTCCTTAACCGCAA 120
QY 4081 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGTTGCTTGTATCAATGTTGGGT 4140
DB 121 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGTTGCTTGTATCAATGTTGGGT 180
QY 4141 TTTAGCTTACTACTTCGAGAGATTATAGAAAGAAAGTGAATCATTTATGAAAGA 4200
DB 181 TTTAGCTTACTACTTCGAGAGATTATAGAAAGAAAGTGAATCATTTATGAAAGA 240
QY 4201 AGAGAACAGAAACCAAAAAAGAAACC 4228
DB 241 AGAGAACAGAAACCAAAAAAGAAACC 268
RESULT 7
ADG25135
ID ADG25135 standard; cDNA; 2148 BP.
XX

AC ADG25135;
XX
XX 26-FEB-2004 (first entry)
XX
XX Thalecress cDNA encoding Aintegumenta, ANT.
DE Thalecress; ss; gene; Aintegumenta; ANT; AP2 domain; plant; seed mass;
XX asexual reproduction; reduced fertility.
XX Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
FH CDS 269..1936
FT /*tag= a
FT /product= "Aintegumenta, ANT"
XX
XX US6639128-B1.
XX
XX 28-OCT-2003.
XX
XX 07-JAN-2000; 2000US-00479855.
XX
XX 08-JAN-1999; 99US-00227421.
XX
XX (NASC-) NAT SCI FOUND.
XX Fischer RL, Mizukami Y;
PI WPI; 2003-842795/78.
DR P-PSDB; ADG25136.
XX
XX New nucleic acid, useful in conferring desired traits on plants, such as
PT increased seed mass, asexual reproduction or reduced fertility.
XX
XX Example 1; SEQ ID NO 1; 25pp; English.
PS
XX
XX The invention relates to an isolated nucleic acid comprising a
CC polynucleotide encoding a polypeptide having at least 90% identity with
CC Canola Aintegumenta, ANT, (appearing as ADG25139) as determined using a
CC BLAST algorithm and comprising two AP2 domains. Also included are an
CC expression cassette comprising a plant promoter operably linked to a
CC heterologous polynucleotide encoding the polypeptide, a vector comprising
CC the expression cassette, a plant comprising the plant promoter operably
CC linked to the heterologous polynucleotide, a method of asexually
CC reproducing a plant and a method of reducing fertility in a plant. The
CC nucleic acid is useful in conferring desired traits on plants, such as
CC increased seed mass, asexual reproduction or reduced fertility. The
CC present sequence encodes Thalecress Aintegumenta, ANT.
XX
XX
SQ Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
Query Match 6.3%; Score 268; DB 10; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.1e-97; Indels 0; Gaps 0;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3961 AGATCCCAACGAGATTCAACAGCAAAATTTGCTTTCCTCTCTCTTATTATATATC 4020
DB 1 AGATCCCAACGAGATTCAACAGCAAAATTTGCTTTCCTCTCTCTTATTATATATC 60
QY 4021 CTCTCAAAAACCTCTCTCTATATCTCTTAAGCCCCCTTCTTGTTCCTTAACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTCTATCTCTTAAGCCCCCTTCTTGTTCCTTAACCGCAA 120
QY 4081 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGTTGCTTGTATCAATGTTGGGT 4140
DB 121 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGTTGCTTGTATCAATGTTGGGT 180
QY 4141 TTTAGCTTACTACTTCGAGAGATTATAGAAAGAAAGTGAATCATTTATGAAAGA 4200
DB 181 TTTAGCTTACTACTTCGAGAGATTATAGAAAGAAAGTGAATCATTTATGAAAGA 240
QY 4201 AGAGAACAGAAACCAAAAAAGAAACC 4228
XX

Db 241 AGAAGCAGAAACCAAAAAAGAAACC 268

RESULT 8
ADG88430
ID ADG88430 standard; cDNA; 2148 BP.
XX
XX ADG88430;
XX
XX 11-MAR-2004 (first entry)
XX
XX Arabidopsis thaliana aintegumenta (ANT) cDNA.
DE
XX plant; genetic engineering; cell proliferation; aintegumenta; ANT;
XX transgenic; transgenic plant; organ mass alteration; fertility;
XX asexual reproduction; gene; ss.
XX
XX Arabidopsis thaliana.
XX
XX
XX Key Location/Qualifiers
XX CDS 269..1936
XX FT /*tag= a
XX FT /product= "Arabidopsis thaliana ANT protein"
XX
XX US2003159180-A1.
XX
XX 21-AUG-2003.
XX
XX 28-JAN-2002; 2002US-00059911.
XX
XX 28-JAN-2002; 2002US-00059911.
XX
XX (REGC) UNIV CALIFORNIA OFFICE TECHNOLOGY.
XX
XX Fischer RL, Mizukami Y;
XX WPI; 2003-787370/74.
XX P-PSDB; ADG88431.
XX
XX Increasing cell proliferation in a plant by introducing into the plant an
XX expression cassette containing a plant promoter operably linked to a
XX nucleic acid encoding a modified ANT polypeptide and selecting plants
XX with increased mass.
XX
XX Example 1; SEQ ID NO 1; s1pp; English.
XX
XX The present invention relates to plant genetic engineering. The invention
XX particularly relates to a method of increasing cell proliferation in a
XX plant. The method involves introducing into the plant an expression
XX cassette containing a plant promoter operably linked to a nucleic acid
XX encoding a modified aintegumenta (ANT) polypeptide comprising an ANT AP2
XX domain and selecting plants the with increased size or mass. The
XX invention is useful to generate transgenic plants. The method is useful
XX for increasing cell proliferation in a plant for altering organ mass,
XX controlling fertility or enhancing asexual reproduction. The present
XX sequence is Arabidopsis thaliana ANT cDNA.
XX
XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
SQ
Query Match 6.3%; Score 268; DB 10; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3961 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATC 4020
Db 1 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATC 60
QY 4021 CTCGCAAAAACCTCTCTATATCTCTAAAGCCCCCTTCTGTTTCTTACCGCA 4080
Db 61 CTCGCAAAAACCTCTCTATATCTCTAAAGCCCCCTTCTGTTTCTTACCGCA 120
QY 4081 CAAAGAAAAACCAAAAGTTTGAAGAAAAATGCTGTTCTGTGTAAACATATGTTGGT 4140

Db 121 CAAAGAAAAACAAAGTTTGAGAAAAATGCTGTTCTGTGTAAACATATGTTGGT 180

QY 4141 TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGAGATGTAATTCATTATTAAGA 4200
Db 181 TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGAGATGTAATTCATTATTAAGA 240

QY 4201 AGAAGCAGAAACCAAAAAAGAAACC 4228
Db 241 AGAAGCAGAAACCAAAAAAGAAACC 268

RESULT 9
AEA17180
ID AEA17180 standard; cDNA; 2148 BP.
XX
XX AEA17180;
XX
XX 25-AUG-2005 (first entry)
XX
XX A. thaliana aintegumenta (ANT) cDNA, seq id 1.
XX
XX plant engineering; growth; cell proliferation; organ mass; fertility;
XX asexual reproduction; aintegumenta; ANT; plant; gene; ss.
XX
XX Arabidopsis thaliana.
XX
XX
XX Key Location/Qualifiers
XX CDS 269..1936
XX FT /*tag= a
XX FT /product= "aintegumenta protein"
XX
XX US2005132445-A1.
XX
XX 16-JUN-2005.
XX
XX 18-JUL-2003; 2003US-00623477.
XX
XX 07-JAN-2000; 2000US-00479855.
XX
XX (REGC) UNIV CALIFORNIA.
XX
XX Fischer RL, Mizukami Y;
XX WPI; 2005-424635/43.
XX P-PSDB; AEA17181.
XX
XX Modulating growth and cell proliferation in a plant, useful in plant
XX genetic engineering, comprises modulating aintegumenta (ANT) gene
XX activity and selecting plants with altered cell number.
XX
XX Claim 9; SEQ ID NO 1; 27pp; English.
XX
XX The invention relates to modulating growth and cell proliferation in a
XX plant comprising modulating aintegumenta (ANT) gene activity and
XX selecting plants with altered cell number. Further disclosed is a method
XX for directing expression of a heterologous nucleic acid in meristematic
XX cells of a plant. The method is useful in plant genetic engineering,
XX specifically for altering organ mass, controlling fertility and enhancing
XX asexual reproduction in plants. The current sequence represents A.
XX thaliana ANT cDNA.
XX
XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
SQ
Query Match 6.3%; Score 268; DB 14; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.1e-97;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3961 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATC 4020
Db 1 AGATCCCAAGGATTCAAAGCAAAATTTGCTTGTCTCTCTATTATATATC 60
QY 4021 CTCGCAAAAACCTCTCTATATCTCTAAAGCCCCCTTCTGTTTCTTACCGCA 4080

Db 61 CTCCTCAAAAACCTCTCTATATCTCTAATAGCCCCCTTCCCTGTTCTCTACCGCA 120
 QY 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGTGTGTCGTGTGTAACCAATGTTGGGT 4140
 Db 121 CAAAGAAAAACAAAGTTTGAGAAAAATGTGTGTCGTGTGTAACCAATGTTGGGT 180
 QY 4141 TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGAGATGAGATACATTATAGAAAGA 4200
 Db 181 TTTAGCTTACTACTTCGAGAGATTATTAAGAAAGAGATGAGATACATTATAGAAAGA 240
 QY 4201 AGAGAAAGCAAAACCAAAAAAGAAACC 4228
 Db 241 AGAGAAAGCAAAACCAAAAAAGAAACC 268
 RESULT 10
 ADM42796
 ID ADM42796 standard; DNA; 1421 BP.
 AC ADM42796;
 XX
 DT 03-JUN-2004 (first entry)
 XX
 DE DNA encoding a murine odourant receptor S19 SeqID 40.
 XX
 KM murine; mouse; ds; gene; chemical sensor system; taste; smell;
 KM artificial sensory organ; olfactory stimulation; food industry;
 KM hygiene inspection; environmental examination; disease diagnosis;
 KM carvone.
 XX
 OS Mus musculus.
 XX
 PN W02003100057-A1.
 XX
 PD 04-DEC-2003.
 XX
 PF 28-MAY-2003; 2003MO-JP006719.
 XX
 PR 28-MAY-2002; 2002JP-00154239.
 PR 13-JUN-2002; 2002JP-00172412.
 PR 14-JAN-2003; 2003JP-00005175.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Seto T, Hirono J, Hamana H, Miyake M, Yoshikawa T, Miyake J;
 XX
 DR WPI; 2004-023356/02.
 DR P-PSDB; ADM42797.
 XX
 PT Chemical sensor systems based on chemical receptors introduced into cells
 PT for immobilization onto support to form chip as component of sensor,
 PT useful in detecting stimuli e.g. taste and smell applicable in food
 PT industry.
 XX
 PS Claim 7; SEQ ID NO 40; 521bp; Japanese.
 XX
 CC This invention relates to a novel chemical sensor system method.
 CC Specifically, it refers to an isolated nucleic acid molecule that encodes
 CC a receptor protein, which binds to chemicals that can stimulate the sense
 CC of taste or smell for example. The present invention describes the
 CC manufacture of a chip that acts as a support to immobilise transfected
 CC cells expressing the receptor gene, such that this chip can be employed
 CC as a component of the chemical sensor model. Furthermore, this chip is
 CC useable as an artificial sensory organ where the chemical receptor
 CC contains an olfactory receptor the sensor can react to olfactory
 CC stimulation. Accordingly, these sensors are useful in the food industry
 CC for analysing freshness of meat, fruit and vegetables, hygiene
 CC inspection, environmental examination and disease diagnosis. Furthermore,
 CC such systems are automatable for high throughput applications under
 CC various conditions, even for differential optical isomers of R(-)-
 CC carvone from S(+)-carvone easily. This polynucleotide sequence is DNA
 CC encoding a murine odourant receptor of the invention.
 XX

SQ Sequence 1421 BP; 341 A; 368 C; 278 G; 434 T; 0 U; 0 Other;
 Query Match 1.3%; Score 55; DB 12; Length 1421;
 Best Local Similarity 100.0%; Pred.No.7.8e-12;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GTGACTTATAGGCTCAGCTGACCTAATACGACTCAGTATAGAGAGCTCGAGATC 55
 Db 387 GTGACTTATAGGCTCAGCTGACCTAATACGACTCAGTATAGAGAGCTCGAGATC 441
 RESULT 11
 ADY55721
 ID ADY55721 standard; DNA; 1421 BP.
 XX
 AC ADY55721;
 XX
 DT 19-MAY-2005 (first entry)
 XX
 DE Mouse odourant receptor S19 gene.
 XX
 KM biocomputer; drug screening; diagnosis; food; cosmetics; agriculture;
 KM analysis; fibronectin; gene; ds.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT CDS 291..1310
 FT /*tag= a
 FT /product= "Mouse odourant receptor S19"
 XX
 PN W02005021744-A1.
 XX
 PD 10-MAR-2005.
 XX
 PF 25-JUN-2004; 2004MO-JP009404.
 XX
 PR 25-JUN-2003; 2003JP-00181915.
 PR 07-AUG-2003; 2003JP-00289469.
 XX
 PA (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
 XX
 PI Miyake M, Yoshikawa T, Miyake J;
 XX
 DR WPI; 2005-262218/27.
 DR P-PSDB; ADY55722.
 XX
 PT Performing data production and presenting cell information under a
 PT similar environment as digital cells, useful e.g. in drug development,
 PT comprises profiling the actual status of cells.
 XX
 PS Example 13; SEQ ID NO 19; 517bp; Japanese.
 XX
 CC The invention relates to a novel method for producing profile data that
 CC relates to cell information in an identical environment. The method
 CC comprises placing several cells on a support in the same environment, and
 CC monitoring the biological factors on or in the cells or their aggregate
 CC chronologically to generate profile data of the cells. The methods and
 CC systems are useful for performing data production by profiling actual
 CC status of cells, and for presenting time-lapse and/or real-time cell
 CC information at a cellular level under a similar environment as well as
 CC digital cells in the form of a library of databases with cell
 CC information, which are particularly useful in drug development, disease
 CC diagnosis and management, as well as in fields including food technology,
 CC cosmetics, agriculture, environmental sciences, in silico computational
 CC biological studies, cell analysis and biotechnology. The methods and
 CC systems are capable of providing information with controllability,
 CC specificity and most importantly directly even in complex systems. This
 CC polynucleotide sequence represents the DNA encoding a mouse odourant
 CC receptor S19 protein used in the method for producing a digital cell
 CC profile of the invention.
 XX
 XX Sequence 1421 BP; 341 A; 368 C; 278 G; 434 T; 0 U; 0 Other;

Query Match 1.3%; Score 55; DB 14; Length 1421;
Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCGCTCACTGAGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 387 GTGACTCTAGGCGCTCACTGAGCTTAATACGACTCACTATAGGAGCTCGAGATC 441

RESULT 12
ID ABB56275
AC ABB56275;
XX 20-OCT-2005 (first entry)
XX
DE Event sequencer related DNA SEQ ID NO 19.
XX
KW analyte detection; ds; gene.
XX
OS unidentified.
XX
PN MO2005073890-A1.
XX
PD 11-AUG-2005.
XX
PF 27-JAN-2005; 2005WO-JP001151.
XX
PR 30-JAN-2004; 2004JP-00024923.
XX
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
XX
PA Miyake M, Yoshikawa T, Miyake J,
XX
PI WPI; 2005-571425/58.
XX
DR P-PSDB; ABB56276.
XX
PT Event sequencer extracts portion of timer series data with peculiar
PT behavior associated with index of system, as event timing, to generate
PT event descriptor described by event timing.
XX
XX
PS Disclosure; SEQ ID NO 19; 281bp; Japanese.
XX
CC The invention relates to an event sequencer that acquires time-series
CC data on an index derived from a system and provides a peculiar behavior
CC associated with the index. A portion of time series data having the
CC peculiar behavior is extracted as an even timing and an event descriptor
CC described by the event timing is generated. The sequencer is useful for
CC analysis of the state of a system. The sequencer performs meaningful
CC analysis of a system state using specific index effectively. The present
CC sequence represents an event sequencer related DNA.
XX
SQ Sequence 1421 BP; 341 A; 368 C; 278 G; 434 T; 0 U; 0 Other;

Query Match 1.3%; Score 55; DB 14; Length 1421;
Best Local Similarity 100.0%; Pred. No. 7.8e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCGCTCACTGAGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 387 GTGACTCTAGGCGCTCACTGAGCTTAATACGACTCACTATAGGAGCTCGAGATC 441

RESULT 13
ID AAT30737
AC AAT30737;
XX
XX 20-OCT-1996 (first entry)

DE Rat cryptdin 2 gene.
XX
XX Cryptdin 2; antibiotic; antimicrobial; defensin; inflammation;
KW antiinflammatory; inflammatory bowel disease; pancreatitis; cancer;
KW tumour; ileitis; ds.
XX
OS Rattus sp.
XX
XX
XX Key Location/Qualifiers
XX FH 1..1345
XX FT exon
XX FT /tag= a
XX FT /codon_start= 1174..1176
XX FT /note="exon 1 codes for the 5' untranslated region and
FT cryptdin-1 prepro sequence"
FT 1345..1930
FT /tag= b
FT 1931..2408
FT /tag= c
FT /note="exon 2 codes for cryptdin-2 and 3' untranslated
FT region"

XX
XX MO9616075-A1.
XX
XX 30-MAY-1996.
XX
XX PD 05-OCT-1995; 95WO-US013328.
XX
XX PF 18-NOV-1994; 94US-00342268.
XX
XX PR 18-NOV-1994; 94US-00342268.
XX
XX PA (REGC) UNIV CALIFORNIA.
XX
XX (SHRI-) SHRINER'S HOSPITAL FOR CRIPPLED CHILDREN.
XX
XX
XX Selected ME, Ouellette AJ;
XX
XX
XX WPI; 1996-268527/27.
XX
XX DR P-PSDB; AAR98787, AAR98792.
XX
XX
XX FT New isolated cryptdin peptide(s) - which have antimicrobial activity,
XX FT used partic. in the detection and treatment of inflammatory pathologies.
XX
XX
XX Claim 31; Page 64-65; 103pp; English.
XX
XX
XX CC The rat cryptdin-2 gene (T30737) codes for the precursor (R98787) of
XX CC cryptdin-2 (R98792), an antimicrobial peptide that exhibits activity
XX CC against a broad range of intestinal and opportunistic pathogens. Rat
XX CC cryptdin-1, -2, and -3 genes (see also T30736 and T30738) were isolated
XX CC from a Sprague-Dawley genomic library cloned in EMBL3. The cryptdin-2
XX CC gene, or corresponding cDNA (see also T30734), can be used to produce
XX CC large amounts of cryptdin-2 for use in treating inflammatory pathologies
XX CC of the intestine
XX
XX
SQ Sequence 2408 BP; 640 A; 531 C; 557 G; 680 T; 0 U; 0 Other;

Query Match 1.3%; Score 55; DB 2; Length 2408;
Best Local Similarity 100.0%; Pred. No. 7.5e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTAGGCGCTCACTGAGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACTCTAGGCGCTCACTGAGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

RESULT 14
ID ABB81284
AC ABB81284;
XX
XX 22-AUG-2002 (first entry)
XX
XX
XX Beet promoter polynucleotide SEQ ID NO 4.
XX
XX Beet; promoter; carbohydrate metabolism; invertase inhibitor;
KW

KW		fructosyl transferase; levan sucrase; nitrogen transporter protein;
KV		pathogen resistance; plant; transgenic; ds.
XX	Beta vulgaris.	
OS		
XX	Key	Location/Qualifiers
FH	Promoter	1..2998
FT	TATA_signal	/tag= a 2877..2883
FT	mRNA	/tag= c 2928..3049
FT		/tag= b
XX		
PN	EP1207204-A1.	
PD	22-MAY-2002.	
PF	16-NOV-2000; 2000EP-00124989.	
XX		
PR	16-NOV-2000; 2000EP-00124989.	
XX	(KWS-) KWS SAAT AG.	
PA		
XX	Hehl R, Kloos D, Stahl DJ;	
PI	WPI; 2002-437465/47.	
XX		
PT	New tissue-specific promoters from Beta vulgaris, useful e.g. for altering carbohydrate metabolism, express transgenes selectively in roots or aerial parts.	
XX		
PS	Claim 1; Page 30-31; 57pp; German.	
XX		
CC	The invention relates to a promoter (A) that is: (i) any of the sequences ABBN1281-ABBN1284; (ii) the complement of (i); or (iii) a sequence that hybridises to (ii). (A) are used, specifically in Beta vulgaris, to control expression of transgenes, particularly to alter carbohydrate metabolism, reduce loss of storage substances; express invertase inhibitor, fructosyl transferase, levan sucrase or genes that encode transport proteins for nitrogen compounds, or increase resistance to, or tolerance of, pathogens. (A) provide tissue-specific transgene expression, either in roots or above-ground parts, so avoid pleiotropic effects, e.g. when expressing invertase inhibitor	
CC		
CQ	Sequence 3049 BP; 783 A; 699 C; 876 G; 691 T; 0 U; 0 Other;	
XX		
Query Match	1.3%; Score 55; DB 6; Length 3049;	
	Best Local Similarity 100.0%; Pred. No. 7.4e-12;	
Matches	55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	1 GTGCACTTAGACCTCACTGGCCTTAATAGACTCACTATTAGGAGCTCGAGATC 55 Db 2656 GTGCAGCTTAGGCCCTCACTGGCCTTAATAGACTCACTATTAGGAGCTCGAGATC 2710 	
RESULT 15		
ABZ82143	ID ABZ82143 standard; DNA; 3869 BP.	
XX		
AC	ABZ82143;	
DT	17-JUN-2003 (first entry)	
XX		
DE	Arabidopsis 9-cis-epoxycarotenoid dioxygenase NCED nucleic acid.	
XX		
NCD	NCED; AtNCED; 9-cis-epoxycarotenoid dioxygenase; enzyme; salt tolerance;	
XX	stress resistance; plant; transgenic plant; gene; ds.	
OS	Arabidopsis thaliana.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1831..3630
FT		/tag= a

FT		/product= "AtNCEBD"
XX		
PN	WO2003020015-A2.	
PD	13-MAR-2003.	
XX		
PF	30-AUG-2002; 2002WO-USO27701.	
XX		
PR	30-AUG-2001; 2001US-0316894P.	
PA	(PURD) PURDUE RES FOUND.	
PI	Ruggiero B, Bressan RA, Hasegawa PW;	
DR	WPI; 2003-300807/29.	
DR	P-PADB; ABP72777.	
PT	Producing transgenic plants resistant to environmental stresses such as salt, drought, cold, osmotic or pathogen, by using 9-cis-epoxycarotenoid dioxygenase nucleic acid.	
PS	Claim 3; Page 27-30; 125pp; English.	
CC	The present sequence is a nucleic acid encoding Arabidopsis thaliana 9-	
CC	cis-epoxycarotenoid dioxygenase (NCED). The NCED nucleic acid can be used	
CC	in the practice of the invention. The invention provides plants that	
CC	exhibit increased salt tolerance or increased stress resistance. These	
CC	comprise: a mutant plant having a mutated NCED gene; a plant having a	
CC	null mutation in an endogenous NCED gene; a transgenic plant comprising	
CC	an isolated NCED nucleic acid (including the present sequence) operably	
CC	linked to a promoter functional in a plant cell; a transgenic plant	
CC	comprising an isolated nucleic acid that encodes an inhibitory NCED RNA	
CC	that inhibits the function of endogenous NCED RNA; and a transgenic plant	
CC	where the inhibitory RNA is complementary to the present sequence or	
CC	hybridises to endogenous RNA encoding NCED. The plants can develop in the	
CC	presence of a concentration of salt that would normally inhibit the	
CC	development of the plant. The plants may be dicots (e.g. soybean) or	
CC	monocots (e.g. corn, rice, rye, oat or wheat) and can be used to produce	
CC	food or feed (all claimed)	
SQ	Sequence 3869 BP; 1155 A; 845 C; 773 G; 1096 T; 0 U; 0 Other;	
OY	Query Match 1.3%; Score 55; DB 8; Length 3869;	
Dn	Best Local Similarity 100.0%; Pred. No. 7.2e-12;	
	Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0	
	1 GTGCAGCTTAGGCGCCTGAATTCACACTCACTAATTGGAGAGCTCGAGATC 55 1 GTGCAGCTTAAAGCCTCACTAGGAGCTTAATTCAGACTCATTAAGAGAGCTCGAGATC 55	
ID	AAS02362 standard; DNA; 11630 BP.	
XX	AAS02362;	
DB	12-SEP-2001 (first entry)	
XX	Galactosyl transferase gene targeting vector.	
XX	Gal alpha(1,3) galactosyl transferase; gene targeting; transgenic animal;	
KV	transplant rejection; immunomodulation; systemic lupus erythematosus;	
KW	immune-haemolytic anaemia; collagen intron targeting construct;	
XX	rheumatoid arthritis; ds.	
OS	Synthetic.	
OS	Sus scrofa.	
FH	Key Location/Qualifiers	
FT	primer_bind 235..260	
FT	/*tag=a	
TT	/note= "PCR primer as displayed in AAS02349"	

```

PT primer_bind complement(4827. .4851)
PT /tag= b
PT /note= "PCR primer as displayed in AAS02350"
FT m18c_feature
FT /tag= c
FT /note= "Site of insertion of the puromycin/bovine growth
FT hormone poly-A signal sequence"
FT primer_bind
FT /tag= d
FT /note= "PCR primer as displayed in AAS02351"
FT primer_bind
FT /tag= e
FT /note= "PCR primer as displayed in AAS02352"
XX WO200123541-A2.
XX 05-APR-2001.
XX 02-OCT-2000; 2000WO-US027065.
XX 30-SEP-1999; 99US-0156953P.
XX (ALEX-) ALEXION PHARM INC.
XX PI Fodor WL, Ramseondar JJ;
XX WPI; 2001-266147/27.
XX Modulating the expression of a eukaryotic gene in a cell, involves
PT transfecting the cell with a nucleic acid construct that disrupts at
PT least a portion of the DNA sequence of the gene to be modulated.
XX Example 2; Fig 7; 86pp; English.
XX The sequence represents Porcine Gal alpha(1,3) galactosyl transferase
CC gene targeting construct. The invention relates to a method for modulating
CC pyrimycin encoding gene. The invention relates to a method for modulating
CC the expression of a eukaryotic gene in a cell. The method involves
CC transfecting the cell with a nucleic acid construct. The construct
CC contains 2 nucleotide sequences which are portions of one or more introns
CC of the eukaryotic gene, and a sequence encoding a selectable marker. The
CC marker sequence is integrated into the gene sequence, so that expression
CC of the marker results in modulation of the expression of the gene. The
CC construct is useful for making a transgenic mammal. The construct is
CC useful for reducing transplant rejection by harvesting cells, tissue, or
CC organs from the offspring of the transgenic mammal, and transplanting the
CC harvested cells, tissue, or organs into a patient in need. The knockout
CC mammals produced by the method are useful for screening drugs for
CC immunomodulation (e.g for systemic lupus erythematosus, rheumatoid
CC arthritis and immune-haemolytic anaemia) and for producing proteins of
CC interest
XX Sequence 11630 BP; 2956 A; 2688 C; 2693 G; 3290 T; 0 U; 3 Other:
SO
Query Match 1.3%; Score 55; DB 4; Length 11630;
Best Local Similarity 100.0%; Pred. No. 6.7e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGACCTTAGGCGCTCACTGACCTAATACGACTCACTAATAGGAGCTCGAGGATC 55
DB 1 GTGACCTTAGGCGCTCACTGACCTAATACGACTCACTAATAGGAGCTCGAGGATC 55

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```

KM mouse; murine; kank; mkank; cancer; gene; ds.
XX Mus musculus.
OS WO2004048568-A1.
XX 10-JUN-2004.
XX 21-NOV-2003; 2003WO-JP014930.
XX 22-NOV-2002; 2002JP-00339909.
XX (NAAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (INFO-) INFO GENES CO LTD.
XX Kiyama R, Kitajima K;
XX WPI; 2004-450380/42.
XX Novel mouse kank protein useful for detecting cancer, treating cancer, in
PT drug discovery for treating cancer.
XX Claim 3; SEQ ID NO 2; 83pp; Japanese.
XX The invention comprises the amino acid and coding sequence of the mouse
CC kank (mkank) protein. The DNA and protein sequences of the invention are
CC useful in the detection and treatment of cancer. The present DNA sequence
CC represents a region of the mouse kank genomic DNA sequence.
XX Sequence 16905 BP; 4333 A; 3945 C; 4066 G; 4561 T; 0 U; 0 Other:
SO
Query Match 1.3%; Score 55; DB 12; Length 16905;
Best Local Similarity 100.0%; Pred. No. 6.5e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 TCGACCTTAGGCGCTCACTGACCTAATACGACTCACTAATAGGAGCTCGAGGATC 56
DB 16905 TCGACCTTAGGCGCTCACTGACCTAATACGACTCACTAATAGGAGCTCGAGGATC 16851

```

```

RESULT 18
ID AAS02354 standard; DNA; 27048 BP.
XX AAS02354;
XX 12-SEP-2001 (first entry)
XX Porcine Gal alpha(1,3) galactosyl transferase gene introns 3-8.
XX Pig; Gal alpha(1,3) galactosyl transferase; intron 3-8; gene targeting;
KM transgenic animal; transplant rejection; immunomodulation;
KM systemic lupus erythematosus; immune-haemolytic anaemia;
KM rheumatoid arthritis; ds.
XX Sub scrofa.
OS
XX Key
PH intron
FT 1.4851
FT /tag= a
FT /number= 3
FT primer_bind
FT /tag= b
FT /number= 4
FT primer_bind
FT /tag= c
FT complement(3998. .4020)
FT /tag= d
FT /tag= e
FT /number= 4
FT /note= "The exon sequence is represented by dashes in the
FT sequence presented in figure 1 in the specification and
FT have been replaced with N's to maintain the sequence
FT numbering"
FT intron
FT 4938. .11715

```

PT		/tag= d
PT	/number= 4	
FT	/note= "This sequence is specifically claimed in claim	
FT	14"	
FT	primer_bind	11521. .11537
FT	/tag= e	
FT	complement(11688. .11716)	
FT	/tag= f	
FT	11716. .11752	
FT	/tag= g	
FT	/number= 5	
FT	/note= "The exon sequence is represented by dashes in the	
FT	sequence presented in figure 1 in the specification and	
FT	have been replaced with N's to maintain the sequence	
FT	numbering"	
FT	intron	11753. .13747
FT	/tag= h	
FT	/number= 5	
FT	13748. .13810	
FT	/tag= i	
FT	/number= 6	
FT	/note= "The exon sequence is represented by dashes in the	
FT	sequence presented in figure 1 in the specification and	
FT	have been replaced with N's to maintain the sequence	
FT	numbering"	
FT	intron	13811. .14358
FT	/tag= j	
FT	/number= 6	
FT	14359. .14463	
FT	/tag= k	
FT	/number= 7	
FT	/note= "The exon sequence is represented by dashes in the	
FT	sequence presented in figure 1 in the specification and	
FT	have been replaced with N's to maintain the sequence	
FT	numbering"	
FT	intron	14464. .21627
FT	/tag= l	
FT	/number= 7	
FT	/note= "This sequence is specifically claimed in claim	
FT	16"	
FT	21628. .21705	
FT	/tag= m	
FT	/number= 8	
FT	/note= "The exon sequence is represented by dashes in the	
FT	sequence presented in figure 1 in the specification and	
FT	have been replaced with N's to maintain the sequence	
FT	numbering"	
FT	intron	21706. .27048
FT	/tag= n	
FT	/number= 8	
FT	/note= "This sequence is specifically claimed in claim	
FT	42"	
XX		
PN	WO200123541-A2.	
XX		
PD	05-APR-2001.	
PE	02-OCT-2000; 2000WO-US027065.	
XX		
PR	30-SEP-1999; 98US-0156953P.	
XX		
PA	(ALEX-) ALEXION PHARM INC.	
XX		
PJ	Fodor WL, Ramamoondar JI;	
XX		
WP	WI; 2001-266147/27.	
XX		
PT	Modulating the expression of a eukaryotic gene in a cell, involves	
PT	transfecting the cell with a nucleic acid construct that disrupts at	
PT	least a portion of the DNA sequence of the gene to be modulated.	
XS		
PS	Example 1; Fig 1; 86pp; English.	
XX		

CC	The sequence represents Porcine Gal alpha(1,3) galactosyl transferase
CC	introns 3-8, a gene used to make a gene targeting construct of the
CC	invention. The invention relates to a method for modulating the
CC	expression of a eukaryotic gene in a cell. The method involves
CC	transfecting the cell with a nucleic acid construct. The construct
CC	contains 2 nucleotide sequences which are portions of one or more introns
CC	of the eukaryotic gene, and a sequence encoding a selectable marker. The
CC	marker sequence is integrated into the gene sequence, so that expression
CC	of the marker results in modulation of the expression of the gene. The
CC	construct is useful for making a transgenic mammal. The construct is
CC	useful for reducing transplant rejection by harvesting cells, tissue, or
CC	organs from the offspring of the transgenic mammal, and transplanting the
CC	harvested cells, tissue, or organs into a patient in need. The knockout
CC	mammals produced by the method are useful for screening drugs for
CC	immunomodulation (e.g. for systemic lupus erythematosus, rheumatoid
CC	arthritis and immune-haemolytic anaemia) and for producing proteins of
CC	interest
SQ	Sequence 27048 BP; 6964 A; 5958 C; 6323 G; 7365 T; 0 U; 438 Other;
Oy	Query Match 1.3%, Score 55; DB 4; Length 27048;
Dn	Best Local Similarity 100.0%; Pred. No. 6.3e-12;
	Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0
	1 GTGCACTTACGGCTCAGCGCCATTAATCGACTACTTTAGGAGCTGAGGATC 55
	1 GTGCAGCTTAGGCGCTCAGCTGCGCTTAATTCGACTCATATTAGGAGAGCTGAGGATC 55
AA502355	RESULT 19
ID	AA502355 standard; DNA; 4026 BP.
XX	AA502355;
DT	12-SEP-2001 (first entry)
DE	Porcine Gal alpha(1,3) galactosyl transferase gene intron 3, 5' sequence.
KW	Pig; Gal alpha(1,3) galactosyl transferase; intron 3; gene targeting;
KM	transgenic animal; transplant rejection; immunomodulation;
XX	systemic lupus erythematosus; immune-haemolytic anaemia;
XX	rheumatoid arthritis; ds.
OS	Sub scrofa.
FH	Key location/Qualifiers
FT	primer_bind 1..23
FT	/tag= a
FT	/note= "PCR primer as displayed in AA502338"
FT	primer_bind Complement(3999..4026)
FT	/tag= b
FT	/note= "PCR primer as displayed in AA502339"
PN	WO200123541-A2.
PD	05-APR-2001.
PP	02-OCT-2000; 2000WO-US027065.
PR	30-SEP-1999; 99US-0156953P.
PA	(ALEX-) ALEXION PHARM INC.
PI	Fodor WL, Ramsoondar JI;
WI	WPJ; 2001-266147/27.
PT	Modulating the expression of a eukaryotic gene in a cell, involves
PT	transfecting the cell with a nucleic acid construct that comprises at
PT	least a portion of the DNA sequence of the gene to be modulated.
PS	Example 1; Fig 3A; 86pp; English.

PF 18-NOV-1997; 97MO-EP006472.
 XX 18-NOV-1996; 96EP-00203213.
 XX (MOGE-) MOGEN INT NV.
 PA Ohl SA, Van Der Lee FM, Goddijn OJM, Klap J, Sijmons PC;
 XX WPI; 1998-312484/27.
 DR
 XX
 PT New Arabidopsis thaliana DNA promoter - useful for, e.g. generating plant
 PT reduced susceptibility to plant parasitic nematodes.
 XX
 PS Claim 1; Page 22-24; 47pp; English.
 XX
 XX This DNA fragment obtainable from Arabidopsis thaliana is capable of
 CC promoting root knot and cyst nematode-inducible transcription of an
 CC associated DNA sequence when reintroduced into a plant. The promoterless
 CC GUS construct binary vector PMO553 was mobilised by triparental mating
 CC to Agrobacterium tumefaciens MOG101 and the resulting strain was used for
 CC Arabidopsis root transformation. Line PMO553H25 was identified as a line
 CC which showed strong GUS expression inside syncytia and giant cells
 CC induced by the cyst nematode Heterodera schachtli and the root knot
 CC nematode Meloidogyne incognita, respectively. Promoter tags from line
 CC PMO553H25 were sequenced. The claimed DNA fragment is nematode feeding
 CC site-specific. Also claimed are: (1) a portion or variant of the above
 CC sequence capable of promoting root knot and cyst nematode inducible
 CC transcription of an associated DNA sequence comprising a DNA fragment as above
 CC plus; (2) a chimeric DNA sequence comprising a DNA fragment as above
 CC plant; (3) a chimeric DNA sequence which is not naturally under its transcriptional
 CC control, and which causes the production of a plant cell-disruptive
 CC substance, preferably barnase; (3) a replicon comprising the chimeric DNA
 CC sequence of (2), or the above DNA and at least 1 restriction endonuclease
 CC recognition site; (4) a microorganism containing the replicon of (3); (5)
 CC a plant cell having incorporated into its genome the chimeric DNA of (2);
 CC (6) a root system of a plant consisting of the cells of (5); (7) a plant
 CC consisting of the cells of (5), preferably a dicotyledonous plant,
 CC especially a potato plant; (8) a plant grafted onto the root system of
 CC (6); (9) a part of a plant, selected from seeds, flowers, tubers, roots,
 CC leaves, fruits, pollen and wood, obtained from the plant of (7) or (8),
 CC and (10) a crop consisting of the plants of (7) or (8). The DNA fragment
 CC can be used to identify subfragments capable of promoting transcription
 CC of an associated DNA sequence in a plant. It can also be used for making
 CC hybrid regulatory DNA sequences. The chimeric DNA sequence of (2) can be
 CC used for transforming plants (all claimed). The DNA sequence can be used
 CC to reduce the susceptibility of a plant to parasitic nematodes. (Updated
 CC on 17-OCT-2003 to standardise OS field)
 CC
 XX
 SQ Sequence 3484 BP; 1143 A; 583 C; 625 G; 1133 T; 0 U; 0 Other;
 Query Match 0.7%; Score 28; DB 2; Length 3484;
 Best Local Similarity 100.0%; Pred. No. 0.56;
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 CTATATGAGACTCACTATAGGAGCTCGA 50
 DB 698 CTATATGAGACTCACTATAGGAGCTCGA 725

OS Eucalyptus grandis.
 XX
 PN MO9730162-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 19-FEB-1997; 97MO-AU000089.
 XX
 XX 19-FEB-1996; 96AU-00008161.
 PR
 XX (FORB-) FORBIO RES PTY LTD.
 PA
 XX Teasdale RD, Mouradov A, Southerton SG, Sawbridge TI;
 PI WPI; 1997-425037/39.
 DR
 XX
 XX
 PT Regulating eukaryotic gene by expressing modulator gene and gene that
 PT regulates the modulator - with two of these genes controlled by inducible
 PT or developmental promoters, particularly used in plants to impart
 PT reversible sterility, nematode or insect resistance, to regulate pigment
 PT production etc.
 PS Disclosure; Fig 13; 87pp; English.
 XX
 XX This sequence represents a promoter used in the method of the invention.
 CC The method of the invention is for regulating a eukaryotic gene by
 CC transforming a cell with a construct. The construct expresses a modulator
 CC gene product that regulates the eukaryotic gene or its product, and a
 CC further gene product that regulates the modulator gene or its product.
 CC Two of the promoters controlling the eukaryotic gene, modulator and
 CC further genes are inducible or developmental promoters from the same or
 CC complementary tissues. The process provides highly specific expression of
 CC the eukaryotic gene in target organs, especially of plants but possibly
 CC also in yeasts and animals. Typical applications include induction of
 CC sterility (which may be reversible); control of root nematodes;
 CC production of pigments, dyes, insecticidal toxins, fragrances etc. A
 CC transformation cassette with the 3 genes under the control of the
 CC specified promoters, provides expression of the eukaryotic gene in target
 CC tissues with increased specificity and reduced promoter leakage
 CC
 XX
 SQ Sequence 1205 BP; 421 A; 218 C; 213 G; 353 T; 0 U; 0 Other;
 Query Match 0.6%; Score 27; DB 2; Length 1205;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 TATATGAGACTCACTATAGGAGCTCGA 50
 DB 72 TATATGAGACTCACTATAGGAGCTCGA 98

RESULT 22
 AAT94303
 ID AAT94303 standard; DNA; 1205 BP.
 XX
 AC AAT94303;
 XX
 DT 18-MAR-1998 (first entry)
 XX
 DE EGM3 gene promoter.
 XX
 KW Promoter; eukaryotic gene regulation; insecticidal toxin production;
 KW sterility induction; root nematode control; amplify; modulator gene;
 KW EGM3 gene; ss.
 XX

RESULT 23
 AAAS1053/C
 ID AAAS1053 standard; DNA; 6975 BP.
 XX
 AC AAAS1053;
 XX
 DT 09-OCT-2000 (first entry)
 XX
 DE Plasmid pMH40-delta.
 XX
 KW S-adenosyl-L-methionine synthetase; SAMS; probe; promoter; embryo;
 KW constitutive; tissue-specific; development-specific;
 KW herbicide resistance; pathogen resistance; pMH40-delta; ss.
 XX
 OS Synthetic.
 XX
 PN MO200037662-A2.
 XX
 PD 29-JUN-2000.
 XX
 PF 17-DEC-1999; 99WO-US030180.
 XX

PR 21-DEC-1998; 98US-0113045P.
XX
XX (DUPO) DU PONT DE NEMOURS & CO E I.
XX
XX Falco SC, L1 Z;
XX
XX WPI; 2000-442682/38.
DR
XX
XX 5'-adenosyl-L-methionine synthetase promoter for expressing target
PT heterologous herbicide-resistance or pathogen-resistance nucleic acid
PT fragments in plants, especially soybean.
XX
XX Example 5; Page 45-47; 50pp; English.
XX
XX The 5'-adenosyl-L-methionine synthetase (SAMS) promoter (see AAB51042) was
CC inserted into plasmid pM40-delta, which contains a 35S promoter::GUS::3'
CC Nos DNA fragment, to form plasmid pS111. The SAMS promoter is active in
CC seedlings and callus and over-expression of a gene in embryo stage can be
CC achieved at an early developing stage using the SAMS promoter. The SAMS
CC promoter may be used as an alternative to cauliflower mosaic virus 35S
CC promoter to drive expression of selectable marker genes. Plant cells
CC transformed with the SAMS constitutive promoter are useful for increasing
CC or decreasing the expression of heterologous nucleic acid fragments in a
CC plant, preferably corn, rice, wheat, barley, palm, Arabidopsis, soybean,
CC oil seed Brassica, peanut, sunflower, safflower, cotton, tobacco, tomato,
CC potato or cocoa. Target heterologous nucleic acid fragments include
CC herbicide resistance or pathogen resistance nucleic acid fragments
XX
SQ Sequence 6975 BP; 1890 A; 1694 C; 1699 G; 1691 T; 0 U; 1 Other;

Query Match 0.6%; Score 27; DB 3; Length 6975;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTATACGACTCACTATAGGAGCTCG 49
Db 4123 CTATACGACTCACTATAGGAGCTCG 4097

RESULT 24
AAC55633/c
ID AAC55633 standard; DNA; 7038 BP.
XX
XX AAC55633;
XX
XX 11-JAN-2001 (first entry)
XX
XX 2-hybrid vector pMAB85 nucleotide sequence.
DE
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; ds.
XX
XX Bacteriophage lambda.
OS Synthetic.
XX
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005432.
XX
XX 02-MAR-1999; 99US-0122389P.
XX 23-MAR-1999; 99US-0126049P.
XX 28-MAY-1999; 99US-0136744P.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT

PT attL1, attL2, attR1, and attR2 nucleotide sequence useful for the
PT recombinational cloning of polypeptides.
XX
XX Disclosure; Fig 98; 459pp; English.
XX
XX The present invention describes isolated nucleic acid molecules (I)
CC encoding an attB1, attB2, attP1, attP2, attL1, attL2, attR1, and attR2
CC nucleotide sequence. Also described are: (1) an isolated nucleic acid
CC molecule (II) comprising one or more att recombination sites comprising
CC at least one mutation in its core region that increases the specificity
CC of interaction between the recombination site and a second att
CC recombination site; and (2) an isolated nucleic acid molecule (III)
CC comprising one or more mutated att recombination sites comprising at
CC least one mutation in its core region that enhances the efficiency of
CC recombination between a first nucleic acid molecule comprising the
CC mutated att recombination site and a second nucleic acid molecule
CC comprising a second recombination site that interacts with the mutated
CC att recombination site. (I), (II), (III), primers, vectors and methods
CC from the present invention are used for the recombinational cloning of
CC nucleic acid molecules. They can be used for changing vectors, targeting
CC gene products to intracellular locations, cleaving fusion tags from
CC desired proteins, operably linking nucleic acid molecules of interest to
CC regulatory genetic sequences, constructing genes for fusion proteins,
CC changing copy number, changing replicons, cloning into phages and
CC cloning. (I), (II), (III), host cells and vectors can be used in the
CC production of polypeptides and antibodies. The present sequence is used
CC in the exemplification of the present invention
XX
SQ Sequence 7038 BP; 2000 A; 1596 C; 1526 G; 1916 T; 0 U; 0 Other;

Query Match 0.6%; Score 27; DB 3; Length 7038;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TAATACGACTCACTATAGGAGCTCGA 50
Db 6005 TAATACGACTCACTATAGGAGCTCGA 5979

RESULT 25
AAC55630/c
ID AAC55630 standard; DNA; 6815 BP.
XX
XX AAC55630;
XX
XX 11-JAN-2001 (first entry)
XX
XX Destination vector pDEST33 nucleotide sequence.
DE
XX Bacteriophage lambda; att; recombination site; attB; attP; attR; attL;
XX mutant; recombinational cloning; entry vector; destination vector;
XX gene product targeting; fusion tag cleavage; ds.
XX
XX Bacteriophage lambda.
OS Synthetic.
XX
XX WO200052027-A1.
XX
XX 08-SEP-2000.
XX
XX 02-MAR-2000; 2000WO-US005432.
XX
XX 02-MAR-1999; 99US-0122389P.
XX 23-MAR-1999; 99US-0126049P.
XX 28-MAY-1999; 99US-0136744P.
XX
XX (LIFE-) LIFE TECHNOLOGIES INC.
XX
XX Hartley JL, Brasch MA, Temple GF, Cheo D;
XX WPI; 2000-543948/49.
XX
XX Isolated nucleic acid molecules encoding an attB1, attB2, attP1, attP2,
PT

	PT	attL1, attL2, attR1, and attR2 nucleotide sequence useful for the recombinational cloning of polypeptides.
	PX	
	PS	Disclosure; Fig 95; 459pp; English.
	XX	The present invention describes isolated nucleic acid molecules (I) encoding an atB1, atB8, atP1, atP2, attL1, attL2, attR1, and attR2 nucleotide sequence. Also described are: (1) an isolated nucleic acid molecule (II) comprising one or more att recombination sites comprising at least one mutation in its core region that increases the specificity of interaction between the recombination site and a second att recombination site; and (2) an isolated nucleic acid molecule (III) comprising one or more mutated att recombination sites comprising at least one mutation in its core region that enhances the efficiency of recombination between a first nucleic acid molecule comprising the mutated att recombination site and a second nucleic acid molecule comprising a second recombination site that interacts with the mutated att recombination site. (I), (II), (III), primers, vectors and methods from the present invention are used for the recombinational cloning of nucleic acid molecules. They can be used for changing vectors, targeting gene products to intracellular locations, cleaving fusion tags from desired proteins, operably linking nucleic acid molecules of interest to regulatory genetic sequences, constructing genes for fusion proteins, changing copy number, changing replicons, cloning into phages and cloning. (I), (II), (III), host cells and vectors can be used in the production of polypeptides and antibodies. The present sequence is used in the exemplification of the present invention.
SQ	XX	Sequence 8815 BP; 2513 A; 1954 C; 1943 G; 2405 T; 0 U; 0 Other;
OY		Query Match 0.6%; Score 27; DB 3; Length 8815; Best Local Similarity 100.0%; Pred. No. 1.3; Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
DG		24 TTATTACGACTCAGCTTAGGGAGTTCGA 50 DB 7782 TAATTCGCAGCTCACTTAAGGAGCTCGA 7756
		RESULT 26 AEA62089/C ID AEA62089 standard; cDNA, 11240 BP. XX AEA62089; AC XX DT 25-AUG-2005 (first entry) XX DB Replication competent hepatitis C virus poly-nucleotide. XX Hepatitis C virus infection; anti-inflammatory; hepatotropic; virucide; KW gastrointestinal disease; drug screening; gene; ss. XX OS Hepatitis C virus. OS Human immunodeficiency virus 1. OS Hepatitis delta virus. OS Encephalomyocarditis virus. OS Chimeric. XX FH Key Location/Qualifiers FT S'UTR 1..341 FT /tag= a FT CDS 342..1457 FT /tag= b FT /product= "Tat2Neo" FT 1458..2076 FT /tag= c FT /function= "IRES" FT CDS 2077..8037 FT /tag= d FT /product= "HCV polypotein" FT 3'UTR 8038..8259 FT /tag= e FT misc feature 8260..8345

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FT      /*tag= f
FT      /function= "Ribozyme"
FN      WO2005053516-A2.
PD      16-JUN-2005.
PP      01-DEC-2004; 2004WO-US040120.
XX      01-DEC-2003; 2003US-0525989P.
XX      (TEXA ) UNIV TEXAS.
XX      Lemon SM, Yi M;
XX      WPI; 2005-418069/42.
XX      P-PSDBJ; AEA62092.
XX      New replication competent polynucleotide comprising a 5' non-translated
XX      region (NTR), a 3' NTR, and a first coding sequence present between the
XX      5' NTR and 3' NTR and encoding a hepatitis C virus polypeptide, useful in
XX      drug discovery.
XX      Disclosure; SEQ ID NO 13; 102pp; English.
XX      The present invention provides replication competent polynucleotides that
XX      include a 5' non-translated region (NTR), a 3' NTR and a coding sequence
XX      encoding a hepatitis C virus (HCV) polypeptide that comprises an Ile
XX      residue at about amino acid 2204, and an adaptive mutation selected from
XX      Arg at about amino acid 1067, Arg at about amino acid 1691, Val at about
XX      amino acid 2080, Ile at about amino acid 1655, Arg at about amino acid
XX      2040, and Arg at about amino acid 1188, or a combination of these. The
XX      polypeptide may include the cleavage products core, E1, E2, P7, NS2, NS3,
XX      NS4A, NS4B, NS5A and NS5B. The polynucleotide may further comprise a
XX      second coding sequence encoding a marker or transactivator, or a
XX      nucleotide sequence having cis-acting ribozyme activity located 3' of the
XX      3' NTR. Also provided are: a method for making the replication component
XX      polynucleotide; a method for using the replication competent
XX      polynucleotide to identify a compound that inhibits replication of the
XX      replication competent nucleotide; a method for selecting a replication
XX      competent polynucleotide; and a method for detecting a replication
XX      competent polynucleotide. The present sequence is that of a replication
XX      competent polynucleotide comprising a 5' NTR, a tat2ANeo
XX      sequence, an encephalomyocarditis virus IRES, a coding sequence for HCV
XX      polypeptide, and the hepatitis delta virus ribozyme.
XX      Sequence 11240 BP; 2431 A; 3214 C; 3038 G; 2557 T; 0 U; 0 Other;
SQ      Query Match          0.6%; Score 27; DB 14; Length 11240;
SQ      Best local Similarity 100.0%; Pwd. No. 1.3;
SQ      Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      23 CTATACGACTCATATAGGAGCTCG 49
DB      8390 CTATACGACTCATATAGGAGCTCG 8364
RESULT 27
ID      ADU81180
XX      ADU81180 standard; cDNA; 21178 BP.
XX      ADU81180;
XX      10-FEB-2005 (first entry)
XX      DT
XX      DE Thale creess diacylglycerol acyltransferase, DGAT, cDNA #2.
XX      KW diacylglycerol acyltransferase; DGAT; plant breeding; crop improvement;
XX      fatty acid biosynthesis; ss.
XX      OS Arabidopsis thaliana.
XX      PN WO2004101793-A1.

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XX 25-NOV-2004.
PD
XX
XX 14-MAY-2004; 2004WO-AU000635.
PF
XX
XX 16-MAY-2003; 2003AU-00902413.
PR
XX
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA
XX (AGRE-) AGRESEARCH LTD.
PI
XX Bryan GT, Burling MF, Roberts NJ, Trollope AJ, Woodfield DR;
DR WPI; 2004-821891/81.
XX
XX New nucleic acid from a ryegrass (Lolium) or fescue (Festuca) species
PT encoding a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
PT polypeptide, useful as a genetic marker or for modifying fatty acid
PT biosynthesis in a plant.
XX
XX Example 2; SEQ ID NO 43; 188bp; English.
PS
XX The invention relates to a new substantially purified or isolated nucleic
CC acid or its fragment from a ryegrass (Lolium) or fescue (Festuca) species
CC encodes a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
CC polypeptide or its fragment or variant. The nucleic acid or nucleic acid
CC fragment and/or its nucleotide sequence information or single nucleotide
CC polymorphism of perennial ryegrass Lolium perenne is useful as a
CC molecular genetic marker or for modifying fatty acid biosynthesis in a
CC plant. The present sequence represents a plant diacylglycerol
CC acyltransferase, DGAT, cDNA.
XX
XX Sequence 21178 BP; 5350 A; 5440 C; 5462 G; 4926 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 27; DB 13; Length 21178;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCG 49
Db 10500 CTATACGACTCACTATAGGAGCTCG 10526
RESULT 28
ADU81181
ID ADU81181 standard; DNA; 22635 BP.
XX
XX ADU81181;
AC
XX
XX 10-FEB-2005 (first entry)
DT
XX
XX Thale cress diacylglycerol acyltransferase, DGAT, DNA #2.
DE
XX
XX diacylglycerol acyltransferase; DGAT; plant breeding; crop improvement;
KM fatty acid biosynthesis; db.
XX
XX Arabidopsis thaliana.
OS
XX
XX WO2004101793-A1.
PN
XX
XX 25-NOV-2004.
PD
XX
XX 14-MAY-2004; 2004WO-AU000635.
PF
XX
XX 16-MAY-2003; 2003AU-00902413.
PR
XX
XX (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.
PA
XX (AGRE-) AGRESEARCH LTD.
PI
XX Bryan GT, Burling MF, Roberts NJ, Trollope AJ, Woodfield DR;
DR WPI; 2004-821891/81.
XX
XX New nucleic acid from a ryegrass (Lolium) or fescue (Festuca) species
PT

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```

PT encoding a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
PT polypeptide, useful as a genetic marker or for modifying fatty acid
PT biosynthesis in a plant.
XX
XX Example 2; SEQ ID NO 44; 188bp; English.
PS
XX The invention relates to a new substantially purified or isolated nucleic
CC acid or its fragment from a ryegrass (Lolium) or fescue (Festuca) species
CC encodes a diacylglycerol acyltransferase 1 (DGAT1) or DGAT1-like
CC polypeptide or its fragment or variant. The nucleic acid or nucleic acid
CC fragment and/or its nucleotide sequence information or single nucleotide
CC polymorphism of perennial ryegrass Lolium perenne is useful as a
CC molecular genetic marker or for modifying fatty acid biosynthesis in a
CC plant. The present sequence represents a plant diacylglycerol
CC acyltransferase, DGAT, cDNA.
XX
XX Sequence 22635 BP; 5760 A; 5684 C; 5710 G; 5481 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 27; DB 13; Length 22635;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCG 49
Db 11957 CTATACGACTCACTATAGGAGCTCG 11983
RESULT 29
AAC60777
ID AAC60777 standard; DNA; 38 BP.
XX
XX AAC60777;
AC
XX
XX 06-FEB-2001 (first entry)
DT
XX
XX Candidate oncogene ZNF217 reverse PCR primer SEQ ID NO:6.
DE
XX
XX Vitamin D 24 hydroxylase; vitamin D receptor; CYP24; VDR; ZNF24;
KM oncogene; breast cancer; chromosome 20; 20q13.2; PCR primer;
KM 25-hydroxyvitamin D3 24-hydroxylase enzyme; cytostatic; ss.
XX
XX Homo sapiens.
OS
XX
XX WO2000060109-A1.
PN
XX
XX 12-OCT-2000.
PD
XX
XX 06-MAR-2000; 2000WO-US005972.
PF
XX
XX 02-APR-1999; 99US-00285292.
PR
XX
XX (REGC ) UNIV CALIFORNIA.
PA
XX
XX Albersson DG, Pinkel D, Collins C, Gray JW, Yestra B;
PI WPI; 2000-656233/63.
DR
XX
XX Detecting a predisposition to or a progression of cancer especially
PT breast cancer in humans comprises detecting levels of CYP24 in a
PT biological sample.
XX
XX Example 1; Page 53; 73pp; English.
PS
XX The present invention describes a method for detecting (I) a
CC predisposition to cancer in an animal. The method comprises detecting the
CC level of CYP24 (25-hydroxyvitamin D3 24-hydroxylase enzyme) in a
CC biological sample from the animal and comparing it with a control sample
CC taken from a normal, cancer-free tissue, where an increased level of
CC CYP24 in the biological sample compared to the control sample indicates a
CC predisposition to cancer in the animal. (I) is useful for detecting a
CC predisposition to cancer in humans, non-human primates, canines, felines,
CC murines, bovine, equine, porcine and lagomorphs. An example from the
CC present invention describes the identification of CYP24 as a driver

```

CC oncogene for amplification at chromosome band 20q13.2; the present
CC sequence represents a PCR primer for the candidate oncogene ZNF217 which
CC is used in this example
XX
SQ Sequence 38 BP, 14 A, 8 C, 9 G, 7 T, 0 U, 0 Other;
Query Match 0.6%; Score 26; DB 3; Length 38;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 TAAATAGCACTCACTATAGGAGCTCG 49
Db 1 TAAATAGCACTCACTATAGGAGCTCG 26
RESULT 30
AAK8214
XX AAK8214 standard; DNA; 40 BP.
AC AAK8214;
XX
XX 10-SEP-1999 (first entry)
DT
XX Oligonucleotide primer 2.
DE
XX Ribozyme; modification; inhibitor; gene expression; gene therapy; primer;
KM retrovirus; probe; nuclease resistant ribonucleic acid; antisense; tRNA;
KM transgenic plant; acylation; aminoacyl-tRNA synthetase; ss.
XX
XX Synthetic.
OS
XX DEL9801153-A1.
PN
XX
XX 15-JUL-1999.
PD
XX 14-JAN-1998; 98DE-01001153.
PF
XX 14-JAN-1998; 98DE-01001153.
PR
XX (JENN/) JENNE A.
PA
XX WPI; 1999-396161/34.
DR
XX
XX Selection of a ribozymes useful for, e.g. inhibiting gene expression and
PT improving nuclease resistance.
PT
XX
PS Example 1; Page 7; 22pp; German.
XX
XX This invention describes a novel method to select a ribozyme that can
CC covalently modify the 2'-OH group of ribonucleic acids in trans. The
CC ribozyme can be used to inhibit gene expression (e.g. in gene therapy) or
CC to fight retroviruses in vitro or in vivo. The ribozyme, DNA encoding it
CC or a vector containing the DNA, can be used as a sequence specific gene
CC probe. They can also be used for manufacture of nuclease resistant
CC ribonucleic acids (especially antisense oligonucleotides) or to produce
CC transgenic plants. The ribozyme can be used to acylate the 3' end of
CC tRNA. In other words, it can be used as an aminoacyl-tRNA synthetase.
CC This sequence represents a primer used in the method of the invention
CC
XX
SQ Sequence 40 BP, 10 A, 12 C, 8 G, 10 T, 0 U, 0 Other;
Query Match 0.6%; Score 26; DB 2; Length 40;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 23 CTAATAGCACTCACTATAGGAGCTC 48
Db 2 CTAATAGCACTCACTATAGGAGCTC 27

XX
XX AEB00576;
AC
XX
XX 25-AUG-2005 (first entry)
DT
XX
XX Drosophila kinase CG7125/T7 promoter reverse PCR primer.
DE
XX
XX Mitosis; kinase; gene silencing; RNA interference; cell cycle;
KM proliferation; ss; PCR; primer; T7 promoter; cancer; cytostatic;
KM psoriasis; antipsoriatic; glomerulonephritis; nephrotic; gene therapy.
XX
XX Drosophila melanogaster.
OS
XX Enterobacteria phage T7.
XX
XX WO2005056802-A2.
PN
XX
XX 23-JUN-2005.
PD
XX
XX 13-DEC-2004; 2004WO-GB005218.
PF
XX
XX 12-DEC-2003; 2003GB-00028928.
PR
XX
XX (CANC-) CANCER RES TECHNOLOGY LTD.
PA
XX
XX Glover DM, Bettencourt-Dias M, Giet R, Sinka R, Carpenter L;
PI WPI; 2005-488189/49.
XX
XX
XX The invention relates to modulating proliferation in a cell or population
CC of cells comprising contacting the cell or population of cells with an
CC agent capable of modulating expression or activity of a target kinase or
CC a regulator of the target kinases listed in table 1 the specification.
CC The modulating agent is a nucleic acid chosen from an anti-sense RNA or
CC DNA, a triple helix-forming molecule, RNAi, siRNA or a ribozyme. The
CC target kinase is a homolog of a Drosophila kinase which, when its
CC expression is modulated by a dsRNA interference molecule, is shown to
CC arrest the cell cycle. Also included are screening for a modulator of
CC cell proliferation, determining the effect of a candidate substance on
CC proliferation of a cell or population of cells, preparing a
CC pharmaceutical composition for the treatment of a proliferative disorder,
CC treating a proliferative disorder in a subject, diagnosing a
CC proliferative disorder, identifying a kinase which is abnormally
CC expressed in a proliferative disorder, a vector (comprising a coding
CC sequence for a kinase (or a regulator of target kinases) listed in the
CC specification operably linked to transcriptional regulatory sequences for
CC use in a method of gene therapy) and a pharmaceutical carrier. The methods and
CC comprising the above vector and a pharmaceutical carrier. The methods and
CC composition (including the vector or nucleic acid or the modulator of
CC expression or activity of the target kinases) are useful for treating
CC proliferative disorders or for manufacturing a medicament for the
CC treatment of proliferative disorders, such as cancer, psoriasis or
CC glomerulonephritis. These may also be used for diagnosing such disorders.
CC The present sequence is a PCR primer that amplifies a region of a
CC Drosophila kinase (which, when its expression is modulated by a dsRNA
CC interference molecule, is shown to arrest the cell cycle). The primer
CC adds a T7 promoter sequence for in-vitro transcription.
CC
XX
SQ Sequence 43 BP, 8 A, 12 C, 9 G, 14 T, 0 U, 0 Other;
Query Match 0.6%; Score 26; DB 14; Length 43;
Best Local Similarity 100.0%; Pred. No. 4.9;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 23 CTAATAGCACTCACTATAGGAGCTC 48
Db 5 CTAATAGCACTCACTATAGGAGCTC 30

ID	AA136342	standard; RNA; 239 BP.
XX	AA136342;	
XX	24-OCT-1997	(first entry)
XX	Human immunodeficiency virus 1 tat ligand, tat7.	
XX	Human immunodeficiency virus type 1, HIV 1, reverse transcriptase;	
KW	high affinity ligand; AIDS; treatment; diagnosis; inhibition;	
KW	acquired immune deficiency syndrome; rev; tat; pol; gag.	
XX	Synthetic.	
OS	W09703085-A1.	
XX	30-JAN-1997.	
PD	10-JUL-1996;	96MO-US011473.
PF	11-JUL-1995;	95US-0000872P.
PR	30-AUG-1995;	95US-00521515.
XX	(NEXS-) NEXSTAR PHARM INC.	
XX	Gold L, Lochrie M, Chen H, Tuerk C;	
PI	WPI, 1997-118979/11.	
XX	Identification of feline immunodeficiency virus reverse transcriptase	
PT	nucleic acid ligands - for treatment and diagnosis of viral infection,	
PT	also treatment of intracellularly mediated diseases.	
XX	Example 3; Page 57; 71pp; English.	
PS	intracellularly mediated conditions such as cancer involving dominant ras	
CC	mutations or infectious diseases including AIDS can be treated by	
CC	administering oligonucleotides (i.e. nucleic acid ligands) which can	
CC	enter the cell and attenuate the condition. In a specific example, RNA	
CC	ligands to HIV-1 tat, rev and reverse transcriptase were generated by the	
CC	SELEX combinatorial method. Fusion of the SELEX ligands to the initiator	
CC	Met RNA used for expressing the ligands in CEMs cell lines either had	
CC	little effect on their affinity (tat7 and rev30A, see AA136342 and	
CC	AA136343, respectively) or reduced it significantly (tw17, see AA136344)	
SO	Sequence 239 BP; 65 A; 61 C; 68 G; 0 T; 45 U; 0 Other;	
Query Match	0.6%; Score 26; DB 2; Length 239;	
Best Local Similarity	76.9%; Pred. No. 4.3;	
Matches	20; Conservative 6; Mismatches 0; Indels 0; Gaps 0	
Cy	23 CTAATACGACCTCATAGGAGCCTC 48	
	: : :	
Db	94 CUAADACGACUCACUADGAGGAGCUC 119	
RESULT 33		
AA235182		
ID	AA235182 standard; cDNA; 6337 BP.	
AC	AA235182;	
XX	13-MAR-2000	(first entry)
XX	Corn delta-12 desaturase fad2-1 gene in plasmid pBN257.	
DE	Corn; maize; transgenic plant; lipid; food; feedstuff; vegetable oil;	
KW	seed oil; Oleic acid; fatty acid desaturase; delta-12 desaturase; fad2-1;	
KW	pBN257; gag.	

[illegible]

XX (SHEN/) SHEN J B.
 XX Shen JB;
 XX WPI; 2003-851762/79.
 XX New nucleic acid fragment comprising a corn oleosin promoter, or encoding
 PT a corn delta-9-steroyl-ACP desaturase, useful for producing corn plant
 PT that produces oil useful in food, animal feed, cooking and industrial
 PT applications.
 XX Claim 22; SEQ ID NO 58; 80pp; English.
 XX The present invention relates to an isolated nucleic acid fragment
 CC comprising a corn oleosin promoter. The invention is useful for producing
 CC corn plant that produces oil useful in food, animal feed, cooking and
 CC industrial applications. The present sequence is plasmid pBN257 DNA
 CC containing fad2-1 (delta-12 desaturase) gene
 XX
 XX Sequence 6337 BP; 1486 A; 1655 C; 1569 G; 1627 T; 0 U; 0 Other;
 SO
 Query Match 0.6%; Score 26; DB 10; Length 6337;
 Best Local Similarity 100.0%; Pred. No. 3.4;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 23 CTAATACGACTCACTATAGGAGCTC 48
 Db 6312 CTAATACGACTCACTATAGGAGCTC 6337
 RESULT 35
 ACN45188/c
 ID ACN45188 standard; DNA; 96499 BP.
 XX ACN45188;
 AC
 XX 18-NOV-2004 (first entry)
 DT
 XX Mouse genomic sequence MCG9393.
 DE
 XX Cytostatic; carcinoma; lymphoma; cancer; murine; gene; ss.
 XX
 XX Mus musculus.
 OS
 XX MO2003073826-A2.
 PN
 XX 12-SEP-2003.
 PD
 XX 28-FEB-2003; 2003WO-US006235.
 PF
 XX 01-MAR-2002; 2002US-00087192.
 PR
 XX (SAGR-) SAGRES DISCOVERY.
 PA
 XX Morris DW;
 PI
 XX WPI; 2003-328604/31.
 DR
 XX Recombinant nucleic acid useful for diagnosis and treatment of carcinoma
 PT comprises a nucleotide sequence.
 PT
 XX Claim 1; SEQ ID NO 2011; 0pp; English.
 PS
 XX The present invention relates to novel DNA and protein sequences which
 CC are associated with carcinomas. The sequences are useful for: (i) for
 CC screening drug candidates; (ii) for screening of bioactive agent capable
 CC of binding to Carcinoma Associated Protein (CAP); (iii) for screening of
 CC a bioactive agent capable of modulating the activity of CAP; (iv) for
 CC evaluating the effect of a candidate carcinoma drug; (v) for diagnosing
 CC carcinoma; (vi) for inhibiting the activity of CAP; (vii) for treating
 CC carcinoma; (viii) for neutralizing the effect of CAP; (ix) as a biochip;
 CC (x) for diagnosing carcinoma or a propensity to carcinoma; and (xi) for

CC determining Carcinoma Associated (CA) gene copy number. In addition, the
 CC CA genes are useful as DNA vaccines and the CAP are useful as markers of
 CC carcinoma including lymphoma. The present sequence is one such CA coding
 CC sequence. Note: This patent is an equivalent to Baetic patent
 CC US2002182586A1, for which no sequence data was published
 XX
 XX Sequence 96499 BP; 25733 A; 19192 C; 19812 G; 28608 T; 0 U; 3154 Other;
 SO
 Query Match 0.6%; Score 26; DB 11; Length 96499;
 Best Local Similarity 100.0%; Pred. No. 2.8;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 3914 ATAAATATAAATAAATAAATAAATAA 3939
 Db 1233 ATAAATATAAATAAATAAATAAATAA 1208
 RESULT 36
 ABD33362/c
 ID ABD33362 standard; DNA; 301477 BP.
 XX ABD33362;
 AC
 XX 18-NOV-2004 (first entry)
 DT
 XX Human cancer-associated (CA) gene HD07-066.
 DE
 XX Human; cancer-associated protein; CAP; cancer-associated gene; CA; gene;
 KW de; cancer; cytostatic.
 XX
 XX Homo sapiens.
 OS
 XX MO2004058146-A2.
 PN
 XX 15-JUL-2004.
 PD
 XX 15-DEC-2003; 2003WO-US040081.
 PF
 XX 17-DEC-2002; 2002US-00322281.
 PR
 XX (SAGR-) SAGRES DISCOVERY INC.
 PA
 XX Morris DW, Malandro MS;
 PI
 XX WPI; 2004-499109/47.
 DR
 XX Novel human cancer associated protein encoded within open reading frame
 PT of cancer associated gene, useful as targets for diagnosing cancer.
 PT
 XX Claim 16; SEQ ID NO 456; 182pp; English.
 PS
 XX The invention relates to cancer-associated proteins (CAP) and the cancer-
 CC associated (CA) nucleic acids encoding them. The invention also relates
 CC to a method for treating cancers involving administering to a patient an
 CC inhibitor of CAP, and a method of screening for anticancer activity in a
 CC potential drug involving providing a cell that expresses a CA gene,
 CC contacting a tissue sample derived from a cancer cell with an anticancer
 CC drug candidate and monitoring the effect of the anticancer drug candidate
 CC on expression of the CA gene. The CAP proteins are useful for detecting
 CC cancer associated with expression of a CAP protein in a test cell sample
 CC and for screening for a bioactive agent capable of modulating the
 CC activity of a CAP protein. The CA nucleic acids are useful for diagnosing
 CC cancer, involving determining the expression of a CA nucleic acid in a
 CC tissue. This sequence represents a human CA gene of the invention. Note:
 CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX
 XX Sequence 301477 BP; 82572 A; 54594 C; 57306 G; 97116 T; 0 U; 9889 Other;
 SO
 Query Match 0.6%; Score 26; DB 13; Length 301477;
 Best Local Similarity 100.0%; Pred. No. 2.6;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAAAAAAAATATAAGTAAA 3935
 DB 105296 AAAAAAAAAATATAAGTAAA 105271

RESULT 37
 ADC64226
 ID ADC64226 standard; DNA; 45 BP.
 AC ADC64226;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Identification of gene function method-related PCR primer #2.
 XX
 CC gene function identification; host cell; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN JP2002306183-A.
 XX
 PD 22-OCT-2002.
 XX
 PF 01-JUN-2001; 2001JP-00166101.
 XX
 PR 02-JUN-2000; 2000JP-00165414.
 XX
 PA (MITU) MITSUBISHI CHEM CORP.
 XX
 DR WPI; 2003-397234/38.
 XX
 PT Identification of gene function by introducing it into a vertebrate cell
 PT and observing changes in the cell.
 XX
 PS Example 3; SEQ ID NO 2; 12pp; Japanese.
 XX
 CC The invention comprises a method for identifying the function of a target
 CC gene - the method involves introducing the sequence into a host cell and
 CC then analysing the change in character of the cell. The method is used
 CC for identifying the function of a target gene. The present DNA sequence
 CC represents a PCR primer that was used in an example of the invention.
 XX
 SQ Sequence 45 BP; 14 A; 10 C; 9 G; 12 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 10; Length 45;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGGCCTAATACGACTCACTATAGCG 43
 DB 15 TGGCCTAATACGACTCACTATAGCG 39

RESULT 38
 AAV45614
 ID AAV45614 standard; DNA; 47 BP.
 XX
 AC AAV45614;
 XX
 DT 04-MAR-1999 (first entry)
 XX
 DE Primer for Mycobacterium identification.
 XX
 CC PCR primer; probe; acid-fast bacteria; human type tubercular bacillus;
 CC Mycobacterium; detection; identification; ss.
 XX
 OS Synthetic.
 XX
 PN JP10323189-A.
 XX
 PD 08-DEC-1998.

XX
 PE 23-MAY-1997; 97JP-00133553.
 XX
 PR 23-MAY-1997; 97JP-00133553.
 XX
 PA (TOYM) TOYOBO KK.
 XX
 DR WPI; 1999-088863/08.
 XX
 CC Novel oligonucleotides - useful for the detection and identification of
 CC acid-fast bacteria.
 XX
 PS Claim 5; Page 13; 15pp; Japanese.
 XX
 CC This sequence represents an oligonucleotide of the invention. The
 CC oligonucleotides of the invention are probes and primers used for the
 CC detection of acid-fast bacteria, human type tubercular bacillus, and
 CC specifically for the identification of Mycobacterium intracellulare,
 CC and M. kansasii. The oligonucleotides allow the simple and rapid
 CC detection and identification of acid-fast bacteria
 XX
 SQ Sequence 47 BP; 11 A; 13 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 47;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCACTATAGGAGCT 47
 DB 5 CTATACGACTCACTATAGGAGCT 29

RESULT 39
 AAZ44303
 ID AAZ44303 standard; DNA; 47 BP.
 XX
 AC AAZ44303;
 XX
 DT 04-APR-2000 (first entry)
 XX
 DE M. tuberculosis 16S rRNA detecting primer 1.
 XX
 KW 16S rRNA; primer; nucleic acid amplification; signal; sensitivity; ss.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN JP11318473-A.
 XX
 PD 24-NOV-1999.
 XX
 PF 27-JAN-1999; 99JP-00018434.
 XX
 PR 17-MAR-1998; 98JP-00066988.
 XX
 PA (TOYM) TOYOBO KK.
 XX
 DR WPI; 2000-100772/09.
 XX
 CC A reagent for nucleic acid amplification and a sequence-specific nucleic
 CC acid amplification - used to inhibit nonspecific reactions to improve
 CC sensitivity and signal.
 XX
 PS Disclosure; Page 9; 10pp; Japanese.
 XX
 CC This invention describes a novel reagent for nucleic acid amplification
 CC containing at least one substance selected from BDTA, nitrofurazone,
 CC acid, uramidacetic acid, trans-1,2-cyclohexanediamine, tetraacetic acid,
 CC diethylenetriaminepentaacetic acid, ethylene glycol bis(2-aminoethyl)
 CC ether diacetate, tetraacetic acid and triethylenetriaminehexaacetic acid.
 CC The method can be used to inhibit nonspecific reactions to improve
 CC sensitivity and signal. AAZ44303-244306 represent primers used in the
 CC method of the invention

SQ Sequence 47 BP; 11 A; 13 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 3; Length 47;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATATGAGCTCACTATAGGAGCT 47
 |||||
 DB 5 CTATATGAGCTCACTATAGGAGCT 29

RESULT 40
 AAF77539
 ID AAF77539 standard; DNA; 47 BP.
 XX AAF77539;
 AC AAF77539;
 XX 23-MAY-2001 (first entry)
 XX
 XX M tuberculosis 16S rRNA gene PCR primer #1.
 DE
 XX Immunological measuring method; antibody; disease diagnosis;
 KW autoimmune disease; cancer; infection; PCR primer; ss.
 XX Mycobacterium tuberculosis.
 OS
 XX JP2001013139-A.
 PN
 XX 19-JAN-2001.
 PD
 XX 28-JUN-1999; 99JP-00182063.
 PF
 XX 28-JUN-1999; 99JP-00182063.
 PR
 XX (TOYM) TOYOBO KK.
 PA
 XX WPI; 2001-248305/26.
 DR
 XX Immunological chemical component measurement for disease diagnosis;
 PT involves detecting amount of standard nucleic acid in antigen mixed
 sample through reaction between nucleic acid and sample at constant
 PT temperature.
 PT
 XX
 PS Disclosure; Page 5; 6pp; Japanese.
 XX
 CC The present invention describes a method of immunological measuring,
 CC involving reacting an antibody or antigens in a biological sample and
 CC measuring the amount of nucleic acid in the antibody/antigen mixed sample
 CC to recognize the target components of sample. This is useful in the
 CC diagnosis of infections due to bacteria, viruses and parasites. It is
 CC also useful for detecting human leukocyte antigen, hormones,
 CC abnormalities in hormones, cancer, and bacteriotoxin in foodstuff
 CC
 XX
 SQ Sequence 47 BP; 11 A; 13 C; 10 G; 13 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 4; Length 47;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATATGAGCTCACTATAGGAGCT 47
 |||||
 DB 5 CTATATGAGCTCACTATAGGAGCT 29

RESULT 41
 AAQ52391
 ID AAQ52391 standard; DNA; 48 BP.
 XX AAQ52391;
 AC AAQ52391;
 XX 25-MAR-2003 (revised)
 DT 13-JUN-1994 (first entry)
 XX

DE PCR primer for amplifying template RNA used in selection process.
 XX
 KW ligand; identification; target; selection; amplification; partition;
 KW detection; binding; affinity; herpes simplex virus; HSV; DNA polymerase;
 KW ss.
 XX
 OS Synthetic.
 XX
 PN US5270163-A.
 PD
 XX 14-DEC-1993.
 PD
 XX 17-AUG-1992; 92US-00931473.
 PF
 XX 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 XX
 XX (UYRE-) UNITV RES CORP.
 PA
 XX Therk C, Gold L;
 PI
 XX WPI; 1993-404920/50.
 DR
 XX Identifying nucleic acids which bind target ligands - by partitioning
 PT increased affinity nucleic acids from candidate mixt. and amplifying
 PT these nucleic acids.
 PT
 XX Example 11; Col 52; 129pp; English.
 PS
 XX A method (SELEX) for identifying nucleic acid ligands which bind target
 CC ligands comprises, contacting a candidate mixture with the target ligand
 CC so that nucleic acids with an increased affinity for the target can be
 CC partitioned from the remainder of the candidate mixture; partitioning the
 CC increased affinity nucleic acids from the remainder of the candidate
 CC mixture and amplifying them. Preferably this procedure is repeated
 CC numerous times to yield a desired level of ligand enrichment. Two primers
 CC (AAQ52390, AAQ52391) were used to amplify the template RNA (AAQ52392)
 CC from which the ligands specific for herpes simplex virus were
 CC synthesized. (updated on 25-MAR-2003 to correct PF field.)
 CC
 XX
 SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TATATGAGCTCACTATAGGAGCTC 48
 |||||
 DB 9 TATATGAGCTCACTATAGGAGCTC 33

RESULT 42
 AAQ62710
 ID AAQ62710 standard; DNA; 48 BP.
 XX
 AC AAQ62710;
 XX
 DT 25-MAR-2003 (revised)
 DT 20-JAN-1995 (first entry)
 XX
 DE Primer for amplification of antibody fragment.
 XX
 KW Amplification; primer; immunoglobulin; light chain; heavy chain; IgG;
 KW gamma; ss.
 XX
 OS Synthetic.
 XX
 PN WO9411507-A2.
 XX
 XX 26-MAY-1994.
 PD
 XX 19-NOV-1993; 93WO-US011295.
 PF
 XX


```

PR 19-NOV-1992; 92US-00978835.
XX
XX (GING/) GINGERAS T R.
PA (KLIN/) KLINMAN N R M D.
PA (STIL/) STILLMAN C A.
PA (LINT/) LINTON P.
PA (DECK/) DECKER D J.
PA (BIER/) BIERER M C.
XX
PI GINGERAS TR, Klilman NRM, Stillman CA, Linton P, Decker DJ;
PI Biery MC;
XX
XX WPI, 1994-183508/22.
XX
XX Obtaining RNA encoding light- or heavy-chain of antibody having desired
PT specificity - comprising in vitro spleen fragment culture and isothermal
PT self-sustained sequence replication, also recombinant prodn. of the
XX antibody.
XX
XX Disclosure; Fig 2; 66pp; English.
XX
XX This primer was used for the amplification of the coding region of the
CC constant light chain region (CL) of an antibody. It may be used in 3SR
CC reactions (isothermal self sustained sequence replication) It hybridises
CC to the sense strand. (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 48 BP; 15 A; 7 C; 14 G; 12 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 TAATACGACTCCTATAGGAGCTC 48
DB 5 TAATACGACTCCTATAGGAGCTC 29
XX
XX
XX RESULT 43
XX AA063026 standard; DNA; 48 BP.
XX
XX AA063026;
XX
XX 25-MAR-2003 (revised)
DT 07-NOV-1994 (first entry)
XX
XX Primer used in SELEX procedure for production of bFGF ligands.
XX
XX Thrombin; coagulation; adhesion; blood clot; clot formation; ligand;
KM binding; SELEX; human immunodeficiency virus; HIV; rev protein;
KM tat protein; basic fibroblast growth factor; bFGF; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FT promoter 10..25
FT /*tag= A
FT /label= T7 promoter.
XX
XX
XX WO9408050-A1.
XX
XX 14-APR-1994.
XX
XX 28-SEP-1993; 93WO-US009296.
XX
XX 29-SEP-1992; 92US-00953694.
PR 21-OCT-1992; 92US-00964624.
PR 06-NOV-1992; 92US-00973333.
PR 22-APR-1993; 93US-00061691.
XX
XX (NEXA-) NEXAGEN INC.
XX
XX Gold LM, Tuerk C, Tasset D, Janjic N,
PI

```

```

XX
XX WPI, 1994-135610/16.
XX
XX Producing target specific nucleic acid ligands - by selection for high
PT affinity then structure determination, esp directed against HIV proteins,
PT thrombin or basic fibroblast growth factor.
XX
XX Example 5; Page 106; 208pp; English.
XX
XX Three oligonucleotides (AA063025-Q63027) were used together in a variable
CC template SELEX procedure (Experiment A) to produce ligands for basic
CC fibroblast growth factor (bFGF). This is a primer used in the procedure.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 TAATACGACTCCTATAGGAGCTC 48
DB 9 TAATACGACTCCTATAGGAGCTC 33
XX
XX
XX RESULT 44
XX AA063022 standard; DNA; 48 BP.
XX
XX AA063022;
XX
XX 25-MAR-2003 (revised)
DT 07-NOV-1994 (first entry)
XX
XX Primer used in SELEX procedure for production of HIV tat ligands.
XX
XX Thrombin; coagulation; adhesion; blood clot; clot formation; ligand;
KM binding; SELEX; human immunodeficiency virus; HIV; rev protein;
KM tat protein; ss.
XX
XX Synthetic.
XX
XX WO9408050-A1.
XX
XX 14-APR-1994.
XX
XX 28-SEP-1993; 93WO-US009296.
XX
XX 29-SEP-1992; 92US-00953694.
PR 21-OCT-1992; 92US-00964624.
PR 06-NOV-1992; 92US-00973333.
PR 22-APR-1993; 93US-00061691.
XX
XX (NEXA-) NEXAGEN INC.
XX
XX Gold LM, Tuerk C, Tasset D, Janjic N,
PI
XX
XX WPI, 1994-135610/16.
XX
XX Producing target specific nucleic acid ligands - by selection for high
PT affinity then structure determination, esp directed against HIV proteins,
PT thrombin or basic fibroblast growth factor.
XX
XX Example 3; Page 91; 208pp; English.
XX
XX Three oligonucleotides (AA063022-Q63024) were used together in a variable
CC template SELEX procedure to produce ligands for the HIV tat protein. This
CC is the 5' primer used in the procedure. (Updated on 25-MAR-2003 to
CC correct PN field.)
XX
XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 25; DB 2; Length 48;

```

Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TAATAGACTCACTATAGGAGCTC 48
Db 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 45

AAT06077 standard; DNA, 48 BP.

AC AAT06077;

DT 12-AUG-1997 (first entry)

DE Substance P ligand library 5' PCR primer.

XX ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KM Systematic Evolution of Ligands by EXponential enrichment; primer; ss;
KM polymerase chain reaction; structure; mimicry; integrase; primer; ss;
KM neuropeptide; rheumatoid arthritis; atherosclerosis; cancer;
KM diabetic retinopathy.

OS Synthetic.

PH Key Location/Qualifiers

FT promoter /tag= a

FT /note= "T7 promoter sequence"

PN MO9530775-A1.

PD 16-NOV-1995.

PF 03-MAY-1995; 95WO-US005600.

PP 06-MAY-1994; 94US-00238863.

PR 24-MAY-1994; 94US-00248632.

PR 09-SEP-1994; 94US-00303362.

PR 21-DEC-1994; 94US-00361795.

XX (UYRE-) UNIV RES CORP.

PA Gold L, Nieuwlandt D, Wecker M, Schneider DJ, Feigon J, Allen P;

PI Sullenger BA, Doudna JA;

DR WPI; 1995-404132/51.

XX Example 6; Fig 8; 209pp; English.

XX The invention relates to a novel method of isolating ligands that bind to

XX target proteins e.g. antibodies or receptors, which bind other proteins

XX or ligands. The method, designated Systematic Evolution of Ligands by

XX exponential enrichment (SELEX), comprises generating a library of random

XX oligonucleotide sequences, about 40-60 nucleotides in length, and binding

XX these sequences to the target proteins. After removal of unbound

XX material, the remaining bound nucleotide sequences are amplified e.g. by

XX PCR, and the newly amplified material is bound again with the target

XX protein. This cycle continues until a sufficiently pure oligonucleotide

XX sequence is isolated. The method allows the isolation of oligonucleotide

XX sequences which structurally mimic the target protein's ligand. The

XX primers AAT06077-8 were used to generate a random oligonucleotide library

XX of length 60 nucleotides to isolate ligands (AAT06081-130) which bind the

XX tachykinin-family neuropeptide Substance P. The ligands can be used to

XX block the activity of Substance P and is useful in the treatment of e.g.

XX rheumatoid arthritis, atherosclerosis, diabetic retinopathy or cancer

XX Sequence 48 BP; 16 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;

Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TAATAGACTCACTATAGGAGCTC 48
Db 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 46

AAT73197 standard; DNA; 48 BP.

AC AAT73197;

DT 26-AUG-1997 (first entry)

DE HIV-1 integrase ligand binding library 3' PCR primer.

XX ligand; antibody; receptor; SELEX; random library; amplification; PCR;
KM Systematic Evolution of Ligands by EXponential enrichment; autoimmunity;
KM polymerase chain reaction; structure; mimicry; integrase; primer; ss;
KM human immunodeficiency virus.

OS Synthetic.

PH Key Location/Qualifiers

FT promoter /tag= a

FT /note= "T7 promoter sequence"

PN MO9530775-A1.

PD 16-NOV-1995.

PF 03-MAY-1995; 95WO-US005600.

PP 06-MAY-1994; 94US-00238863.

PR 24-MAY-1994; 94US-00248632.

PR 09-SEP-1994; 94US-00303362.

PR 21-DEC-1994; 94US-00361795.

XX (UYRE-) UNIV RES CORP.

PA Gold L, Nieuwlandt D, Wecker M, Schneider DJ, Feigon J, Allen P;

PI Sullenger BA, Doudna JA;

DR WPI; 1995-404132/51.

XX Example 13; Page 98; 209pp; English.

XX The invention relates to a novel method of isolating ligands that bind to

XX target proteins e.g. antibodies or receptors, which bind other proteins

XX or ligands. The method, designated Systematic Evolution of Ligands by

XX exponential enrichment (SELEX), comprises generating a library of random

XX oligonucleotide sequences, about 40-60 nucleotides in length, and binding

XX these sequences to the target proteins. After removal of unbound

XX material, the remaining bound nucleotide sequences are amplified e.g. by

XX PCR, and the newly amplified material is bound again with the target

XX protein. This cycle continues until a sufficiently pure oligonucleotide

XX sequence is isolated. The method allows the isolation of oligonucleotide

XX sequences which structurally mimic the target protein's ligand. The

XX primers AAT73197-8 were used to generate a random sequence (AAT73196)

XX containing a 30 nucleotide random sequence for generating a random

XX oligonucleotide library to isolate ligands (AAT06139-93) which bind the

XX human immunodeficiency virus type 1 (HIV-1) integrase protein. The

XX ligands can be used to inhibit integrase activity and thus be used to

XX treat HIV-1 infections

```
XX
SQ Sequence 48 BP, 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCCTATAGGAGCTC 48
Db 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 47
AAQ98306
ID AAQ98306 standard; DNA; 48 BP.
XX
AC AAQ98306;
XX
DT 07-AUG-1996 (first entry)
XX
DE SELEX primer 1 molecule for isolation of bFGF ligands (experiment A).
XX
KM Family 1; family 2; ligand; thrombin;
KM systematic evolution of ligands by exponential enrichment; SELEX;
KM heparin; selection; region of homology; inhibitor; ss.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT promoter 10..25
FT /*tag= a
FT /note= "T7 promoter"
XX
XX WO5521853-A1.
XX
XX 17-AUG-1995.
XX
XX 06-FEB-1995; 95WO-US001458.
XX
XX 10-FEB-1994; 94US-00195005.
XX
XX 28-MAR-1994; 94US-00219012.
XX
XX (NEXS-) NEXSTAR PHARM INC.
XX
XX Janjic N, Gold L, Taeset D;
XX
XX WPI; 1995-293073/38.
XX
PT Identification of ligands to basic fibroblast growth factor and thrombin
PT - which can be modified for increased in vivo stability.
XX
XX Example 2; Page 69; 236pp; English.
XX
XX The sequences given in AAQ98306-07 are primers which were used in the
XX isolation of ligands to thrombin. The ligands were isolated using
XX systematic evolution of ligands by exponential enrichment (SELEX). DNA
XX nucleotides such as the one in AAQ98305, containing a region of 30 random
XX nucleotides flanked by constant sequence regions, were synthesized. The
XX random region was generated by utilizing an equimolar mixture of the four
XX nucleotides during oligonucleotide synthesis. The constant regions were
XX designed to contain PCR primer annealing sites, allowing cDNA synthesis
XX and containing a T7 RNA promoter region. An initial pool of RNA molecules
XX was prepared by in vitro transcription of the double stranded DNA
XX template. Transcription mixtures were incubated at 37 deg.C for 2-3 hours
XX which resulted in a typical amplification of 10-100 fold. Selection of
XX the high affinity ligands was done by incubating with bFGF for 10 mins a
XX buffer solution at 37 deg. C then separating the protein-RNA complexes by
XX filtration. After 10 rounds of selection, no additional improvement in
XX binding was seen. The experiment was repeated using the sequences given
XX in AAQ98308-10, using heparin as a competitor for binding of randomised
XX RNA to bFGF. The isolated ligands fell into two families, family 1 having
XX a consensus sequence of CTAACGAGG and family two having the consensus
XX sequence given in AAQ98434
```

```
XX
SQ Sequence 48 BP, 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCCTATAGGAGCTC 48
Db 9 TAATACGACTCCTATAGGAGCTC 33

RESULT 48
AAQ89173
ID AAQ89173 standard; RNA; 48 BP.
XX
AC AAQ89173;
XX
DT 25-MAR-2003 (revised)
DT 16-JAN-1996 (first entry)
XX
DE VEGF RNA binding ligand amplification primer (1).
XX
DE Nucleic acid; ligand; thrombin; elastase; theophylline; caffeine;
KM pharmaceutical; diagnosis; vascular endothelial growth factor; VEGF;
KM gene therapy; RNA; DNA; ss.
XX
OS Synthetic.
XX
XX WO9507364-A1.
XX
XX 16-MAR-1995.
XX
XX 08-SEP-1994; 94WO-US010306.
XX
XX 08-SEP-1993; 93US-00117991.
XX
XX 07-OCT-1993; 93US-00134028.
XX
XX 22-FEB-1994; 94US-00195507.
XX
XX 25-APR-1994; 94US-00233012.
XX
XX 28-APR-1994; 94US-00234997.
XX
XX (NEXA-) NEXAGEN INC.
XX
XX Gold L, Pleken W, Taeset D, Janjic N, Kirscheneuter GP;
XX Polisky B, Jayasena S, Biesacker G, Smith D, Jenison RD;
XX
XX WPI; 1995-123436/16.
XX
PT Identifying nucleic acid ligands for target molecules - by partitioning
PT increased affinity nucleic acids from a candidate mixt. and amplifying.
XX
XX Example 12; Fig 26; 251pp; English.
XX
XX The sequences given in AAQ89173-74 are primers which were used to amplify
XX the target sequence given in AAQ89172. The amplified sequences represent
XX vascular endothelial growth factor (VEGF) RNA ligands (see also AAQ88982-
XX AAQ89965). The amplified ligand sequences were identified using the
XX method of the invention. This method comprises contacting a candidate
XX mixture with the target molecule (i.e. VEGF) where the nucleic acids
XX which have an increased affinity to the target relative to the candidate
XX mixture can be partitioned from the remainder of the candidate mixture.
XX The increased affinity nucleic acids are partitioned from the remainder
XX of the candidate mixture and the isolated nucleic acids are amplified to
XX yield a ligand-enriched mixture of nucleic acids, in which the nucleic
XX acid ligands can be identified. The isolated ligands may be used as
XX pharmaceutical, diagnostic agents and in gene therapy. The ligands may
XX be RNA or DNA molecules. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 48 BP, 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 24 TATACGACTCACTATAGGAGCTC 48
 |||
 DB 9 TATACGACTCACTATAGGAGCTC 33

RESULT 49

AAQ89176
 ID AAQ89176 standard; RNA; 48 BP.

AC AAQ89176;

DT 25-MAR-2003 (revised)

DT 16-JUN-1996 (first entry)

DE VEGF RNA binding ligand amplification primer, 5G1.

KM Nucleic acid; ligand; thrombin; elastase; theophylline; caffeine;

KM pharmaceutical; diagnosis; vascular endothelial growth factor; VEGF;

KM gene therapy; RNA; DNA; ss.

OS Synthetic.

PN WO9507364-A1.

PD 16-MAR-1995.

PF 08-SEP-1994; 94MO-US010306.

XX 08-SEP-1993; 93US-00117991.

XX 07-OCT-1993; 93US-00134028.

PR 22-FEB-1994; 94US-00199507.

PR 25-APR-1994; 94US-00233012.

PR 28-APR-1994; 94US-00234997.

XX (NEXA-) NEXAGEN INC.

XX Gold L, Pleken W, Tasset D, Janjic N, Kirscheneuter GP;

PI Policky B, Jayasena S, Biesecker G, Smith D, Jensen RD;

XX WPI; 1995-123436/16.

XX Identifying nucleic acid ligands for target molecules - by partitioning

PT increased affinity nucleic acids from a candidate mixt. and amplifying.

PS Example 12; Fig 46; 251p; English.

XX The sequences given in AAQ89176-77 are primers which were used to amplify

CC the target sequence given in AAQ89175. The amplified sequences represent

CC vascular endothelial growth factor (VEGF) RNA ligands (see also AAQ8982-

CC AAQ89065). The amplified ligand sequences were identified using the

CC method of the invention. This method comprises contacting a candidate

CC mixture with the target molecule (i.e. VEGF) where the nucleic acids

CC which have an increased affinity to the target relative to the candidate

CC mixture can be partitioned from the remainder of the candidate mixture.

CC The increased affinity nucleic acids are partitioned from the remainder

CC of the candidate mixture and the isolated nucleic acids are amplified to

CC yield a ligand-enriched mixture of nucleic acids, in which the nucleic

CC acid ligands can be identified. The isolated ligands may be used as

CC pharmaceutical, diagnostic agents and in gene therapy. The ligands may

CC be RNA or DNA molecules. (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

QY Query Match 0.6%; Score 25; DB 2; Length 48;

DB Best Local Similarity 100.0%; Pred. No. 12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 50
 AAT07688
 ID AAT07688 standard; cDNA; 48 BP.

AC AAT07688;

DT 25-MAR-2003 (revised)

DT 15-JUL-1996 (first entry)

DE Amplification primer #2 for SELEX of HSV-1 DNA polymerase.

XX DNA polymerase; gp43; ligand; cell sorting; inhibitor; probe; primer;

KM systematic evolution of ligands by exponential enrichment; SELEX; PCR;

KM bacteriophage coat protein; serine protease; mammalian receptor; amplify;

KM mammalian hormone; mammalian growth factor; ribosomal protein; T7;

KM viral rev protein; polymerase chain reaction; HSV-1; ss.

OS Synthetic.

PN US5475096-A.

PD 12-DEC-1995.

PF 10-JUN-1991; 91US-00714131.

XX 11-JUN-1990; 90US-00536428.

XX (UYRE-) UNITV RES CORP.

XX Tuerk C, Gold L;

XX WPI; 1996-039557/04.

XX Artificial nucleic acid ligands - for selected target proteins.

XX Example 11; Col 49; 133p; English.

XX This sequence represents an amplification primer used as the PCR primer 2

CC in a systematic evolution of ligands by exponential enrichment (SELEX)

CC reaction on HSV-1 DNA polymerase. This sequence amplifies a portion of

CC the T7 RNA polymerase promoter. The primer represented by AAT07687 is

CC also used in this reaction. In a SELEX reaction, a target molecule (such

CC as T7 RNA polymerase) is contacted with a mixture of random nucleic acids

CC under conditions favourable for binding. Unbound nucleic acids are then

CC separated from those bound to the target, and the nucleic acid-target

CC pairs are dissociated. The dissociated nucleic acids are amplified (using

CC a primer such as this) to give a ligand enriched mixture. These steps are

CC repeated until the specific ligand is obtained. This procedure can also

CC be carried out for ligands for bacteriophage coat proteins, serine

CC proteases, mammalian receptors, mammalian hormones, mammalian growth

CC factors, ribosomal proteins, DNA polymerases and viral rev proteins. The

CC ligands identified (such as the sequences represented by AAT07653-T07660)

CC may be used in assays, diagnostic procedures, or cell sorting as an

CC inhibitor of the target molecule function. It may also be used as a probe

CC or sequestering agent, and also possess catalytic activity. (Updated on

XX 25-MAR-2003 to correct PF field.)

QY Query Match 0.6%; Score 25; DB 2; Length 48;

DB Best Local Similarity 100.0%; Pred. No. 12;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 51

AAT84603

ID AAT84603 standard; DNA; 48 BP.

XX AAT84603;

XX 25-MAR-2003 (revised)
 DT 17-DEC-1997 (first entry)
 XX
 XX RNA ligand to HIV-1 nucleocapsid 3' PCR primer.
 DE
 XX
 XX Human immunodeficiency virus type 1; HIV-1; nucleocapsid; RNA ligand;
 KW inhibitor; SELEX; therapy; diagnosis; primer; PCR;
 KM polymerase chain reaction; ss.
 XX
 XX Synthetic.
 OS
 XX US5654151-A.
 PN
 XX 05-AUG-1997.
 PD
 XX 07-JUN-1995; 95US-00477530.
 PF
 XX 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 PR 17-AUG-1992; 92US-00931473.
 PR 21-OCT-1992; 92US-00964624.
 PR 08-SEP-1993; 93US-00117991.
 PR 21-DEC-1994; 94US-00361795.
 PR 19-MAY-1995; 95US-00447172.
 XX
 XX (NEXS-) NEXSTAR PHARM INC.
 PA
 XX Gold L, Allen PN;
 PI
 XX WPI; 1997-401842/37.
 DR
 XX
 XX Identifying nucleic acid ligands specific for viral nucleocapsid by the
 PT SELEX method - particularly to identify high affinity ligands for human
 PT immunodeficiency virus nucleocapsid, potentially useful as diagnostic and
 PT therapeutic agents.
 PS
 XX Example 1; Col 21-22; 17pp; English.
 XX
 XX This sequence comprises a 3' PCR primer for a random pool of 10 power 14
 CC DNA oligomers (see AAT84602). It includes a 5' HindIII site and a T7
 CC promoter sequence. A 5' primer (AAT84604) is also provided. Oligomers in
 CC the random pool have 5' and 3' proximal ends of fixed sequence to allow
 CC PCR amplification, while the central region consists of 30 randomised
 CC positions. They are used in a SELEX (Systematic Evolution of Ligands by
 CC Exponential enrichment) method to select RNA ligands (see AAT84605-26) to
 CC HIV-1 nucleocapsid. The method involves contacting the oligomers with HIV
 CC -1 nucleocapsid, partitioning nucleic acids of relatively high affinity
 CC and specificity, and amplifying these nucleic acids. The isolated RNA
 CC ligands are inhibitors of HIV-1 nucleocapsid and are potentially useful
 CC as diagnostic and therapeutic agents. (Updated on 25-MAR-2003 to correct
 CC PF field.)
 CC
 XX
 SO Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 24 TAATACGACTCACTATAGGAGCTC 48
 Db 9 TAATACGACTCACTATAGGAGCTC 33
 RESULT 52
 AAT79124
 ID AAT79124 standard; DNA; 48 BP.
 XX
 XX AAT79124;
 AC
 XX
 XX 25-MAR-2003 (revised)
 DT 07-OCT-1997 (first entry)
 XX

DE 3' primer for SELEX template for HIV-1 nucleocapsid ligands.
 XX
 XX Human immunodeficiency virus; HIV; nucleocapsid; SELEX; infection;
 KW inhibit; ss.
 XX
 XX Synthetic.
 OS
 XX US5635615-A.
 PN
 XX 03-JUN-1997.
 PD
 XX 07-JUN-1995; 95US-00477530.
 PF
 XX 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 PR 17-AUG-1992; 92US-00931473.
 PR 21-OCT-1992; 92US-00964624.
 PR 08-SEP-1993; 93US-00117991.
 PR 21-DEC-1994; 94US-00361795.
 PR 19-MAY-1995; 95US-00447172.
 XX
 XX (NEXS-) NEXSTAR PHARM INC.
 PA
 XX Gold L, Allen P;
 PI
 XX WPI; 1997-309884/28.
 DR
 XX
 XX Nucleic acids that are HIV-1 nucleocapsid ligands - for treatment of
 PT diagnosis or HIV-1 infection.
 PT
 XX
 XX Example 1; Col 19-20; 17pp; English.
 PS
 XX
 XX AAT79124 and AAT79125 are PCR primers used for the amplification of a
 CC SELEX template molecule having a stretch of 40 randomised nucleotides.
 CC The template was used for the production of nucleic acid (especially RNA)
 CC ligands for the nucleocapsid of human immunodeficiency virus type 1 (HIV-
 CC 1). The ligands bind the nucleocapsid and inhibit its function; they can
 CC be used in the treatment and diagnosis of HIV-1 infection. (Updated on 25
 CC -MAR-2003 to correct PF field.)
 CC
 XX
 SO Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 24 TAATACGACTCACTATAGGAGCTC 48
 Db 9 TAATACGACTCACTATAGGAGCTC 33
 RESULT 53
 AAT87307
 ID AAT87307 standard; DNA; 48 BP.
 XX
 XX AAT87307;
 AC
 XX
 XX 24-NOV-1997 (first entry)
 DT
 XX
 XX SELEX PCR primer 2 for hTNF-alpha ligand amplification.
 DE
 XX
 XX high affinity ligand; cytokine; interferon-gamma; IFN-gamma; RANTES;
 KW interleukin-4; IL-4; tumour necrosis factor-alpha; TNF-alpha;
 KW Systematic Evolution of Ligands by Exponential enrichment; SELEX;
 KW diagnosis; inflammatory response; septic shock; arthritis;
 KW graft-vs-host reaction; primer; PCR; amplify; ss.
 XX
 XX Synthetic.
 OS
 XX WO9640717-A1.
 PN
 XX 19-DEC-1996.
 PD
 XX

PF 04-JUN-1996; 96MO-US009537.
 XX
 XX 07-JUN-1995; 95US-00477527.
 PR 07-JUN-1995; 95US-00481710.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 XX
 PI Tasseet D, Pagratia N, Jayasena S, Gold L;
 XX WPI; 1997-087049/08.
 DR
 XX
 PT Identification of nucleic acid ligands that bind cytokine(s) - by
 PT partitioning the ligands from a nucleic acid mixture, using SELEX
 PT techniques.
 XX
 PS Example 7; Page 73; 175pp; English.
 XX
 XX AAT87306-07 are primers used to begin a new round of SELEX (Systematic
 CC Evolution of Ligands by Exponential enrichment) used to evolve high
 CC affinity ligands to human tumour necrosis factor (hTNF)-alpha (using
 CC AAT87305 as a template). Nucleic acid (NA) ligands to a cytokine can be
 CC identified using SELEX. A candidate mixture of NA's are contacted with a
 CC cytokine where the NA's having an increased affinity to the cytokine
 CC relative to the candidate mixture may be partitioned from the rest of the
 CC mixture. The NA's with increased affinity are amplified to yield a
 CC mixture of NA's enriched for the NA sequences and relatively higher
 CC affinity and selectivity for binding to the cytokine. The NA ligands are
 CC useful in diagnostic and therapeutic applications especially to prevent
 CC or treat diseases or medical conditions in human patients, e.g.
 CC associated with excessive cytokine production such as inflammatory
 CC responses mediated by IFN-gamma or interleukin-4, septic shock, arthritis
 CC or graft-vs-host reactions mediated by hTNF-alpha
 XX

SO Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
 DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 54

AAV00777
 ID AAV00777 standard; DNA; 48 BP.

AC AAV00777;

DT 25-MAR-1998 (first entry)

DE PCR primer #2 for isolating SELEX ligands to HSV-1 DNA polymerase.

XX Systematic evolution of ligands by exponential enrichment; SELEX;
 KM binding affinity; diagnosis; inhibitor; probe; catalytic; template;
 KM herpes simplex virus type 1; HSV1; DNA polymerase; ss.

XX Synthetic.

OS Herpes simplex virus type 1.

PN US5670637-A.

PD 23-SEP-1997.

XX 27-MAR-1995; 95US-00412110.

PR 11-JUN-1990; 90US-00536428.

PR 10-JUN-1991; 91US-00714131.

XX (NEXS-) NEXSTAR PHARM INC.

PA Tuerk C, Gold L;

XX WPI; 1997-479527/44.
 DR
 XX
 PT Nucleic acid ligands for binding proteins - obtained by systematic
 PT evolution of ligands by exponential enrichment procedures.
 XX
 PS Example 11; Col 49; 133pp; English.
 XX
 CC This primer was used to primer cDNA synthesis for generating the template
 CC AAV00778 for use in a SELEX method to isolate nucleic acid ligands that
 CC bind the herpes simplex virus type 1 DNA polymerase. The ligands are
 CC isolated by the systematic evolution of ligands by exponential enrichment
 CC (SELEX) method of the invention. This method is especially used to
 CC isolate novel non-naturally occurring nucleic acid ligands having a
 CC specific binding affinity for a target molecule, where the target
 CC molecule is a protein and the nucleic acid ligand is not a nucleic acid
 CC known to bind the target molecule. The nucleic acid ligands can be used,
 CC e.g. in assay methods, diagnostic procedures, cell sorting, as inhibitors
 CC of target molecule function, as probes, as sequestering agents, for
 CC therapy or as catalysts
 XX

SO Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATAGACTCACTATAGGAGCTC 48
 DB 9 TAATAGACTCACTATAGGAGCTC 33

RESULT 55

AAV14558
 ID AAV14558 standard; cDNA; 48 BP.

AC AAV14558;

DT 21-MAY-1998 (first entry)

DE Primer for HSV-1 DNA polymerase.

XX High affinity RNA ligand motif; polymer binding; cell sorting; inhibitor;
 KM sequestering agent; HSV-1 DNA polymerase; PCR primer; amplify; ss.

XX Synthetic.

OS Herpes simplex virus unknown type.

PN US5696249-A.

PD 09-DEC-1997.

XX 24-MAR-1995; 95US-00409442.

PR 11-JUN-1990; 90US-00536428.

PR 10-JUN-1991; 91US-00714131.

XX (NEXS-) NEXSTAR PHARM INC.

PA Tuerk C, Gold L;

DR WPI; 1998-041356/04.

PT Synthetic nucleic acid ligands - that bind to target molecules other than
 PT nucleic acids.

PS Example 11; Col 48; 137pp; English.

CC This sequence represents a primer for the herpes simplex virus 1 (HSV-1)
 CC DNA polymerase. The amplified sequence is used to identify ligands of the
 CC invention. The ligands are non-naturally occurring nucleic acid ligand
 CC with specific binding affinity for a target molecule, where: the target
 CC molecule is not a polynucleotide that binds to the ligand by Watson-Crick

CC base pairing or triple helix binding; the ligand is not a nucleic acid
CC having the known physiological function of being bound by the target
CC molecule; and the ligand is obtained by: (a) contacting the target
CC molecule with a candidate mixture of nucleic acids, each having a region
CC of randomised sequence; (b) separating the nucleic acids having the
CC highest affinity for the target; and (c) amplifying the separated nucleic
CC acids, ligands as above that bind to natural or synthetic polymers, e.g.
CC proteins, polysaccharides, glycoproteins, hormones, receptors, cell
CC surfaces, drugs, metabolites, cofactors, transition-state analogues or
CC toxins, may be useful in assays, diagnostic procedures or cell sorting,
CC as inhibitors of target molecule function, as probes, as sequestering
CC agents, etc., or may have catalytic activity
XX

SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCATATAGGAGCTC 48
|||||
9 TAATACGACTCATATAGGAGCTC 33

Db

RESULT 56
AAV79637
ID AAV79637 standard; DNA; 48 BP.
XX
AC AAV79637;
XX
DT 24-FEB-1999 (first entry)
XX
DE HSV-1 DNA polymerase cDNA amplifying primer 1.
XX
XX Target molecule; detection; measuring; high-affinity; ligand; SELEX;
KM systematic evolution of ligands by exponential enrichment; assay;
KM diagnostic; cell sorting; metabolite; HSV-1; DNA polymerase; RNA ligand;
KM PCR primer; ss.
XX
OS Synthetic.
OS Herpes simplex virus unknown type.
XX
XX US6843653-A.
PN
XX
PD 01-DEC-1998.
XX
PF 06-JUN-1995; 95US-00469609.
XX
PR 11-JUN-1990; 90US-00536428.
PR 10-JUN-1991; 91US-00714131.
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
XX
PI Tuerk C, Gold L;
XX
XX WPI; 1999-044566/04.
DR
XX
PT Detection of target molecule - by detecting binding of nucleic acid
PT ligand.
XX
XX
PS Example 11; Col 48; 138bp; English.
XX
XX The invention provides methods for detecting the presence or absence of a
CC target molecule in a sample and measuring the amount of a target molecule
CC using high-affinity nucleic acid ligands. The nucleic acid ligands are
CC identified by the method of the invention referred to as the systemic
CC evolution of ligands by exponential enrichment (SELEX). The nucleic acid
CC products are useful in assay methods, diagnostic procedures, cell
CC sorting, as inhibitors of target molecule function etc. The methods are
CC used to detect or determine the amount of a protein, small molecule,
CC controlled substance or metabolite in a biological sample. The present
CC sequence represents a primer used for amplifying the cDNA encoding a
CC Herpes simplex virus (HSV-1) DNA polymerase. This is used in the isolation

CC of RNA ligands for HSV-1 DNA polymerase by the method of the invention
XX

SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 2; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCATATAGGAGCTC 48
|||||
9 TAATACGACTCATATAGGAGCTC 33

Db

RESULT 57
AAA92737
ID AAA92737 standard; DNA; 48 BP.
XX
AC AAA92737;
XX
DT 10-JAN-2001 (first entry)
XX
DE HSV-1 DNA polymerase PCR primer # 2.
XX
XX Nucleic acid ligand; assay method; diagnostic procedure; cell sorting;
KM inhibitor; probe; sequestering agent; PCR primer; ss.
XX
OS Herpes simplex virus unknown type.
XX
PN US6110900-A.
XX
PD 29-AUG-2000.
XX
PF 27-AUG-1998; 98US-00143190.
XX
XX
PR 11-JUN-1990; 90US-00536428.
PR 10-JUN-1991; 91US-00714131.
PR 24-MAR-1995; 95US-00409442.
PR 27-MAR-1995; 95US-00412110.
PR 25-APR-1995; 95US-00428964.
PR 06-JUN-1995; 95US-00469609.
XX
XX
PA (NEXS-) NEXSTAR PHARM INC.
XX
XX Gold L, Tuerk C;
XX
XX WPI; 2000-571430/53.
DR
XX
XX
PT Diagnostic composition comprising a nucleic acid ligand useful in binding
PT reaction e.g. assay methods, diagnostic procedures, cell sorting,
PT inhibitors of target molecule function, as probes, as sequestering
PT agents.
XX
XX
PS Example 10; Col 49; 138bp; English.
XX
XX The present invention relates to a diagnostic composition comprising a
CC nucleic acid ligand. The present sequence is a PCR primer for
CC bacteriophage T7 RNA polymerase. The ligands of the present invention are
CC identified from a candidate mixture of nucleic acids by contacting the
CC candidate mixture with the target molecule; partitioning increased
CC affinity nucleic acids from the remainder of the candidate mixture; and
CC amplifying the increased affinity nucleic acids to yield a ligand.
CC enriched mixture of nucleic acids. The ligands of the present invention
CC are useful for detecting a target molecule in a sample, and also in any
CC binding reaction such as assay methods, diagnostic procedures, cell
CC sorting, inhibitors of target molecule function, as probes, and as
CC sequestering agents. The present sequence was used in the isolation of
CC ligands of the present invention
XX
XX

SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 3; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 |||||
 Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 58
 AAF70540
 ID AAF70540 standard; DNA; 48 BP.
 XX
 AC AAF70540;
 XX
 DT 20-APR-2001 (first entry)
 XX
 DE SELEX experiment oligonucleotide #2.
 XX
 KM Ligand; basic fibroblast growth factor; bFGF; gene therapy; vascular;
 KW atherosclerosis; angioplasty; stability; ss.
 XX
 OS Unidentified.
 XX
 PN US6177557-B1.
 XX
 PD 23-JAN-2001.
 XX
 PF 05-AUG-1996; 96US-00687421.
 XX
 PR 11-JUN-1990; 90US-00536428.
 PR 10-JUN-1991; 91US-00714131.
 PR 06-NOV-1992; 92US-00973333.
 PR 10-FEB-1994; 94US-00195005.
 PR 28-MAR-1994; 94US-00219012.
 XX
 PA (NEXS-) NEXSTAR PHARM INC.
 XX
 PI Janjic N, Gold L, Tasset D;
 XX
 DR WPI; 2001-158583/16.
 XX
 PT Novel nucleic acid ligands to basic fibroblast growth factor that are
 PT useful as inhibitors of basic fibroblast growth factors and 2'-amino
 PT modified RNA ligands, exhibit increased in vivo stability.
 XX
 PS Example 19; Col 36; 153pp; English.
 XX
 CC The present invention relates to a purified and isolated non-naturally
 CC occurring DNA ligands to basic fibroblast growth factor (bFGF). The
 CC ligands are useful as part of gene therapy treatments and for diagnosing
 CC pathogenesis of vascular diseases including initiation and progression of
 CC atherosclerosis, acute coronary syndromes, vein graft disease and
 CC restenosis following coronary angioplasty. The ligands have improved
 CC stability in vivo
 CC
 XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 SQ

Query Match 0.6%; Score 25; DB 4; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 |||||
 Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 59
 AAD44075
 ID AAD44075 standard; DNA; 48 BP.
 XX
 AC AAD44075;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 XX PCR primer #1a used to illustrate the method of the invention.

XX
 KM Target compound; detector molecule; food; environmental; effluent sample;
 KW water; PCR; primer; ss.
 XX
 OS Unidentified.
 XX
 PN US2002051974-A1.
 XX
 PD 02-MAY-2002.
 XX
 PF 24-NOV-1999; 99US-00449204.
 XX
 PR 30-NOV-1998; 98US-0110259P.
 XX
 PA (DODG/) DODGE A H.
 PA (MENG/) MENG Y G.
 PA (SIMS/) SIMS P W.
 PA (SINI/) SINICROPI D V.
 PA (WILL/) WILLIAMS P M.
 PA (WONG/) WONG W L.
 XX
 PI Dodge AH, Meng YG, Sims PW, Sinicropi DV, Williams PM, Wong WL;
 XX
 DR WPI; 2002-453890/48.
 XX
 PT Method for quantitating or detecting the presence of a target compound in
 PT a sample using a nucleic acid detector molecule useful for detecting
 PT target compounds in clinical diagnosis.
 XX
 PS Example 1; Page 13; 37pp; English.
 XX
 CC The invention relates to a method for quantitating or detecting the
 CC presence of a target compound in a sample comprising a nucleic acid
 CC detector molecule, amplification and quantitation or detection of the
 CC detector molecule. The methods are useful for the detection of target
 CC compounds in clinical diagnosis of physiological conditions in the same
 CC way as ELISA, immuno-PCR and ELONA. The methods may also be used to
 CC detect the presence of a target compound in food, environmental, water
 CC and effluent samples. The present sequence is a PCR primer used to
 CC illustrate the method of the invention
 CC
 XX Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
 SQ

Query Match 0.6%; Score 25; DB 6; Length 48;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
 |||||
 Db 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 60
 ABK61113
 ID ABK61113 standard; DNA; 48 BP.
 XX
 AC ABK61113;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE SELEX process primer sequence #3.
 XX
 KM SELEX; systematic evolution of ligands by exponential enrichment; ss;
 KW endocrine; hormone reaction modifier; primer.
 XX
 OS Synthetic.
 XX
 PN US6331398-B1.
 XX
 PD 18-DEC-2001.
 XX
 PF 10-FEB-2000; 2000US-00502344.
 XX

PR 11-JUN-1990; 90US-00536428.
PR 25-APR-1995; 95US-00428964.
PR 06-JUN-1995; 95US-00469609.
PR 27-AUG-1998; 98US-00143190.
PA (GILE-) GILEAD SCI INC.
XX
PI Gold L, Tuerk C;
XX
DR WPI; 2002-113091/15.
XX
PT Identifying a function-modifying nucleic acid ligand, useful in
PT diagnostic assays and inhibiting biological function of a target
PT molecule, comprises contacting with target molecule and evaluating
PT whether the ligand modifies the target.
XX
PS Example 11; Col 47; 137pp; English.
XX
CC The invention relates to nucleic acid ligands which bind specifically to
CC a desired target compound or molecule. A function-modifying nucleic acid
CC ligand can be identified by contacting a candidate nucleic acid ligand
CC with the target molecule and evaluating whether the ligand modifies the
CC function of the target molecule. The nucleic acid ligands each have a
CC unique sequence and the property of binding specifically to a desired
CC target compound or molecule. The method, also known as the SELEX method
CC (systematic evolution of ligands by exponential enrichment), can be used
CC to detect proteins which are not known to bind nucleic acids as part of
CC their biological function, meaning that the ligands can be employed in a
CC manner similar to conventional antibody- based diagnostics. The ligands
CC identified are useful as diagnostic assay reagents and have therapeutic
CC uses as sequestering agents, drug delivery vehicles and modifiers of
CC hormone reactions. This sequence represents a primer used in the scope of
CC the invention.
XX
SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 6; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 TAATACGACTCCTATAGGAGCTC 48
Db 9 TAATACGACTCCTATAGGAGCTC 33
RESULT 61
ADP67501 standard; DNA; 48 BP.
XX
AC ADP67501;
XX
DT 12-FEB-2004 (first entry)
XX
DE SELEX cDNA synthesis PCR primer 2.
XX
KM ss; SELEX; systematic evolution of ligands by exponential enrichment;
KM ligand; diagnostic agent; cell sorting; inhibitor; probe;
KM sequestering agent.
XX
OS Synthetic.
XX
PN US2003157487-A1.
XX
PD 21-AUG-2003.
XX
PF 18-OCT-2001; 2001US-00037986.
XX
PR 11-JUN-1990; 90US-00536428.
PR 10-JUN-1991; 91US-00714131.
PR 24-MAR-1995; 95US-00409442.
PR 27-MAR-1995; 95US-00412110.
PR 25-APR-1995; 95US-00428964.
PR 06-JUN-1995; 95US-00469609.
PR 27-AUG-1998; 98US-00143190.

PR 27-AUG-1998; 98US-00143190.
PR 10-FEB-2000; 2000US-00502344.
PA (GOLD/) GOLD L.
PA (TUEK/) TUEK C.
XX
PI Gold L, Tuerk C;
XX
DR WPI; 2003-897816/82.
XX
PT Composition useful as a diagnostic agent for detecting the presence or
PT absence of a target molecule in a sample comprises nucleic acid ligands.
XX
PS Example 11; SEQ ID NO 37; 138pp; English.
XX
XX The invention relates to a composition comprising nucleic acid ligands,
CC typically an RNA molecule selected using the technique of SELEX
CC (systematic evolution of ligands by exponential enrichment). The
CC composition is used as a diagnostic agent for detecting the presence or
CC absence of target molecules (e.g. natural and synthetic polymers
CC including proteins, polysaccharides, glycoproteins, hormones, receptors
CC and cell surfaces), and small molecules in a sample, as a diagnostic
CC agent to measure the amount of a target molecule in a sample, in assay
CC methods, cell sorting, as inhibitors of target molecule function, as
CC probes and sequestering agents. The nucleic acids have capacity for
CC forming a variety of two and three dimensional structures and chemical
CC versatility available within their monomers to act as ligands with
CC virtually any chemical compound, whether monomeric or polymeric. The
CC nucleic acids possess unique sequences, which help the nucleic acids to
CC specifically bind to a desired target compound or molecule. The present
CC sequence is an oligonucleotide used in the construction of a SELEX
CC library or starting sequence.
XX
SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;
Query Match 0.6%; Score 25; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 24 TAATACGACTCCTATAGGAGCTC 48
Db 9 TAATACGACTCCTATAGGAGCTC 33
RESULT 62
ADG39049 standard; DNA; 48 BP.
XX
AC ADG39049;
XX
DT 26-FEB-2004 (first entry)
XX
DE cDNA primer #3.
XX
KM ss; SELEX; systematic evolution of ligands by exponential enrichment;
KM cell sorting; unique sequence specificity; unique binding specificity;
KM PCR; primer.
XX
OS Synthetic.
XX
PN US2003198989-A1.
XX
PD 23-OCT-2003.
XX
PF 03-APR-2003; 2003US-00408085.
XX
PR 11-JUN-1990; 90US-00536428.
PR 24-MAR-1995; 95US-00409442.
PR 27-MAR-1995; 95US-00412110.
PR 25-APR-1995; 95US-00428964.
PR 06-JUN-1995; 95US-00469609.
PR 27-AUG-1998; 98US-00143190.
PR 10-FEB-2000; 2000US-00502344.

```
PR 18-OCT-2001; 2001US-00037986.
XX
XX (GILE-) GILEAD SCI INC.
XX
XX Gold L, Therk C;
XX
XX WPI; 2004-059537/06.
XX
PT Diagnostic composition useful for detecting the presence or absence of a
PT target molecule comprises a nucleic acid ligand.
XX
PS Example 11; SEQ ID NO 37; 149bp; English.
XX
CC The invention relates to a diagnostic composition which comprises a
CC nucleic acid ligand. The invention is useful for detecting the presence
CC or absence of a target molecule and as diagnostic reagent to measure the
CC amount of target molecule in a sample; in assay methods, diagnostic
CC procedures, cell sorting, as inhibitors of target molecule function, as
CC probes and as sequencing agent. The nucleic acids in the composition
CC have unique sequences and binding specificities; capacity for forming a
CC variety of 2- or 3-dimensional structures; chemical versatility within
CC their monomers; and broad range of functions of the nucleic acid ligands.
CC The composition has ability of binding specifically to a desired target
CC molecule or compound facilitating qualitative and quantitative detection.
CC The present sequence is used in the exemplification of the invention.
XX
SQ Sequence 48 BP; 18 A; 12 C; 9 G; 9 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 12; Length 48;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAATACGACTCACTATAGGAGCTC 48
DB 9 TAATACGACTCACTATAGGAGCTC 33

RESULT 63
ABL88785
ID ABL88785 standard; DNA; 59 BP.
XX
XX ABL88785;
XX
DT 22-MAY-2002 (first entry)
XX
DE HIV-1 reverse transcriptase primer 3' ET21-T7 SEQ ID NO:7.
XX
XX Binding molecule; HIV-1; human immunodeficiency virus type 1;
XX reverse transcriptase; binding group; PCR primer; ss.
XX
OS Human immunodeficiency virus 1.
OS Synthetic.
XX
XX EP1174518-A1.
XX
XX 23-JAN-2002.
XX
XX 20-JUL-2000; 2000EP-00202611.
XX
XX 20-JUL-2000; 2000EP-00202611.
XX
XX (AMST-) AMSTERDAM SUPPORT DIAGNOSTICS BV.
XX
XX Loukachov VV, Van Gemen B, Goudsmit J;
XX
XX WPI; 2002-156696/21.
XX
XX Collection of binding groups for determining or typing samples,
XX especially clinical samples, has groups capable to identify essentially
XX all members of the family of nucleic acids of relatively high
XX significance.
XX
PS Example 5; Page 6; 166bp; English.
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```
XX
XX The present invention describes a collection of binding groups for a
XX family of nucleic acids comprising members of relative high and relative
XX low significance, where the binding groups are selected to be capable to
XX identify, alone or in combination, essentially all members of the family
XX of nucleic acids of relatively high significance. The collection of
XX binding groups is useful for typing of nucleic acid in a clinical sample,
XX by contacting the nucleic acid with the collection and determining
XX whether one or more binding groups bound to the nucleic acid of the
XX sample. This method is useful for determining whether the sample
XX comprises at least a part of a member of relatively high significance of
XX a family of nucleic acids. The collection of binding groups is useful for
XX diagnosing the severity of a disease caused by a pathogen containing a
XX member of a family of nucleic acids. ABL88779 to ABL89321 represent
XX oligonucleotide sequences used in the exemplification of the present
XX invention
XX
SQ Sequence 59 BP; 15 A; 12 C; 12 G; 20 T; 0 U; 0 Other;

Query Match 0.6%; Score 25; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTATACGACTCACTATAGGAGCT 47
DB 5 CTATACGACTCACTATAGGAGCT 29

RESULT 64
ABL41041
ID ABL41041 standard; DNA; 59 BP.
XX
XX ABL41041;
XX
DT 12-AUG-2002 (first entry)
XX
XX GUS mRNA UTR fragment amplifying primer 7.
XX
DE Translation; untranslated region; UTR; pathogen; virus; GUS; PCR; primer;
XX ss.
XX
OS Synthetic.
XX
XX JP2002095483-A.
XX
XX 02-APR-2002.
XX
XX 25-SEP-2000; 2000JP-00291084.
XX
XX 25-SEP-2000; 2000JP-00291084.
XX
XX (TOYT ) TOYOTA JIDOSHA KK.
XX (KONP-) KONPON KENKYUSHO KK.
XX
XX WPI; 2002-439991/47.
XX
XX Screening potential translational control factors of mRNA, useful for
XX preventative research on pathogenic viruses, involves introducing random
XX oligonucleotide sequences into an untranslated region.
XX
XX Example 1; Page 7; 16bp; Japanese.
XX
XX The invention relates to a method of screening potential translational
XX control factors of mRNA. The method involves synthesizing an mRNA
XX containing a cap structure and a poly(A) chain sequence in which a random
XX oligonucleotide sequence which is a candidate for translational control
XX factor is introduced in the 5'- untranslated region (UTR) and the mRNA in
XX which the translation efficiency is changed compared to the untreated is
XX selected. The method can be used for preventive researches on pathogenic
XX viruses. Sequences ABL41035-42 represent primers used for amplifying the
XX UTRs of GUS mRNA
XX
SQ Sequence 59 BP; 26 A; 13 C; 12 G; 8 T; 0 U; 0 Other;
```

```

Query Match      0.64; Score 25; DB 6; Length 59;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 GGCTTAATAGCACTCACTATAGGGA 44
      |||
DB      4 GGCTTAATAGCACTCACTATAGGGA 28

RESULT 65
ABL41037
ID ABL41037 standard; DNA; 63 BP.
XX
XX ABL41037;
AC
XX 12-AUG-2002 (first entry)
XX
XX GUS mRNA UTR fragment amplifying primer 3.
DE
XX Translation; untranslated region; UTR; pathogen; virus; GUS; PCR; primer;
KM 89.
XX
XX Synthetic.
OS
XX JP2002095483-A.
XX
XX 02-APR-2002.
XX
XX 25-SEP-2000; 2000JP-00291084.
XX
XX 25-SEP-2000; 2000JP-00291084.
XX
XX (TOYT ) TOYOTA JIDOSHA KK.
XX
XX (KONP-) KONPON KENKYUSHO KK.
XX
XX WPI; 2002-439991/47.
XX
XX Screening potential translational control factors of mRNA, useful for
PT preventative research on pathogenic viruses, involves introducing random
PT oligonucleotide sequences into an untranslated region.
XX
XX Example 1; Page 7; 16pp; Japanese.
XX
XX The invention relates to a method of screening potential translational
CC control factors of mRNA. The method involves synthesizing an mRNA
CC containing a cap structure and a poly(A) chain sequence in which a random
CC oligonucleotide sequence which is a candidate for translational control
CC factor is introduced in the 5'- untranslated region (UTR) and the mRNA in
CC which the translation efficiency is changed compared to the untreated is
CC selected. The method can be used for preventive researches on pathogenic
CC viruses. Sequences ABL41035-42 represent primers used for amplifying the
CC UTRs of GUS mRNA
XX
XX
SQ Sequence 63 BP; 16 A; 19 C; 13 G; 15 T; 0 U; 0 Other;

Query Match      0.64; Score 25; DB 6; Length 63;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      20 GGCTTAATAGCACTCACTATAGGGA 44
      |||
DB      9 GGCTTAATAGCACTCACTATAGGGA 33

RESULT 66
ADN14395
ID ADN14395 standard; DNA; 123 BP.
XX
XX ADN14395;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX

```

```

DE PCR primer 1 to construct dsRNA with stabilising hairpin & linker region.
XX
XX 89; RNA complex; immunosuppressive; cytostatic; cancer;
KM systemic lupus erythematosus; Alzheimer's; Huntington's disease;
KM salivary gland carcinoma; melanoma; brain tumour; leukaemia; lymphoma;
KM gene therapy; PCR; primer.
XX
XX Synthetic.
OS
XX
XX Key Location/Qualifiers
FH misc_binding 5..123
FT /*cag= a
FT /bound_molety= "Reverse primer (2)"
FT /note= "Forms double stranded region with nucleotides 123
FT -5"
XX
XX WO2004035765-A2.
XX
XX 29-APR-2004.
XX
XX 20-OCT-2003; 2003WO-US033466.
XX
XX 18-OCT-2002; 2002US-0419532P.
XX
XX 28-OCT-2002; 2002US-0421757P.
XX
XX (NUCL-) NUCLEONICS INC.
XX
XX Pachuk CV, Satishchandran C, Mccallue DE;
XX
XX WPI; 2004-348454/32.
XX
XX
XX New substantially pure ribonucleic acid (RNA) complex comprising a first
PT strand and a second strand that hybridize to each other, useful for
PT treating cancer, systemic lupus erythematosus, Alzheimer's disease or
PT Huntington's disease.
XX
XX
XX Example 10; Page 126; 204pp; English.
XX
XX This invention relates to double stranded ribonucleic acid (RNA)
CC structures and constructs. Specifically, it comprises first and second
CC RNA strands that hybridize to each other under physiological conditions
CC to form a double-strand region, wherein the double-strand region contains
CC one or more mismatched regions that result in two or more double-stranded
CC segments. Furthermore, the mismatched regions may be cleaved by single-
CC strand ribonuclease enzymes. The present invention describes expression
CC vectors that encode dsRNAs with an intron containing exemplary target
CC genes such as anti-folate resistance genes. Accordingly, using gene
CC therapy, these RNA complexes exhibit immunosuppressive and cytostatic
CC activities and can be used to treat cancer, systemic lupus erythematosus,
CC Alzheimer's and Huntington's disease. The cancer is selected from,
CC amongst others, prostate, breast, ovarian, salivary gland carcinoma,
CC melanoma, brain tumour, leukaemia and lymphoma. This oligonucleotide
CC sequence is a PCR primer given in an exemplification of the invention.
XX
XX
SQ Sequence 123 BP; 32 A; 32 C; 27 G; 32 T; 0 U; 0 Other;

Query Match      0.64; Score 25; DB 12; Length 123;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 GGCTTAATAGCACTCACTATAGGGA 45
      |||
DB      4 GGCTTAATAGCACTCACTATAGGGA 28

RESULT 67
AAQ23256
ID AAQ23256 standard; DNA; 136 BP.
XX
XX AAQ23256;
AC
XX
XX 25-MAR-2003 (revised)
DT
XX 31-JUL-1992 (first entry)

```

```

XX DE Plasmid pGENE 8459.
XX XX Synthetic ribozyme; virus resistant plants; antiviral agents.
XX OS Synthetic.
XX FT Key Location/Qualifiers
XX FT promoter 1..27 /*tag= a
XX FT m1sc_feature /note= "T7 promoter"
XX FT /tag= b
XX FT /note= "SFL1 ribozyme RNA coding region"
XX PN JF03219874-A.
XX PD 27-SEP-1991.
XX PF 19-DEC-1989; 89JP-00329831.
XX PR 19-DEC-1989; 89JP-00329831.
XX PA (AGEN ) AGENCY OF IND SCI & TECHNOLOGY.
XX DR WPI; 1992-107687/14.
XX PT New synthetic ribozyme with hair pin structure - using DNA fragment with
XX PT ribozyme RNA code sequence and 2nd sequence that cleaves transcribed
XX PS Disclosure; Fig 3; 8pp; Japanese.
XX CC The sequence is that of plasmid pGENE 8459 which contains a T7 promoter
XX CC upstream of a Sfl ribozyme and a 3' terminal self-processing ribozyme.
XX CC The plasmid is ligated into pUC19 and can then be used to prepare virus
XX CC resistant plants or new antiviral agents. Its hairpin structure is
XX CC extremely stable against exonucleases in vivo. See also AAQ23255.
XX CC (Updated on 25-MAR-2003 to correct PA field.)
XX SQ Sequence 136 BP; 34 A; 31 C; 42 G; 29 T; 0 U; 0 Other;
XX
Query Match 0.6%; Score 25; DB 2; Length 136;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

XX PA (CHIR ) CHIRON CORP.
XX XX Morris DW, Malandro MS;
XX PI WPI; 2005-273395/28.
XX DR
XX PT Nucleic acid array useful for detecting cancer associated nucleic acid,
XX PT comprises two or more nucleic acid probes.
XX PS Disclosure; SEQ ID NO 966; 198pp; English.
XX
XX CC The invention relates to a nucleic acid array for detecting a cancer
XX CC associated (CA) nucleic acid, comprising two or more nucleic acid probes.
XX CC The invention also relates to a peptide array comprising two or more
XX CC isolated polypeptides encoded by a CA nucleic acid sequence, a compound
XX CC that binds to a polypeptide, an isolated antibody or its fragment which
XX CC binds to a polypeptide, which is prepared by immunizing a host animal
XX CC with a composition comprising the polypeptide or its antigen binding
XX CC fragment and collecting cells from the host expressing antibodies against
XX CC the antigen or its antigen binding fragment, a composition comprising the
XX CC antibody and a carrier, a method of screening for anticancer activity, a
XX CC method of detecting a CA nucleic acid, a method of diagnosing cancer, a
XX CC method of treating cancer and a method of inhibiting expression of a CA
XX CC nucleic acid in a cell. The CA nucleic acids are useful for detecting CA
XX CC nucleic acids. The antibody is useful for detecting the presence or
XX CC absence of cancer cells in an individual which involves contacting cells
XX CC from the individual with the antibody and detecting a complex of a CA
XX CC protein from the cancer cells and the antibody, where the detection of
XX CC the complex correlates with the presence of cancer cells in the
XX CC individual. The composition is useful for inhibiting growth of cancer
XX CC cells in an individual or for delivering a therapeutic agent to cancer
XX CC cells in an individual. The invention is also useful for diagnosing
XX CC cancer, for treating cancer and for inhibiting expression of a CA gene in
XX CC a cell. This sequence represents human cancer-associated genomic DNA of
XX CC the invention.
XX SQ Sequence 243934 BP; 66213 A; 49129 C; 53448 G; 74301 T; 0 U; 843 Other;
XX
Query Match 0.6%; Score 25; DB 14; Length 243934;
Best Local Similarity 100.0%; Pred. No. 6.6;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

XX Tang DG, Honn KV;
 XX WPI, 1999-130388/11.
 XX
 XX In vitro method for determining the effectiveness of compound in
 PT producing apoptosis - comprises, providing tumour cells which are known
 PT to produce 12-lipoxygenase, exposing tumour cells compound which inhibits
 PT 12-lipoxygenase, determining apoptosis.
 XX
 XX Disclosure; Col 13; 26pp; English.
 XX
 XX An in vitro method has been developed for determining the effectiveness
 CC of a compound in producing apoptosis. The method comprises: (a) providing
 CC tumour cells which are known to produce 12-lipoxygenase, using normal
 CC cells as a control; (b) exposing the tumour cells and the normal cells to
 CC a compound (1) which inhibits 12-lipoxygenase which is to be tested in
 CC vitro in a culture medium; and (c) determining if the tumour cells have
 CC undergone apoptosis as a result of exposure to (1), without producing
 CC apoptosis in normal cells. (1) is selected from: a cyclic hydroxamic acid
 CC (1a); an aryl aliphatic acid (1b); nordihydro-guaiaric acid (1c); N-
 CC benzyl-N-hydroxy-5-phenylpentanamide (1d); baicalin (1e); and an
 CC antisense segment of DNA which selectively binds to DNA encoding 12-
 CC lipoxygenase (1f). The process is used to determine the effectiveness of
 CC (1) in producing apoptosis, also to induce selective apoptosis of tumour
 CC cells, and to test, detect and compare tumour apoptosis caused by (1).
 CC The process can effectively identify new candidate chemotherapeutic
 CC agents that can be used in the clinical treatment of cancer patients. The
 CC present sequence represents a T7 RNA polymerase promoter sequence from
 CC the present invention. (Updated on 27-AUG-2003 to correct OS field.)
 XX
 XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 24; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CCTAATACGACTCCTATAGGAG 45
 Db 5 CCTAATACGACTCCTATAGGAG 28

RESULT 70
 ABK31899
 ID ABK31899 standard; DNA; 29 BP.
 XX
 AC ABK31899;
 XX
 XX 29-AUG-2003 (revised)
 DT 23-APR-2002 (first entry)
 XX
 XX Bacteriophage T7 DNA sequence relating to *Candida tropicalis* invention.
 DE
 XX CPERA, CPERB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A;
 KM CYP52A5B, CYP52A8A, CYP52A8B, CYP52D4A, URA3A; cytochrome P450;
 KM NADPH2 reductase; omega-hydroxylase complex; dicarboxylic acid; de.
 XX
 XX Enterobacteria phage T7.
 OS
 XX US6331420-B1.
 PN
 XX
 XX 18-DEC-2001.
 PD
 XX
 XX 30-APR-1999; 99US-00302620.
 PF
 XX
 XX 01-MAY-1998; 98US-0083798P.
 PR 05-OCT-1998; 98US-0103099P.
 PR 10-MAR-1999; 99US-0123555P.
 XX
 XX (WILS/) WILSON C R.
 PA (CRAF/) CRAFT D L.
 PA (EIRI/) EIRICH L D.
 PA (ESHO/) ESHOO M.

PA (MADD/) MADDURI K M.
 PA (CORN/) CORNETT C A.
 PA (BREN/) BRENNER A A.
 PA (TANG/) TANG M.
 PA (LOPE/) LOPEZ J C.
 PA (GLEE/) GLEESON M.
 XX
 PI Wilson CR, Craft DL, Birch LD, Eshoo M, Madduri KM, Cornett CA;
 PI Brenner AA, Tang M, Loper JC, Gleeson M;
 XX
 XX WPI; 2002-138383/18.
 DR
 XX
 XX Novel isolated nucleic acid encoding cytochrome P450 and NADPH reductase
 PT enzymes of omega-hydroxylase complex of *Candida tropicalis*, useful for
 PT increasing production of dicarboxylic acids.
 XX
 XX Disclosure; Col 16; 173pp; English.
 XX
 XX The present invention relates to the isolation of *Candida tropicalis*
 CC 20336 novel genes (CPERA, CPERB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A,
 CC CYP52A3B, CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B, CYP52D4A and URA3A)
 CC which encode cytochrome P450 and NADPH2 reductase enzymes of the omega-
 CC hydroxylase complex. Also disclosed are vectors containing these genes
 CC and methods of producing these enzymes. The genes and vectors are useful
 CC for increasing production of a dicarboxylic acid by providing a host cell
 CC having a naturally occurring number of the genes of the invention and
 CC increasing in the host cell, the number of genes encoding these enzymes.
 CC The present sequence represents a Bacteriophage T7 DNA sequence of
 CC unknown function. Note: The present sequence is given in the sequence
 CC listing but is not mentioned elsewhere in the specification. (Updated on
 CC 29-AUG-2003 to standardise OS field)
 XX
 XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 SQ
 Query Match 0.6%; Score 24; DB 6; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 CCTAATACGACTCCTATAGGAG 45
 Db 5 CCTAATACGACTCCTATAGGAG 28

RESULT 71
 ADC44990
 ID ADC44990 standard; DNA; 29 BP.
 XX
 AC ADC44990;
 XX
 XX 18-DEC-2003 (first entry)
 DT
 XX
 XX T7 promoter consensus sequence.
 DE
 XX T7, promoter; de; omega oxygenase complex; cytochrome P450 monooxygenase;
 KM CYP, NADPH reductase enzymes; CPER, CPERA, CPERB, CYP52A1A, CYP52A2A,
 KM CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B,
 KM CYP52D4A, dicarboxylic acid; diester; polymer; thermoplastic;
 KM plasticising agent; lubricant; hydraulic fluid; agricultural chemical;
 KM pharmaceutical; dye; surfactant; adhesive; QC-RT-PCR;
 KM quantitative competitive reverse transcription PCR.
 KM
 XX
 XX Enterobacteria phage T7.
 OS
 XX US2003049821-A1.
 PN
 XX
 XX 13-MAR-2003.
 PD
 XX
 XX 03-MAY-2002; 2002US-00138638.
 PF
 XX
 XX 01-MAY-1998; 98US-0083798P.
 PR 05-OCT-1998; 98US-0103099P.
 PR 10-MAR-1999; 99US-0123555P.
 PR 30-APR-1999; 99US-00302620.

```

PR 12-OCT-2001; 2001US-00976800.
XX (WILS/) WILSON C R.
PA (CRAF/) CRAFT D L.
PA (BIRI/) BIRICH L D.
PA (ESHO/) ESHOO M.
PA (MADD/) MADDURI K M.
PA (CORN/) CORNETT C A.
PA (BREN/) BRENNER A A.
PA (TANG/) TANG M.
PA (LOPE/) LOPER J C.
PA (GLEE/) GLEESON M.
XX Wilson CR, Craft DL, Birch LD, Eshoo M, Madduri KM, Cornett CA;
PI Brenner AA, Tang M, Loper JC, Gleeson M;
XX WPI; 2003-777150/73.
XX
XX New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes
PT (e.g. CPRa, CPRb or CYP52A1A), useful for producing dicarboxylic acids
PT that may be utilized as industrial intermediates in manufacturing
PT diesters and polymers.
XX
XX Example 11; SEQ ID NO 109; 196pp; English.
XX
XX The invention relates to an isolated nucleic acid selected encoding
CC Candida tropicalis omega oxygenase complex enzymes (CYP) designated CPRa,
CC monooxygenase (CYP) and NADPH reductase enzymes (CPR) designated CPRa,
CC CPRb, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A,
CC CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A) or their coding regions. Also
CC included are the CPR/CYP proteins, a vector comprising the nucleic acid
CC cited above, a host cell transfected or transformed with the above
CC nucleic acid, producing the proteins, discriminating members of a gene
CC family by quantifying the amount of target mRNA in a sample, increasing
CC production of a dicarboxylic acid and increasing the production of the
CC proteins cited above. The host cell is C. tropicalis is specifically
CC H5343 ura-. The nucleic acid is useful for producing dicarboxylic acids
CC that may be utilized as industrial intermediates in the manufacture of
CC diesters and polymers (e.g. as thermoplastic, plasticizing agents,
CC lubricants, hydraulic fluids, agricultural chemicals, pharmaceuticals,
CC dyes, surfactants or adhesives). The present sequence is a T7 promoter
CC consensus sequence incorporated into a quantitative competitive reverse
CC transcription (QC-RT) PCR primer used to assay the levels of CYP, CPR or
CC control FOX mRNA in response to exogenously added substrates.
XX
XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 24; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 CCTAATACGACTCATATAGGAG 45
Db 5 CCTAATACGACTCATATAGGAG 28
RESULT 72
ADCA5560
ID ADC45560 standard; DNA; 29 BP.
XX
XX ADC45560;
AC
XX 18-DEC-2003 (first entry)
DT
XX
XX T7 promoter consensus sequence.
DE
XX
XX T7 promoter; ds; omega oxygenase complex; cytochrome P450 monooxygenase;
KM CYP; NADPH reductase enzymes; CPR; CPRa; CPRb; CYP52A1A; CYP52A2A;
KM CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A; CYP52A5B; CYP52A8A; CYP52A8B;
KM CYP52D4A; dicarboxylic acid; diester; polymer; thermoplastic;
KM plasticizing agent; lubricant; hydraulic fluid; agricultural chemical;
KM pharmaceutical; dye; surfactant; adhesive; QC-RT-PCR;
KM quantitative competitive reverse transcription PCR.

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XX
XX OS Enterobacteria phage T7.
XX
XX US2003049822-A1.
XX
XX 13-MAR-2003.
XX
XX 03-MAY-2002; 2002US-00139031.
XX
XX 01-MAY-1998; 98US-0063798P.
PR 05-OCT-1998; 98US-0103099P.
PR 10-MAR-1999; 99US-0123555P.
PR 30-APR-1999; 99US-00302620.
PR 12-OCT-2001; 2001US-00976800.
XX
XX (WILS/) WILSON C R.
PA (CRAF/) CRAFT D L.
PA (BIRI/) BIRICH L D.
PA (ESHO/) ESHOO M.
PA (MADD/) MADDURI K M.
PA (CORN/) CORNETT C A.
PA (BREN/) BRENNER A A.
PA (TANG/) TANG M.
PA (LOPE/) LOPER J C.
PA (GLEE/) GLEESON M.
XX
XX Wilson CR, Craft DL, Birch LD, Eshoo M, Madduri KM, Cornett CA;
PI Brenner AA, Tang M, Loper JC, Gleeson M;
XX WPI; 2003-765370/72.
XX
XX New nucleic acid encoding cytochrome P450 and NADPH reductase enzymes
PT (e.g. CPRa, CPRb or CYP52A1A), useful for producing dicarboxylic acids
PT that may be utilized as industrial intermediates in manufacturing
PT diesters and polymers.
XX
XX Example 11; SEQ ID NO 109; 196pp; English.
XX
XX The invention relates to an isolated nucleic acid selected encoding
CC Candida tropicalis omega oxygenase complex enzymes (CYP) designated CPRa,
CC monooxygenase (CYP) and NADPH reductase enzymes (CPR) designated CPRa,
CC CPRb, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B, CYP52A5A,
CC CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A) or their coding regions. Also
CC included are the CPR/CYP proteins, a vector comprising the nucleic acid
CC cited above, a host cell transfected or transformed with the above
CC nucleic acid, producing the proteins, discriminating members of a gene
CC family by quantifying the amount of target mRNA in a sample, increasing
CC production of a dicarboxylic acid and increasing the production of the
CC proteins cited above. The host cell is C. tropicalis is specifically
CC H5343 ura-. The nucleic acid is useful for producing dicarboxylic acids
CC that may be utilized as industrial intermediates in the manufacture of
CC diesters and polymers (e.g. as thermoplastic, plasticizing agents,
CC lubricants, hydraulic fluids, agricultural chemicals, pharmaceuticals,
CC dyes, surfactants or adhesives). The present sequence is a T7 promoter
CC consensus sequence incorporated into a quantitative competitive reverse
CC transcription (QC-RT) PCR primer used to assay the levels of CYP, CPR or
CC control FOX mRNA in response to exogenously added substrates.
XX
XX Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
SQ
Query Match 0.6%; Score 24; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 22 CCTAATACGACTCATATAGGAG 45
Db 5 CCTAATACGACTCATATAGGAG 28
RESULT 73
ADE52071
ID ADE52071 standard; DNA; 29 BP.
XX

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AC ADE52071;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE T7 promoter consensus sequence.
 XX
 KM T7 promoter; ds: cytochrome P450; CYP; NADPH reductase; CPR;
 KM omega-hydroxylase complex; omega-oxidation; long chain fatty acid;
 KM QC-RT PCR; Quantitative competitive reverse transcriptase PCR.
 XX
 OS Enterobacteria phage T7.
 XX
 PN US2003073220-A1.
 XX
 PD 17-APR-2003.
 XX
 PF 03-MAY-2002; 2002US-00138916.
 XX
 PR 01-MAY-1998; 98US-0083798P.
 PR 05-OCT-1998; 98US-0103099P.
 PR 10-MAR-1999; 99US-0123555P.
 PR 30-APR-1999; 99US-00302620.
 PR 12-OCT-2001; 2001US-00976800.
 XX
 PA (WLS/) WILSON C. R.
 PA (CRAP/) CRAFT D. L.
 PA (EIRI/) EIRICH L. D.
 PA (ESHO/) ESHOO M.
 PA (MADD/) MADDURI K. M.
 PA (CORN/) CORNETT C. A.
 PA (BREN/) BRENNER A. A.
 PA (TANG/) TANG M.
 PA (LOPE/) LOPEZ J. C.
 PA (GLEE/) GLEESON M.
 XX
 PI Wilson CR, Craft DL, Eirich LD, Bshoo M, Madduri KM, Cornett CA;
 PI Brenner AA, Tang M, Loper JC, Gleeson M;
 DR WPI; 2003-625522/59.
 XX
 PT New cytochrome P450 and NADPH oxidoreductase, i.e. CPR and CYP, genes and
 PT proteins, useful for discriminating members of a gene family by
 PT quantifying the amount of target mRNA in a sample, or for omega-oxidation
 PT of long chain fatty acids.
 XX
 PS Example 11; SEQ ID NO 109; 194bp; English.
 XX
 CC The invention relates to isolated nucleic acids encoding cytochrome P450
 CC (CYP) and NADPH reductase (CPR) enzymes of the omega-hydroxylase complex
 CC of Candida tropicalis. Also included are the CYP and CPR proteins
 CC (comprising CPR, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B,
 CC CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B, or CYP52D4A), a vector comprising
 CC any one of the nucleic acid sequences cited above, a host cell
 CC transfected or transformed with the nucleic acid, methods of producing
 CC the CPR or CYP proteins, a method for discriminating members of a gene
 CC family by quantifying the amount of target mRNA in a sample and methods
 CC for increasing the production of a dicarboxylic acid, (or the CPR/CYP
 CC proteins). The CPR and CYP genes and proteins are useful for
 CC discriminating members of a gene family by quantifying the amount of
 CC target mRNA in a sample, for increasing production of a dicarboxylic
 CC acid, or for omega-oxidation of long chain fatty acids. The technique of
 CC Quantitative competitive reverse transcriptase PCR (QC-RT PCR) was used
 CC to quantitate the CPR/CYP mRNA in RNA sample. The present sequence is a
 CC T7 promoter consensus sequence incorporated into a QC-RT PCR primer used
 CC in the analysis.
 XX
 SQ Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 0.6%; Score 24; DB 10; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 CCTAATCGACTCACTATAGGAG 45

DB 5 CCTAATCGACTCACTATAGGAG 28
 RESULT 74
 ID ADF72378
 XX ADF72378 standard; DNA; 29 BP.
 XX
 AC ADF72378;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Bacteriophage T7 promoter consensus sequence seq id 109.
 XX
 KM CYP52A2B; cytochrome P450; NADH reductase; dicarboxylic acid production;
 KM organic substrate oxidation; fatty acid oxidation;
 KM gene integration vector; CYP; CPR; Bacteriophage T7; promoter; ds.
 XX
 OS Enterobacteria phage T7.
 XX
 PN US2003077795-A1.
 XX
 PD 24-APR-2003.
 XX
 PF 12-OCT-2001; 2001US-00976800.
 XX
 PR 10-MAR-1999; 99US-0123555P.
 XX
 PA (WLS/) WILSON C. R.
 PA (CRAP/) CRAFT D. L.
 PA (EIRI/) EIRICH L. D.
 PA (ESHO/) ESHOO M.
 PA (MADD/) MADDURI K. M.
 PA (CORN/) CORNETT C. A.
 PA (BREN/) BRENNER A. A.
 PA (TANG/) TANG M.
 PA (LOPE/) LOPEZ J. C.
 PA (GLEE/) GLEESON M.
 XX
 PI Wilson CR, Craft DL, Eirich LD, Bshoo M, Madduri KM, Cornett CA;
 PI Brenner AA, Tang M, Loper JC, Gleeson M;
 DR WPI; 2003-810780/76.
 XX
 PT New nucleic acids encoding a CYP52A2B protein useful for increasing the
 PT production of dicarboxylic acid for oxidizing organic substrates such as
 PT fatty acids.
 XX
 PS Example 11; SEQ ID NO 109; 188bp; English.
 XX
 CC The invention describes an isolated nucleic acid encoding a CYP52A2B
 CC protein comprising the fully defined sequence of 522 amino acids, as
 CC given in the specification, and comprising a coding region defined by
 CC nucleotides 1072-2640 of a fully defined sequence of 3755 base pairs, as
 CC given in the specification. The nucleic acids encoding the cytochrome
 CC P450 and NADH reductase enzymes of Candida tropicalis are useful for
 CC increasing the production of dicarboxylic acid for oxidizing organic
 CC substrates such as fatty acids. This sequence represents the
 CC bacteriophage T7 promoter consensus sequence used in the isolation of RNA
 CC for a quantitative competitor reverse transcriptase PCR assay to determine
 CC the level of CYP52A5 RNA in a sample.
 XX
 SQ Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;
 XX
 Query Match 0.6%; Score 24; DB 10; Length 29;
 Best Local Similarity 100.0%; Pred. No. 32;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 CCTAATCGACTCACTATAGGAG 45
 DB 5 CCTAATCGACTCACTATAGGAG 28

```

RESULT 75
ADFI1818
ID ADFI1818 standard; DNA; 29 BP.
XX
AC ADFI1818;
XX
DT 12-FEB-2004 (first entry)
XX
DE T7 promoter consensus sequence.
XX
KM CPRA; CPRB; CYP52A1A; CYP52A2A; CYP52A2B; CYP52A3A; CYP52A3B; CYP52A5A;
XX CYP52A5B; CYP52A8A; CYP52A8B; CYP52D4A; gene family; ds.
XX
OS Enterobacteria phage T7.
XX
PN US2003153060-A1.
XX
PD 14-AUG-2003.
XX
PF 03-MAY-2002; 2002US-00139218.
XX
PR 01-MAY-1998; 98US-0083798P.
PR 05-OCT-1998; 98US-0103099P.
PR 10-MAR-1999; 99US-0123555P.
PR 30-APR-1999; 99US-00302620.
PR 12-OCT-2001; 2001US-00976800.
XX
PA (WILS/) WILSON C R.
PA (CRAF/) CRAFT D L.
PA (EIRI/) EIRICH L D.
PA (ESHO/) ESHOO M.
PA (MADD/) MADDURI K M.
PA (CORN/) CORNETT C A.
PA (BREN/) BRENNER A A.
PA (TANG/) TANG M.
PA (LOPE/) LOPER J C.
PA (GLEE/) GLEESON M.
XX
PI Wilson CR, Craft DL, Eirich LD, Eshoo M, Madduri KM, Cornett CA,
PI Brenner AA, Tang M, Loper JC, Gleeson M;
XX
DR WPI; 2003-897719/82.
XX
PT New CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B,
PT CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A gene, useful for
PT increasing production of dicarboxylic acid.
XX
PS Example 11; SEQ ID NO 109; 194bp; English.
XX
CC The invention relates to a new isolated nucleic acid which encodes a
CC CPRA, CPRB, CYP52A1A, CYP52A2A, CYP52A2B, CYP52A3A, CYP52A3B,
CC CYP52A5A, CYP52A5B, CYP52A8A, CYP52A8B or CYP52D4A protein. The nucleic acid is
CC useful for discriminating between members of a gene family by quantifying
CC the amount of mRNA in a sample. The present sequence represents the T7
CC promoter consensus sequence.
XX
SQ Sequence 29 BP; 9 A; 6 C; 8 G; 6 T; 0 U; 0 Other;

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Query Match 0.6%; Score 24; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 22 CCTAATACGACTCATCTATAGGAG 45
DB 5 CCTAATACGACTCATCTATAGGAG 28

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Search completed: February 27, 2006, 20:48:05
 Job time : 1592 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 20:48:17 ; Search time 10434 Seconds
(without alignments)
18958.768 Million cell updates/sec

Title: US-10-623-477-3

Sequence score: 4228
1 gtcagctcagcgcctcactg.....agaacacacacacacacac

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 0

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: listing first 100 summaries

Database :

- EST.*
- 1: gb_gaet1.*
 - 2: gb_gaet2.*
 - 3: gb_gaet3.*
 - 4: gb_hic.*
 - 5: gb_gaet4.*
 - 6: gb_gaet5.*
 - 7: gb_gaet6.*
 - 8: gb_gaet7.*
 - 9: gb_gaet8.*
 - 10: gb_gaet9.*
 - 11: gb_gaet10.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	417	9.9	581	10 BX290871	BX290871 Arabidops
2	278	6.6	652	9 B62389	B62389 T2110TR TA
3	233	5.5	437	9 CC056828	CC056828 SALK_1112
4	193	4.6	234	10 AL936239	AL936239 Arabidops
5	176	4.2	300	11 CR402297	CR402297 Arabidops
6	154	3.6	162	10 AL759737	AL759737 Arabidops
7	140	3.3	276	11 CR402298	CR402298 Arabidops
8	139	3.3	415	9 B2379137	B2379137 SALK_1129
9	135	3.2	2106	4 CNS0A2BQ	BX826541 Arabidops
10	127	3.0	192	10 AL759736	AL759736 Arabidops
11	112	2.6	112	9 CC455690	CC455690 SALK_0857
12	103	2.4	323	9 CC797115	CC797115 SALK_1444
13	91	2.2	92	10 AL769520	AL769520 Arabidops
14	91	2.2	418	10 AL769556	AL769556 Arabidops
15	84	2.0	2315	4 CNS0A2BQ	BX826540 Arabidops
16	80	1.9	92	10 AL754990	AL754990 Arabidops
17	75	1.8	424	3 BP561373	BP561373 Arabidops
18	73	1.7	694	3 BH934314	BH934314 Ode65910.
19	71	1.7	268	10 AL756782	AL756782 Arabidops
20	68	1.6	594	6 CB260786	CB260786 65-B9572-
21	65	1.5	110	10 AL769557	AL769557 Arabidops
22	61	1.4	96	10 AL754991	AL754991 Arabidops

23	45	1.1	381	9 BH481919	BH481919 BOGEA30TR
24	45	1.1	673	9 BH676371	BH676371 BOHXV80TR
25	43	1.0	56	9 B2380049	B2380049 SALK_1145
26	32	0.8	335	9 BH451280	BH451280 BOGNW77TR
27	32	0.8	796	9 BH510257	BH510257 BOHKU78TR
28	27	0.6	897	10 CW938563	CW938563 TGB18.3.F
29	27	0.6	901	10 CW938873	CW938873 TGB19.1.C
30	26	0.6	288	2 BP925688	BP925688 CME-NT015
31	25	0.6	225	2 BE145442	BE145442 IL5-HT019
32	25	0.6	388	10 CE734860	CE734860 L1gr-g88-
33	25	0.6	488	9 AZ088538	AZ088538 RPCI-23-4
34	25	0.6	715	10 AG013324	AG013324 Homo sapi
35	25	0.6	755	10 CNS01002	AL153762 Anopheles
36	25	0.6	793	9 BH510250	BH510250 BOHKU78TF
37	25	0.6	798	10 CW949303	CW949303 TGB33.4.F
38	25	0.6	860	10 AG409273	AG409273 Mus muscu
39	25	0.6	898	10 CW940939	CW940939 TGB22.1.A
40	25	0.6	924	10 AG400158	AG400158 Mus muscu
41	25	0.6	1036	10 CW937215	CW937215 TGB16.1.F
42	24	0.6	161	7 CK121482	CK121482 202020.PI
43	24	0.6	191	9 AQ955990	AQ955990 LERPA18TR
44	24	0.6	278	7 CK573161	CK573161 1172 Plab
45	24	0.6	278	8 DR973784	DR973784 CHUT008P1
46	24	0.6	310	9 AQ955989	AQ955989 LERPA18TF
47	24	0.6	318	9 BH451271	BH451271 BOGNW77TF
48	24	0.6	320	7 CV263561	CV263561 WS02022.B
49	24	0.6	339	9 CE127892	CE127892 L1gr-g88-
50	24	0.6	349	9 BM163414	BM163414 EST565948
51	24	0.6	350	10 AG229188	AG229188 Lotus cor
52	24	0.6	390	9 B239509	B239509 CH230-456
53	24	0.6	392	3 BM163358	BM163358 EST565881
54	24	0.6	394	9 AQ081838	AQ081838 RPCI11-55
55	24	0.6	398	3 BM163834	BM163834 EST566357
56	24	0.6	399	3 BM966009	BM966009 ko20F03.Y
57	24	0.6	418	11 CRO57094	CRO57094 Forward s
58	24	0.6	423	9 AZ301311	AZ301311 UP 315-19
59	24	0.6	429	9 AQ955959	AQ955959 LERPA17TF
60	24	0.6	440	3 BM171421	BM171421 EST573944
61	24	0.6	444	9 AQ959560	AQ959560 LERPA17TR
62	24	0.6	454	9 AQ028235	AQ028235 CIT-HSP-2
63	24	0.6	469	3 BM166570	BM166570 EST569093
64	24	0.6	478	5 BU303919	BU303919 603737371
65	24	0.6	478	5 BU396654	BU396654 603533803
66	24	0.6	487	2 BF558277	BF558277 UI-R-A1-e
67	24	0.6	511	1 AL720059	AL720059 AL720059
68	24	0.6	523	1 AL720155	AL720155 AL720155
69	24	0.6	525	1 AL715025	AL715025 AL715025
70	24	0.6	529	8 DR576414	DR576414 MS00743.C
71	24	0.6	540	1 AL723652	AL723652 AL723652
72	24	0.6	564	3 BM168186	BM168186 EST570709
73	24	0.6	581	9 B2293554	B2293554 CG0392.11
74	24	0.6	631	3 BM170115	BM170115 EST572638
75	24	0.6	637	10 CE784932	CE784932 L1gr-g88-
76	24	0.6	668	10 AG366559	AG366559 Mus muscu
77	24	0.6	673	1 AL726822	AL726822 AL726822
78	24	0.6	675	9 AZ393711	AZ393711 IM0156723
79	24	0.6	679	10 AG077514	AG077514 Pan trogl
80	24	0.6	680	9 BH426079	BH426079 BOHIW87TR
81	24	0.6	687	10 AG069432	AG069432 Pan trogl
82	24	0.6	698	9 BH936859	BH936859 Ccd82912.
83	24	0.6	698	6 CA966306	CA966306 CcdX07a27
84	24	0.6	706	9 AG108940	AG108940 Pan trogl
85	24	0.6	708	1 AL722577	AL722577 AL722577
86	24	0.6	715	10 AG099910	AG099910 Pan trogl
87	24	0.6	718	10 AG106672	AG106672 Pan trogl
88	24	0.6	720	10 AG117860	AG117860 Pan trogl
89	24	0.6	721	3 BM160799	BM160799 EST563322
90	24	0.6	721	10 AG101726	AG101726 Pan trogl
91	24	0.6	738	8 CV908369	CV908369 Ptdpcd.36
92	24	0.6	740	10 AL726847	AL726847 AL726847
93	24	0.6	742	10 AG418452	AG418452 Mus muscu
94	24	0.6	756	10	
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c	98	24	0.6	781	6	CA405371	CA405371
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ALIGNMENTS

RESULT 1
BX290871/c
LOCUS
DEFINITION
Arabis thaliana T-DNA flanking sequence GK-440605-018216,
genomic survey sequence.
ACCESSION
BX290871
VERSION
BX290871.1
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (chale creas)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
AUTHORS
TITLE
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weishaar, B.
GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
Bioinformatics 19 (11), 1441-1442 (2003)

JOURNAL
PUBMED
12874060
AUTHORS
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

JOURNAL
PUBMED
14756321
AUTHORS
Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)

JOURNAL
PUBMED
14682050
AUTHORS
Strizhov, N., Li, Y., Rosso, M.G. and Weishaar, B.
Direct Submission
Submitted (31-MAR-2004) Weishaar, B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

COMMENT
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1. 581
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/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACT161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

FEATURES

source

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 417; DB 10; Length 581;
Matches 417; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1152	GTGCTGTTGACTAATTTCTCAGAGTGAGTGTAATCAAGAACTAATATTCGAAA	1211
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Qy	1212	AGAAAGAAAAAAGCAGAAAACTATGTCGAAAAGACATTAATGACCTAAATTTGG	1271
Db	464	AGAAAGAAAAAAGCAGAAAACTATGTCGAAAAGACATTAATGACCTAAATTTGG	405
Qy	1272	ATTATTTAAATGATATATGTTGGTGAATTTTAATCAATTAACAAATCAAGAA	1231
Db	404	ATTATTTAAATGATATATGTTGGTGAATTTTAATCAATTAACAAATCAAGAA	345
Qy	1332	GGAGAGGAGGACCTCTTCGCTTATGATTTCCCTCTTAACAACAGCTCCACTATCCT	1391
Db	344	GGAGAGGAGGACCTCTTCGCTTATGATTTCCCTCTTAACAACAGCTCCACTATCCT	285
Qy	1392	TTTTTACTTCGACAAATATCATTACACGAGAAATCTGCTGTGATCATTTTCATGCA	1451
Db	284	TTTTTACTTCGACAAATATCATTACACGAGAAATCTGCTGTGATCATTTTCATGCA	225
Qy	1452	AAATTAACATAATTTTGGATTTTGTGCAAGTTCTGCTTTTAAGTCGATATTTTG	1511
Db	224	AAATTAACATAATTTTGGATTTTGTGCAAGTTCTGCTTTTAAGTCGATATTTTG	165
Qy	1512	GTAATCTATATGTGATATACATCATCAAGCTATCAATTAATGATCTCTTC	1568
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RESULT 2
B62389/c
LOCUS
DEFINITION
T21110TR T21110 Arabidopsis thaliana genomic clone T21110, genomic survey sequence.
ACCESSION
B62389
VERSION
B62389.1
KEYWORDS
GSS.
SOURCE
Arabidopsis thaliana (chale creas)
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
AUTHORS
Rounale, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Adams, M.D. and Venter, J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3
Unpublished (1997)
Other GSSs: T21110TF
Contact: Steve Rounale
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: rounale@tigr.org
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 652.

location/Qualifiers
1. 652
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FEATURES
source

ORIGIN

ORIGIN

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/note="Vector: Belobacit; Site 1: HindIII; Site 2: HindIII; Produced by Rod Wing"

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DB 278 GTATAATATATACAAATTTAATTAAGTATGATTTACTATCTCAAACTTACC 219
QY 2344 ATCTTCAACATTAATATGATCAATTTTATTTTACTAAACTTCTCCACTTAAA 2403
DB 218 ATCTTCAACATTAATATGATCAATTTTATTTTACTAAACTTCTCCACTTAAA 159
QY 2404 AAATGCAAAAGAGATATATTTAATTAAGTAAAGTAAAGATGATGGATGATCT 2463
DB 158 AAATGCAAAAGAGATATATTTAATTAAGTAAAGTAAAGATGATGGATGATCT 99
QY 2464 TCAGCAAAAGCGCCCGCTAGAGTGTCTTATCTTACATTAAGCTGGGTTGGCAGACA 2523
DB 98 TCAGCAAAAGCGCCCGCTAGAGTGTCTTATCTTACATTAAGCTGGGTTGGCAGACA 39
QY 2524 TCATAGGGCTTACGATATTTTACGCTTACTGTACGTA 2561
DB 38 TCATAGGGCTTACGATATTTTACGCTTACTGTACGTA 1

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LOCUS SALK_111232.51.45.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_111232.51.45.x, genomic survey sequence.

ACCESSION CC056828
VERSION CC056828.1 GI:29476492
KEYWORDS Arabidopsis thaliana (chale crees)
SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana (chale crees)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Chauk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Becker,J.R.

A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

Unpublished (2001)

CONTACT: Joseph R. Becker
Salk Institute Genomic Analysis Laboratory (SIGNAL)

The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA

Tel: 858 453 4100 x1752
Fax: 858 558 6379

Email: jbecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.

Class: TDNA tagged.

Location/Qualifiers

1. 437

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/ecotype="Col-0"

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/clone.lib="Arabidopsis thaliana TDNA insertion lines"

/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html

ORIGIN

Query Match 5.5%; Score 233; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 4.6e-88; Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 2394 TCCACTAAAAAAGAGATATATTTAATTAAGTAAAGTAAATGAATGAT 2453
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QY 2454 GGGTATTTCTTACGCAAAAGCGCCGCTAGAGTGTCTTATCTTACATTAAGCTGGGTT 2513
DB 121 GGGTATTTCTTACGCAAAAGCGCCGCTAGAGTGTCTTATCTTACATTAAGCTGGGTT 180
QY 2514 GTGGCAGACATCATAGGCGCTACGATATTTTACGCTTACTGTAAAGCT 2566
DB 181 GTGGCAGACATCATAGGCGCTACGATATTTTACGCTTACTGTAAAGCT 233

RESULT 4 234 bp DNA linear GSS 01-APR-2004
LOCUS AL936239/c
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-047A09-016076, genomic survey sequence.

ACCESSION AL936239
VERSION AL936239.1 GI:24367864
KEYWORDS Arabidopsis thaliana (chale crees)
SOURCE Arabidopsis thaliana

ORGANISM Arabidopsis thaliana (chale crees)
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.

GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

Bioinformatics 19 (11), 1441-1442 (2003)

REFERENCE Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.

An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

Plant Mol. Biol. 53 (1-2), 247-259 (2003)

REFERENCE Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.

High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

Biotechniques 35 (6), 1164-1168 (2003)

REFERENCE 4 (bases 1 to 234)

Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.

Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BNC clone T8119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Location/Qualifiers

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/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at

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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 5.9e-71;
Matches 193; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1092 TAGCGTTTCACGTTTGGCTTCCTCGCGCAACTTGGCGGTGTGACTTTTCTTAT 1151
DB 213 TAGGGTTACGTTTGGCTTCCTCGCGCAACTTGGCGGTGTGACTTTTCTTAT 154
QY 1152 GTCGTTGTTGACTAATTTCTCAGAGTGAAGTATCAAGAACTAATATTCGAAA 1211
DB 153 GTCGTTGTTGACTAATTTCTCAGAGTGAAGTATCAAGAACTAATATTCGAAA 94

QY 1212 AGAAGAGAAAAAGGAGAAAACTATTGTGAAAAAGACTAAATATGG 1271
DB 93 AGAAGAGAAAAAGGAGAAAACTATTGTGAAAAAGACTAAATATGG 34

QY 1272 ATTTATTTAAATG 1284
DB 33 ATTTATTTAAATG 21

RESULT 5
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LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-853H05-025756,
ACCESSION CR402297
VERSION CR402297.1 GI:46943025
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4
AUTHORS Li,Y., Rosso,M.G., Strizhov,N. and Weisshaar,B.

```

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TITLE Direct Submission
JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linn-Weeg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.

FEATURES
source
1. .300
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/clone_1b="GK-853H05-025756"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 4.2%; Score 176; DB 11; Length 300;
Best Local Similarity 100.0%; Pred. No. 1.1e-63;
Matches 176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2109 TTTAATTCCTCTCGTCGACACTTGCAGGACTTGCACCAAGCACTATATGAAAGC 2168
DB 273 TTTAATTCCTCTCGTCGACACTTGCAGGACTTGCACCAAGCACTATATGAAAGC 214
QY 2169 AAATATCCACCAAGGATAGAGGTTAGATCCCACTCAATATCTTTGTCTTGTTA 2228
DB 213 AAATATCCACCAAGGATAGAGGTTAGATCCCACTCAATATCTTTGTCTTGTTA 154
QY 2229 TTTATGAAAAACAATTTTATCAGGAAAAACGTTTCTTCTTACGTGATTAAG 2244
DB 153 TTTATGAAAAACAATTTTATCAGGAAAAACGTTTCTTCTTACGTGATTAAG 98

RESULT 6
AL759737 162 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-190B10-014641,
ACCESSION AL759737
VERSION AL759737.1 GI:21498085
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3

```

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050

REFERENCE 4 (bases 1 to 162)

AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone 728119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1..162

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="GK-190B10-014641"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 3.6%; Score 154; DB 10; Length 162;

Best Local Similarity 100.0%; Pred. No. 2.8e-54;

Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2117 TCTCTGCTGCTACTTTCAGGCAATTTGACCAACGACTATACATATTTGAAAGCAAAATATC 2116

Db 5 TCTCTGCTGCTACTTTCAGGCAATTTGACCAACGACTATACATATTTGAAAGCAAAATATC 64

QY 2177 CACCAAGGATGATAGGGTTAGATCCACATTCATATCTTTGCTTTGTTATTATGAA 2236

Db 65 CACCAAGGATGATAGGGTTAGATCCACATTCATATCTTTGCTTTGTTATTATGAA 124

QY 2237 AAACAAATATTTATCAGAAAAAAGCTTTCTTC 2270

Db 125 AAACAAATATTTATCAGAAAAAAGCTTTCTTC 158

RESULT 7

CR402298/c 276 bp DNA linear GSS 02-MAY-2004

LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-853H05-025845,

ACCESSION CR402298

VERSION CR402298.1 GI:46943026

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1

AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.

TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

PUBMED 12874060

REFERENCE

AUTHORS 2 Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)

PUBMED 14756321

REFERENCE 3

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050

REFERENCE 4 (bases 1 to 276)

AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone 728119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES

source

1..276

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="GK-853H05-025845"

/clone_lib="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Col-0"

/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 3.3%; Score 140; DB 11; Length 276;

Best Local Similarity 100.0%; Pred. No. 2.6e-48;

Matches 140; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2145 CCAACGCTTACATATTGAAAGCAAAATATCCACCGGATGATAGGTTATCCAC 2204

Db 206 CCAACGCTTACATATTGAAAGCAAAATATCCACCGGATGATAGGTTATCCAC 147

QY 2205 ATTCAATATCTTTGCTTTGTTATTATGAAAAACAATATTATCAGAAAAAAGCT 2264

Db 146 ATTCAATATCTTTGCTTTGTTATTATGAAAAACAATATTATCAGAAAAAAGCT 87

QY 2265 TTCTTCTAGTGTATAG 2284

Db 86 TTCTTCTAGTGTATAG 67

RESULT 8

B2379137 415 bp DNA linear GSS 26-NOV-2002

LOCUS Arabidopsis thaliana T-DNA insertion lines

DEFINITION SALK_112909.37.05.x Arabidopsis thaliana T-DNA insertion lines

ACCESSION B2379137

VERSION B2379137.1 GI:25470664

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050

REFERENCE 4 (bases 1 to 276)

AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

TITLE Direct Submission

JOURNAL Submitted (01-MAY-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone 728119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 415)

REFERENCE
AUTHORS
Alonso, J.M., Leisner, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeake, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmermann, J., and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)

JOURNAL
COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.
Location/Qualifiers
1. .415
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_112909.37.05.x"
/note="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 3.3%; Score 139; DB 9; Length 415;
Best Local Similarity 100.0%; Pred. No. 6,6e-48;
Matches 139; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2146 CAACGATATACATATGAAAGCAAAATATCCACGAGATGATGGTTAGATCCACA 2205
DB 1 CAACGATATACATATGAAAGCAAAATATCCACGAGATGATGGTTAGATCCACA 60

QY 2206 TTCAATATCTTTGCTCTTGTATTTATGAAAAACAATATTTATCGAAAAAAAGCTT 2265
DB 61 TTCAATATCTTTGCTCTTGTATTTATGAAAAACAATATTTATCGAAAAAAAGCTT 120

QY 2266 TCTTCTAGTGTATTAAG 2284
DB 121 TCTTCTAGTGTATTAAG 139

RESULT 9
CNS044GJ
LOCUS 2106 bp mRNA linear HTC 06-FEB-2004
DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSLTFB37ZE02 of flowers and buds of strain col-0 of Arabidopsis thaliana (thale cress).
ACCESSION BX826541
VERSION BX826541.1 GI:42462514
KEYWORDS HTG; GSUT cDNA.
SOURCE Arabidopsis thaliana
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 2106)
Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C., Menard, M., Crund, C., Querier, F., Scarpetelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J., and Salanoubat, M.
Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation

Unpublished
2 (bases 1 to 2106)

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Direct Submission
Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr - Web : www.genoscope.cns.fr)
The sequences are based on single pass reads.
Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G.
Genoscope members carried out sequencing and annotation : Castelli V., Aury J.M., Jallion O., Wincker P., Menard M., Crund C., Schachter V., Weissenbach J., Salanoubat M.
URGV INRA : Clepet C., Caboche M.
Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full_length
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

FEATURES
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Location/Qualifiers
1. .2106
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/db_xref="taxon:3702"
/clone="GSLTFB37ZE02"
/tissue_type="flowers and buds"
/ecotype="Col-0"
/plasmid="pCMVSPORT_6"
1. .2106
/gene="At4g37750"

ORIGIN

Query Match 3.2%; Score 135; DB 4; Length 2106;
Best Local Similarity 100.0%; Pred. No. 3e-46;
Matches 135; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3968 AACGATTCACACAGCAAAATTTGCTTGTCTCTCTATTAATATCTCTCA 4027
DB 1 AACGATTCACACAGCAAAATTTGCTTGTCTCTCTATTAATATCTCTCA 60

QY 4028 AAACCTTCTCTATCTCTCAAGCCGCCCTCTCTTCTCTCAACCAAGAA 4087
DB 61 AAACCTTCTCTATCTCTCAAGCCGCCCTCTCTTGTCTCAACCAAGAA 120

QY 4088 AAAACAAAGTTGA 4102
DB 121 AAAACAAAGTTGA 135

RESULT 10
AL759736
LOCUS 192 bp DNA linear GSS 01-APR-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-190B10-014640, genomic survey sequence.
ACCESSION AL759736
VERSION AL759736.1 GI:21498084
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1
Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weisshaar, B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
12874060
Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

TITLE
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics

JOURNAL
Plant Mol. Biol. 53 (1-2), 247-259 (2003)

REFERENCE
14756321

AUTHORS
3
Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and Weisshaar,B.

TITLE
High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines

JOURNAL
Biotechniques 35 (6), 1164-1168 (2003)

REFERENCE
14682050

AUTHORS
4 (bases 1 to 192)
Li,Y., Strizhov,N., Rosso,M.G. and Weisshaar,B.

TITLE
Direct Submission

JOURNAL
Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany

COMMENT
This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
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/clone_11b="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 3.0%; Score 127; DB 10; Length 192;
Best Local Similarity 100.0%; Pred. No. 9.4e-43;
Matches 127; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
2148 ACGACTATACATATGAAAGCAAAATATCCACGAGATAGGTTAGATCCACATT 2207
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Db 56 ACGACTATACATATGAAAGCAAAATATCCACGAGATAGGTTAGATCCACATT 115

Qy
2208 CAATATCTTTTGTCTTTGTTATTTATGAAAAAAATTTATTCAGAAAAAAACGTTTC 2267
|||||
Db 116 CAATATCTTTTGTCTTTGTTATTTATGAAAAAAATTTATTCAGAAAAAAACGTTTC 175

Qy
2268 TTCTCTA 2274
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Db 176 TTCTCTA 182

RESULT 11
CC455690 112 bp DNA linear GSS 30-MAY-2003
LOCUS SALK_085740.55.25.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_085740.55.25.x, genomic survey sequence.

ACCESSION
CC455690

VERSION
CC455690.1 GI:31215945

KEYWORDS
GSS.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
1 (bases 1 to 112)

AUTHORS
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab,C., Jeake,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL
Unpublished (2001)

COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.

FEATURES
source
1..112
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_085740.55.25.x"
/clone_11b="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 2.6%; Score 112; DB 9; Length 112;
Best Local Similarity 100.0%; Pred. No. 2.5e-36;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
57 TTTAGTTAGAAAAAATCTTCTTTAGCTGTGTGTGTTTAACTTAACTTAACT 116
|||||
Db 1 TTTAGTTAGAAAAAATCTTCTTTAGCTGTGTGTGTTTAACTTAACTTAACT 60

Qy
117 AGTCACATGATATCAATATATATTTGAAATTTGAAATTTATTTA 168
|||||
Db 61 AGTCACATGATATCAATATATATTTGAAATTTGAAATTTATTTA 112

RESULT 12
CC797115 323 bp DNA linear GSS 01-JUL-2003
LOCUS SALK_144490.54.40.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_144490.54.40.x, genomic survey sequence.

ACCESSION
CC797115

VERSION
CC797115.1 GI:32392338

KEYWORDS
GSS.

SOURCE
Arabidopsis thaliana (thale cress)

ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
1 (bases 1 to 323)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrihab,C., Jeake,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.

TITLE
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome

JOURNAL
Unpublished (2001)

COMMENT
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu

This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES
source
Location/Qualifiers

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1. .323
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
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/clone="SALK_14490.54.40.x"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna\_protocols.html"
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ORIGIN

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Best Local Similarity 99.4%; Pred. No. 1.6e-32;
Matches 153; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2676 CAATTTCTAACTAATCTATACAACTGAATGTTGTTGTAATTTATCTTAA 2735
Db 153 CAATTTCTAACTAATCTATACAACTGAATGTTGTTGTAATTTATCTTAA 212
Qy 2736 CCAAGTTTGAATGTCATGCGAGCTACACTCTAGTCCCTTTTCCCAATTA 2795
Db 213 CCAAGTTTGAATGTCATGCGAGCTACACTCTAGTCCCTTTTCCCAATTA 272
Qy 2796 TCTCCTTACATCGACCGGTTAAAGTATTTAAAC 2829
Db 273 TCTCCTTACATCGACCGGTTAAAGTATTTAAAC 306

RESULT 13
AL769520 92 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-087A04-011968,
genomic survey sequence.
ACCESSION AL769520
VERSION AL769520.1 GI:21531722
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 92)
AUTHORS Rosso,M.G., Strizhov,N., Li,Y. and Weisshaar,B.
TITLE Direct Submission

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linn-We 10, Koeln, 50829, Germany.
COMMENT This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T28119. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
Location/Qualifiers

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1. .92
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-087A04-011968"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (Genbank accession number: J2537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."
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ORIGIN

Query Match 2.2%; Score 91; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 2.4e-27;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2184 GATGATAGGTTGATGATCCGATTCATCTTTGCTTGTATTATGAAAAACAA 2243
Db 2 GATGATAGGTTGATGATCCGATTCATCTTTGCTTGTATTATGAAAAACAA 61
Qy 2244 TATTATCAGAAAAAAACGTTTCTCTTA 2274
Db 62 TATTATCAGAAAAAAACGTTTCTCTTA 92

RESULT 14
AL769556 418 bp DNA linear GSS 01-APR-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-087D01-012260,
genomic survey sequence.
ACCESSION AL769556
VERSION AL769556.1 GI:21531758
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weisshaar,B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (PST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2
AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
Weisshaar,B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3
AUTHORS Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)

PUBMED 14682050
 REFERENCE 4 (bases 1 to 418)
 AUTHORS Strizhov,N., Rosso,M.G., Li,Y. and Weishaar,B.
 TITLE Direct Submision
 JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
 source
 1. .418
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-087D01-012260"
 /clone_1b="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
 Query Match 2.2%; Score 91; DB 10; Length 418;
 Best Local Similarity 100.0%; Pred. No. 2.1e-27;
 Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2184 GATGATAGGTTGATCCCATTCATATCTTGTCTGTATTATGAAAAACAA 2243
 DB 8 GATGATAGGTTGATCCCATTCATATCTTGTCTGTATTATGAAAAACAA 67

QY 2244 TATTATCAGAAAAACGTTCTCTCTA 2274
 DB 68 TATTATCAGAAAAACGTTCTCTCTA 98

RESULT 15
 CDS0A2BQ 2315 bp mRNA linear HTC 06-FEB-2004
 LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 DEFINITION GSLTJS902C06 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).
 ACCESSION BX827650.1 GI:42459424
 VERSION BX827650
 KEYWORDS HTC; GSUT cDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsi.

REFERENCE 1 (bases 1 to 2315)
 CastellI,V., Aury,J.M., Jallion,O., Wincker,P., Clepet,C., Menard,M., Cruaud,C., Quetier,F., Scairelli,C., Schachter,V., Temple,G., Caboche,M., Weissenbach,M. and Salanoubat,M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2315)
 Genoscope.
 AUTHORS Direct Submision
 TITLE Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 JOURNAL BP 191 91006 Evry cedex - FRANCE (E-mail : seque@genoscope.cns.fr
 PUBMED - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads.

Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G, Genoscope members carried out sequencing and annotation : CastellI V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C., Schachter V., Weissenbach J., Salanoubat M.
 UNIV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis genome released by MRS (Munich information center for Protein Sequences) . 5 prime and 3 prime are assembled with Phrap.
http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/FullLength
<http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis>.

FEATURES
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 1. .2315
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="GSLTJS902C06"
 /clone_1b="Adult vegetative tissue"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"
 1. .2315
 /gene="Atg37750"

ORIGIN
 gene
 Query Match 2.0%; Score 84; DB 4; Length 2315;
 Best Local Similarity 100.0%; Pred. No. 1.8e-24;
 Matches 84; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3999 TCTTCTCTTATATATATCGTCGAAACCCCTGCTATATCTCGTAAAGCCCC 4058
 DB 1 TCTTCTCTTATATATATCGTCGAAACCCCTGCTATATCTCGTAAAGCCCC 60

QY 4059 CTTCCTGTCTCTACCGCAACA 4082
 DB 61 CTTCCTGTCTCTACCGCAACA 84

RESULT 16
 AL754990 92 bp DNA linear GSS 01-APR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-060001-013874,
 DEFINITION genomic survey sequence.
 ACCESSION AL754990
 VERSION AL754990.1 GI:21487488
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weishaar,B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 PUBMED 12874060

REFERENCE 2
 Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 PUBMED 14756321

REFERENCE 3
 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weishaar,B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050
 REFERENCE 4 (bases 1 to 92)

AUTHORS Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.
TITLE Direct Submission
JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
FEATURES Location/Qualifiers
 source
 1..92
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-060D01-013874"
 /clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACT1 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
 Query Match 1.9%; Score 80; DB 10; Length 92;
 Best Local Similarity 100.0%; Pred. No. 1.2e-22;
 Matches 80; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 GGGTTGATCCGCATTCATATCTTTGCTTTGTTATTTAGAAAACAATATTTAT 2250
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 |||||
DB 9 GGGTTGATCCGCATTCATATCTTTGCTTTGTTATTTAGAAAACAATATTTAT 68
 |||||
 |||||
QY 2251 CAGAAAAAAGCTTCTTC 2270
 |||||
 |||||
DB 69 CAGAAAAAAGCTTCTTC 88
 |||||
 |||||

RESULT 17 424 bp mRNA linear EST 24-NOV-2004
BP561373 BP561373 RAFL6 Arabidopsis thaliana cDNA clone RAFL06-86-P19 5',
 mRNA sequence.
ACCESSION BP561373 GI:56086434
VERSION BP561373.2
KEYWORDS EST.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 424)
 Seki, M., Narusaka, M., Kamliya, A., Ishida, J., Satou, M., Sakurai, T., Nakajima, M., Enju, A., Akiyama, K., Oono, Y., Muramatsu, M., Hayakawa, T., Kawai, J., Carninci, P., Itoh, M., Ishii, Y., Arakawa, A., Shibata, K., Shinagawa, K. and Shinzaki, K.
 Functional annotation of a full-length Arabidopsis cDNA collection
 11910074 (5565), 141-145 (2002)
 On Jun 20, 2004 this sequence version replaced gi:48977139.
COMMENT Contact: Motoaki Seki
 Plant Functional Genomics Research Group
 RIKEN Genomic Sciences Center
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
 Tel: 81-298-36-4359
 Fax: 81-298-36-9060
 Email: mseki@rkc.riken.go.jp
 An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al., 1998). This clone is in a

modified plusucscript vector as a Setai/XhoI insert. Please visit our web site (<http://figweb.gsc.riken.go.jp/>) for further details.
FEATURES Location/Qualifiers
 source
 1..424
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="RAFL06-86-P19"
 /dev_stage="plants at various developmental stages from germination to mature seeds"
 /lab_host="DH10B"
 /clone_1lb="RAFL6"
 /note="Site 1: Setai; Site 2: XhoI; subjected to dehydration (1, 2, 5, 10, 24 hr) and cold (1, 2, 5, 10, 24 hr) treatments"

ORIGIN
 Query Match 1.8%; Score 75; DB 3; Length 424;
 Best Local Similarity 100.0%; Pred. No. 1.4e-20;
 Matches 75; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4154 TTGGAAGTTTATAGAAAGAAAGTGAAGTACATTATAGAAAGAAAGCAAGAA 4213
 |||||
 |||||
DB 85 TTGGAAGTTTATAGAAAGAAAGTGAAGTACATTATAGAAAGAAAGCAAGAA 144
 |||||
 |||||
QY 4214 CCAAAAAAGAAACC 4228
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 |||||
DB 145 CCAAAAAAGAAACC 159
 |||||
 |||||

RESULT 18 694 bp DNA linear GSS 01-OCT-2002
BH934314 BH934314
 od65g10.g1 B. oleracea002 Brassica oleracea genomic, genomic survey
 sequence.
ACCESSION BH934314 GI:23414380
VERSION BH934314.1
KEYWORDS GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 694)
 Mash, W., Rabinowicz, P.D. and Wilson, R.K.
 Whole genome shotgun reads from Brassica oleracea
 unpublished (2002)
 Contact: Richard K. Wilson
 Genome Sequencing Center
 Washington University School of Medicine
 Email: submissions@wustl.wustl.edu
 Plate: od65 row: 9 column: 10
 Seq primer: -28RPpOT reverse
 Class: shotgun
 High quality sequence stop: 551.
FEATURES Location/Qualifiers
 source
 1..694
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /db_xref="taxon:3712"
 /clone_1lb="B.oleracea002"
 /note="Vector: pOTW13; Whole genome shotgun library from flowering buds. DNA was purified from a crude nuclear prep using Brassica oleracea TO1000DH3 buds provided by Thomas Osborn at the University of Wisconsin. Genomic DNA was provided by Pablo Rabinowicz (CSHL) and the shotgun library prepared at Washington University Genome Sequencing Center."

ORIGIN
 Query Match 1.7%; Score 73; DB 9; Length 694;
 Best Local Similarity 100.0%; Pred. No. 9.9e-20;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3928 AAGTAAGAAAGCTTTTCTCATTAAGACACGATCCCGAGATTCAACAGCAAT 3987
 DB 75 AAGTAAGAAAGCTTTTCTCATTAAGACACGATCCCGAGATTCAACAGCAAT 134

QY 3988 TTGGGCTTGCTC 4000
 DB 135 TTGTGCTTGCTC 147

RESULT 19
 LOCUS AL756782 268 bp DNA linear GSS 01-APR-2004
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-113A12-012505,
 genomic survey sequence.
 ACCESSION AL756782
 VERSION AL756782.1 GI:21489280
 KEYWORDS GSS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weisshaar, B.
 TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for
 the identification of T-DNA insertion mutants in Arabidopsis
 thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 PUBMED 12874060

REFERENCE 2
 AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and
 Weisshaar, B.
 TITLE An Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for
 flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 PUBMED 14756321

REFERENCE 3
 AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and
 Weisshaar, B.
 TITLE High-throughput generation of sequence indexes from T-DNA
 mutagenised Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 PUBMED 14682050

REFERENCE 4 (bases 1 to 268)
 AUTHORS Li, Y., Rosso, M.G., Strizhov, N. and Weisshaar, B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
 Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 COMMENT This sequence has been recovered from the left border of the T-DNA.
 It indicates an insertion within the locus defined by BAC clone
 T88119. Details on the protocols used for generation of the
 sequence are described in References 1-3. The sequences are
 generated at the MPI for Plant Breeding Research in the context of
 the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
 program designated 'GABI'. Information on line availability can be
 found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
 source
 1..268
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-113A12-012505"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector PAC161 (GenBank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

ORIGIN

Query Match 1.7%; Score 71; DB 10; Length 268;
 Best Local Similarity 100.0%; Fred. No. 7.7e-19;
 Matches 71; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2026 TAGTAATTACACATTTTAAACCGTCCATCCAGATTGTAATAGTGAACAAATCGAACA 2085
 DB 29 TAGTAATTACACATTTTAAACCGTCCATCCAGATTGTAATAGTGAACAAATCGAACA 88

QY 2086 TTTTCTTTTCTT 2096
 DB 89 TTTTCTTTTCTT 99

RESULT 20
 LOCUS CB260786 594 bp mRNA linear EST 06-NOV-2003
 DEFINITION 65-B9572-012-004-B17-T7R MPZ-ADIS-012 Arabidopsis thaliana cDNA
 clone MPZP769B174Q 5'-PRIME, mRNA sequence.
 ACCESSION CB260786
 VERSION CB260786.1 GI:32885559
 KEYWORDS EST.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1
 AUTHORS Schmidt, K.J., Soerensen, T.R., Stracke, R., Torjek, O., Altman, T.,
 Mitchell-Olds, T. and Weisshaar, B.
 TITLE Large-scale identification and analysis of genome-wide
 single-nucleotide polymorphisms for mapping in Arabidopsis thaliana
 Genome Res. 13 (6), 1250-1257 (2003)
 PUBMED 12799357

COMMENT Contact: Weisshaar B
 ADIS DNA core facility at MPZ
 Max-Planck-Institute for Plant Breeding Research
 Carl-von-Linne Weg 10, 50829 Koeln, Germany
 Fax: 00492215062851
 Email: weisshaar@mpiz-koeln.mpg.de
 Insert Length: 594 Std Error: 0.00
 Plate: 4 row: B column: 17
 Seq primer: T7R; CTATACGACTCATTATAGGA.
 Location/Qualifiers
 1..594
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /ecotype="landsberg erecta"
 /db_xref="GABI:590183"
 /db_xref="taxon:3702"
 /clone="MPZP769B174Q"
 /tissue_type="whole plant"
 /dev_stage="adult plant, mixed stressses"
 /lab_host="E. coli XL1-Blue MRF"
 /note="Vector: pSPORT1; Site 1: SalI; Site 2: NotI; cDNA
 library from Arabidopsis thaliana, accession landsberg
 erecta; six weeks old total plants grown under long-day
 conditions in soil, whole adult plants were treated for 24
 hours with different stressses, (1) at 4N-0 C in the dark,
 (2), at 37 Grad C in the dark, (3) lying in the lab after
 removing from soil, (4) in the greenhouse after wounding
 leaves with a forceps, (5) in the lab watering with a 150
 mM NaCl solution, (6) at 26 Grad C in the light/UV; equal
 quantities of stressed plant material were pooled; library
 was made at the Max-Planck-Institute for Plant Breeding
 Research, Cologne, Germany; cloning sites SalI-NotI,
 primer sites and orientation:
 T7-SalI-CCACCGTCGCG-5prime-cDNA-polyA-CC-NotI-SP6; Note:
 Sequencing granted in the context of the GABI Arabidopsis
 Verbund II: Genetic Diversity, 'Establishment of
 high-efficiency SNP-based mapping tools and development of

methods for genome-wide mutation detection, Pi: Bernd Weisshaar Sequence submission managed by RZPD/GABI-Primary database: <http://gabi.rzpd.de>. This clone is available from RZPD; contact RZPD (clone@rzpd.de) for further information."

ORIGIN

Query Match 1.6%; Score 68; DB 6; Length 594;
Best Local Similarity 99.2%; Pred. No. 1.4e-11; Indels 0; Gaps 0;
Matches 118; Conservative 0; Mismatches 1;

Qy 4110 GGTGTCTTCTGTGTAACCAATGATGGTTTACCTTACTTCTGAGATTATTAAG 4169

Db 24 GGTGTCTTCTGTGTAACCAATGATGGTTTACCTTACTTCTGAGATTATTAAG 83

Qy 4170 AAGAAAGATGAGATCACTTATAGAAAGAGAGCAAAACCAAAAGAAACC 4228
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Db 84 AAGAGAGATGAGATCACTTATAGAAAGAGAGCAAAACCAAAAGAAACC 142

RESULT 21
AL769557 110 bp DNA linear GSS 01-APR-2004

LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-087D01-012440,
DEFINITION genomic survey sequence.
ACCESSION AL769557
VERSION AL769557.1 GI:21531759

KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.
TITLE GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana

JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)

PUBMED 12874060

REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

JOURNAL Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
PUBMED Plant Mol. Biol. 53 (1-2), 247-259 (2003)

REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

JOURNAL High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
PUBMED Biotechniques 35 (6), 1164-1168 (2003)

REFERENCE 4
AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
PUBMED This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

COMMENT

location/Qualifiers
1. 110
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-087D01-012440"

FEATURES
source

/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/notes="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 1.5%; Score 65; DB 10; Length 110;
Best Local Similarity 100.0%; Pred. No. 3e-16;
Matches 65; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2210 ATATCTTTTGTCTTTGTATTTAGAAAACAATTTATTCGGAAGAAAAAGCTTTCTT 2269

Db 46 ATATCTTTTGTCTTTGTATTTAGAAAACAATTTATTCGGAAGAAAAAGCTTTCTT 105

Qy 2270 CTCTA 2274
|||||
Db 106 CTCTA 110

RESULT 22
AL754991 96 bp DNA linear GSS 01-APR-2004

LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-060D01-013875,
DEFINITION genomic survey sequence.
ACCESSION AL754991
VERSION AL754991.1 GI:21487489

KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoveer, P. and Weisshaar, B.

JOURNAL GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
PUBMED Bioinformatics 19 (11), 1441-1442 (2003)

REFERENCE 2
AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weisshaar, B.

JOURNAL Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
PUBMED Plant Mol. Biol. 53 (1-2), 247-259 (2003)

REFERENCE 3
AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoveer, P., Dekker, K.A. and Weisshaar, B.

JOURNAL High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
PUBMED Biotechniques 35 (6), 1164-1168 (2003)

REFERENCE 4
AUTHORS Rosso, M.G., Strizhov, N., Li, Y. and Weisshaar, B.

JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
PUBMED This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

COMMENT

location/Qualifiers
1. 96
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-060D01-013875"

FEATURES
source

/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-060D01-013875"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana vector pDCL61 (Genbank accession number: A0337514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN

Query Match 1.4%; Score 61; DB 10; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.6e-14;
Matches 61; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2191 GGGTTAGATCCCATTCATATCTTTGCTTTGTTATTTATGAAAACCAATTTAT 2250
DB 13 GGGTTAGATCCCATTCATATCTTTGCTTTGTTATTTATGAAAACCAATTTAT 72

QY 2251 C 2251
DB 73 C 73

RESULT 23
BH481919 381 bp DNA linear GSS 13-DEC-2001
LOCUS BOGEA30TR BOGE Brassica oleracea genomic clone BOGEA30, genomic
DEFINITION survey sequence.
ACCESSION BH481919
VERSION BH481919.1 GI:17690023
KEYWORDS GSS.

SOURCE
ORGANISM Brassica oleracea

Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS 1 (bases 1 to 381)
Ayale, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utechtack, T.R., Wortman, J.R., White, O.R. and Town, C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)

JOURNAL
PUBMED 15805490
COMMENT Other_GSSs: BOGEA30TR
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source location/Qualifiers
1..381
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOGEA30"
/clone_1lb="BOGE"

/note="Vector: pHOS1, Site 1: BcXI, 2-3 kb sheared
genomic DNA inserted into pHOS1 using BcXI linkers"

ORIGIN

Query Match 1.1%; Score 45; DB 9; Length 381;
Best Local Similarity 100.0%; Pred. NO. 9.5e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3007 TATATATGTCGGTCATTAGAGCCGTGACCAAAAGTTTCGTCT 3051
DB 181 TATATATGTCGGTCATTAGAGCCGTGACCAAAAGTTTCGTCT 225

RESULT 24
BH676371/c 673 bp DNA linear GSS 19-FEB-2002
LOCUS BOHX80TR BO_2_3_KB Brassica oleracea genomic clone BOHX80,
DEFINITION genomic survey sequence.
ACCESSION BH676371
VERSION BH676371.1 GI:18746814
KEYWORDS GSS.

SOURCE
ORGANISM Brassica oleracea

Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS 1 (bases 1 to 673)
Ayale, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S.,
Utechtack, T.R., Wortman, J.R., White, O.R. and Town, C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)

JOURNAL
PUBMED 15805490
COMMENT Other_GSSs: BOHX80TR
Contact: Chris Town

TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES
source location/Qualifiers
1..673
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHX80"
/clone_1lb="BO_2_3_KB"

/note="Vector: pHOS1, Site 1: BcXI, 2-3 kb sheared
genomic DNA inserted into pHOS1 using BcXI linkers"

ORIGIN

Query Match 1.1%; Score 45; DB 9; Length 673;
Best Local Similarity 100.0%; Pred. NO. 9.1e-08;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3007 TATATATGTCGGTCATTAGAGCCGTGACCAAAAGTTTCGTCT 3051
DB 602 TATATATGTCGGTCATTAGAGCCGTGACCAAAAGTTTCGTCT 558

RESULT 25
BZ380049 56 bp DNA linear GSS 26-NOV-2002
LOCUS SALK_114519.40.05.x Arabidopsis thaliana TDNA insertion lines
DEFINITION Arabidopsis thaliana genomic clone SALK_114519.40.05.x, genomic
survey sequence.
ACCESSION BZ380049
VERSION BZ380049.1 GI:25472515
KEYWORDS GSS.

SOURCE
ORGANISM Arabidopsis thaliana (thale cress)

Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
AUTHORS 1 (bases 1 to 56)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R.,
Gadrinab, C., Jeeke, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L.,

TITLE Shim, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
JOURNAL Unpublished (2001)
COMMENT Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
Class: TDNA tagged.

FEATURES

source

1. .56
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone_lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/cdna_protocols.html"

ORIGIN

Query Match 1.0%; Score 43; DB 9; Length 56;
Best Local Similarity 100.0%; Pred. No. 7.9e-07;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2524 TCATAGGCGCTTACGTATTTGAGCTTACTGTAAGTAAAGCT 2566

Db 14 TCATAGGCGCTTACGTATTTGAGCTTACTGTAAGTAAAGCT 56

RESULT 26
BH451280/c 335 bp DNA linear GSS 12-DEC-2001
LOCUS BOGNN777R BOGN Brassica oleracea genomic clone BOGNN77, genomic
DEFINITION Survey sequence.
VERSION BH451280
KEYWORDS BH451280.1 GI:117636991
GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 335)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
TIGR
Contact: Chris Town
Other GSSs: BOGNN777F
912 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES

source

1. .335
Location/Qualifiers
/organism="Brassica oleracea"
/mol_type="genomic DNA"

/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BOGNN77"
/clone_lib="BOGN"
/note="Vector: pHOS1, Site 1: BexXI, 2-3 kb sheared
genomic DNA inserted into pHOS1 using BexXI linkers"

ORIGIN

Query Match 0.8%; Score 32; DB 9; Length 335;
Best Local Similarity 100.0%; Pred. No. 0.034;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2855 GTACAAACATGTCACTATATAGACAGACAT 2886

Db 96 GTACAAACATGTCACTATATAGACAGACAT 65

RESULT 27
BH510257/c 796 bp DNA linear GSS 13-DEC-2001
LOCUS BOHKU787R BOHK Brassica oleracea genomic clone BOHKU78, genomic
DEFINITION Survey sequence.
VERSION BH510257
KEYWORDS BH510257.1 GI:11718347
GSS.
SOURCE Brassica oleracea
ORGANISM Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 796)
Ayele,M., Haas,B.J., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utterback,T.R., Wortman,J.R., White,O.R. and Town,C.D.
Whole genome shotgun sequencing of Brassica oleracea and its
application to gene discovery and annotation in Arabidopsis
Genome Res. 15 (4), 487-495 (2005)

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT
TIGR
Contact: Chris Town
Other GSSs: BOHKU787F
912 Medical Center Drive, Rockville, MD 20850, USA.
Tel: 301-838-3523
Fax: 301-838-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.

FEATURES

source

1. .796
Location/Qualifiers
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
/clone_lib="BOHKU78"
/clone_lib="BOHK"
/note="Vector: pHOS1, Site 1: BexXI, 2-3 kb sheared
genomic DNA inserted into pHOS1 using BexXI linkers"

ORIGIN

Query Match 0.8%; Score 32; DB 9; Length 796;
Best Local Similarity 100.0%; Pred. No. 0.032;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2855 GTACAAACATGTCACTATATAGACAGACAT 2886

Db 644 GTACAAACATGTCACTATATAGACAGACAT 613

RESULT 28
CW938563/c 897 bp DNA linear GSS 20-DEC-2004
LOCUS TCBI8.3_F08_T7 Tribolium BAC library Tribolium castaneum genomic,
DEFINITION genomic survey sequence.

ACCESSION CM938563
VERSION CM938563.1 GI:56721176
SOURCE Tribolium castaneum (red flour beetle)
ORGANISM Tribolium castaneum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiforma; Tenebrionidae; Tribolium.
REFERENCE 1 (bases 1 to 897)
AUTHORS Savard,J. and Tautz,D.
TITLE Tribolium castaneum BAC-ends sequencing project
JOURNAL Unpublished (2003)
COMMENT Contact: Savard, J.
Abteilung fur Evolutionsgenetik, AG Tautz
Institut fur Genetik, Universitat zu Koin
Weyertal 121, 50931 Koin, Germany
Tel: 49 221 470 6911
Fax: 49 221 470 5975
Email: savard@uni-koeln.de
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..901
/organism="Tribolium castaneum"
/mol_type="genomic DNA"
/strain="GA-2"
/db_xref="taxon:7070"
/clone_lib="Tribolium BAC library"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

ORIGIN
Query Match 0.6%; Score 27; DB 10; Length 897;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 TAATACGACTCATTAGGAGCTCGA 50
67 TAATACGACTCATTAGGAGCTCGA 41

RESULT 29
LOCUS CM938873 901 bp DNA linear GSS 20-DEC-2004
DEFINITION TB19.1.C07.T7 Tribolium BAC library Tribolium castaneum genomic,
genomic survey sequence.
ACCESSION CM938873
VERSION CM938873.1 GI:56721486
KEYWORDS GSS.
SOURCE Tribolium castaneum (red flour beetle)
ORGANISM Tribolium castaneum
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiforma; Tenebrionidae; Tribolium.
REFERENCE 1 (bases 1 to 901)
AUTHORS Savard,J. and Tautz,D.
TITLE Tribolium castaneum BAC-ends sequencing project
JOURNAL Unpublished (2003)
COMMENT Contact: Savard, J.
Abteilung fur Evolutionsgenetik, AG Tautz
Institut fur Genetik, Universitat zu Koin
Weyertal 121, 50931 Koin, Germany
Tel: 49 221 470 6911
Fax: 49 221 470 5975
Email: savard@uni-koeln.de
Class: BAC ends.

FEATURES
source
Location/Qualifiers
1..901
/organism="Tribolium castaneum"
/mol_type="genomic DNA"
/strain="GA-2"
/db_xref="taxon:7070"
/clone_lib="Tribolium BAC library"
/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

ORIGIN Library constructed by Exelixis Inc."

Query Match 0.6%; Score 27; DB 10; Length 901;
Best Local Similarity 100.0%; Pred. No. 4.4;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 TAATACGACTCATTAGGAGCTCGA 50
70 TAATACGACTCATTAGGAGCTCGA 44

RESULT 30
LOCUS BF925688 298 bp mRNA linear EST 19-JAN-2001
DEFINITION CM2-NT0192-291100-578-h07 NT0192 Homo sapiens cDNA, mRNA sequence.
ACCESSION BF925688
VERSION BF925688.1 GI:12322245
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 298)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W.Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the PAPSP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?cl=CM2&c2=CM2-NT0192-291100-578-h07&r3=2000-11-29&c4=1)
Seq primer: puc 18 forward
High quality sequence start: 27
High quality sequence stop: 298.
Location/Qualifiers
1..298
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="adult"
/clone_lib="NT0192"
/note="Organ: nervous tumor; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORSTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN
Query Match 0.6%; Score 26; DB 2; Length 298;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3910 AAAAATAAAATTAATTAAGTAA 3935
249 AAAAATAAAATTAATTAAGTAA 274

[illegible]

ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Canis familiaris	1 (bases 1 to 388)	Kirkness, E.F., Bafna, V., Halpern, A.L., Levy, S., Remington, K., Ruch, D.B., Delcher, A.L., Pop, M., Wang, W., Fraser, C.M. and Venter, J. C.	The dog genome: survey sequencing and comparative analysis	Science 301 (5641), 1998-1903 (2003)	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.					
Canis familiaris EF					
Contact: Kirkness EF					
The Institute for Genomic Research					
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive, Rockville, MD 20850, USA					
Tel: 301-838-0200					
Fax: 301-838-0208					
Email: ekirkness@tigr.org					
Class: shotgun.					
Location/Qualifiers					
1..388					
/organism="Canis familiaris"					
/mol_type="genomic DNA"					
/strain="Standard Poodle"					
/db_xref="taxon:9615"					
/clone_lib="Dog Library"					
/note="Site 1: BactxI; Libraries were prepared from peripheral blood"					
ORIGIN					
Query Match	0.6%	Score 25;	DB 10;	Length 388;	
Best Local Similarity	100.0%	Pred. No. 33;			
Matches 25; Conservative 0;		Mismatches 0;	Indels 0;	Gaps 0;	
Cy	3911	AAATATAAATAAATAAAGTAA	3935		
Dd	128	AAATATAAATAAATAAAGTAA	104		
RESULT 33					
LOCUS	AZ088538	488 bp	DNA	linear	GSS 08-MAY-2000
DEFINITION	RPCT-23-470D9.T1 RPCT-23	Mus musculus genomic clone	RPCT-23-470D9,		
ACCESSION	AZ088538				
VERSION	AZ088538.1	GI:7730586			
KEYWORDS	GSS.				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Murioidea; Muridae; Murinae; Mus.				
REFERENCE	1 (bases 1 to 488)				
AUTHORS	Zhao, S., Nieman, W., Feldblum, T., Malek, J., Shatman, S., Akintet, B., Levins, M., McGann, S., Tesgaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.				
TITLE	Mouse BAC End Sequences from Library RPCT-23				
JOURNAL	Unpublished (1999)				
COMMENT	Other GSSs: RPCT-23-470D9.TV Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCT-23. For BAC library availability, please contact Pieter de Jong (pieter@tigr.org; med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm) or from Resea ch Genetics (info@resgen.com). BAC end page: http://www.tigr.org/tdb/bac/ends/mouse/bac_end_intro.html Plate: 470 row: D column: 9				

Seq primer: SP6
Class: BAC ends.

FEATURES
Source Location/Qualifiers

1..488
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-470D9"
/sex="Female"
/lab_host="DH10B"
/clone_1lb="RPCI-23"
/note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1:
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI MethyIase. Size
selected DNA was cloned into the pBAC3.6 vector at the
EcoRI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."

ORIGIN

Query Match 0.6%; Score 25; DB 9; Length 488;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 73 TTTCTTTGTAGTGTGTGTGTGT 97
DB 339 TTTCTTTGTAGTGTGTGTGTGT 363

RESULT 34
AG013324/c

LOCUS Homo sapiens genomic DNA, 21q region, clone: S82AN, genomic survey
DEFINITION
ACCESSION AG013324 AG005647
VERSION AG013324.2 GI:55788761
KEYWORDS GSS.

SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.

REFERENCE
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Homo sapiens genomic DNA, chromosome 21q
JOURNAL Published Only in Database (1998)
REFERENCE
AUTHORS Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
TITLE Direct Submission
JOURNAL Submitted (03-SEP-1998) Masahira Hattori, RIKEN Genomic Sciences
Center, RIKEN Yokohama Institute, Yokohama Research Promotion
Division, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa,
230-0045, Japan (E-mail:hattori@gscc.riken.jp, Tel:81-45-503-9111,
Fax:81-45-503-9113)

COMMENT
AG005647: Submitted (07-Mar-1998).
On Nov 16, 2004 this sequence version replaced gi:3513370.

FEATURES
Source Location/Qualifiers

1..715
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="21"
/map="21q"
/clone="S82AN"

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 715;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GCCTAATACGACTCCTATAGGAG 45
|||||

DB 510 GCCTAATACGACTCCTATAGGAG 486

RESULT 35
CNS01002/c

LOCUS Anopheles gambiae GSS SP6 end of clone 26M24 of NotreDamel library
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),
genomic survey sequence.

ACCESSION AL153762
VERSION AL153762.1 GI:7014681
KEYWORDS GSS.

SOURCE
ORGANISM Anopheles gambiae (African malaria mosquito)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;
Culicidae; Anophelinae; Anopheles.

REFERENCE
AUTHORS 1 (bases 1 to 755)
TITLE Genoscope.

JOURNAL Direct Submission

Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqret@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

REFERENCE
AUTHORS 2 (bases 1 to 755)
TITLE Roch,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
JOURNAL Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr.
Roux, Paris 75015, France

COMMENT
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
Pasteur.

FEATURES
Source Location/Qualifiers

1..755
/organism="Anopheles gambiae"
/mol_type="genomic DNA"
/strain="PEST"
/db_xref="taxon:7165"
/clone="26M24"
/clone_1lb="NotreDamel"
/note="End : SP6"

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 755;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3910 AAAATTAATAATAATAATAAGTAA 3934
DB 653 AAAATTAATAATAATAATAAGTAA 629
|||||

RESULT 36
BHS10250

LOCUS BHKU78TR BOHK Brassica oleracea genomic clone BHKU78, genomic
DEFINITION survey sequence.
ACCESSION BHS10250
VERSION BHS10250.1 GI:17718340
KEYWORDS GSS.

SOURCE
ORGANISM Brassica oleracea

Brassicaceae
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE
AUTHORS 1 (bases 1 to 793)
Aylee,M., Haas,B.U., Kumar,N., Wu,H., Xiao,Y., Van Aken,S.,
Utechtack,T.R., Wortman,J.R., White,O.R. and Town,C.D.

JOURNAL Whole genome shotgun sequencing of Brassica oleracea and its
Genome Res. 15 (4), 487-495 (2005)

COMMENT
PUBMED 15805490
Other_GSSs: BHKU78TR

Contact: Chris Town
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA.

Tel: 301-838-3523

Fax: 301-838-0208

Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.

Seq primer: TP

Class: sheared ends.

FEATURES

Source

1..793
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="T01000DH3"
/db_xref="taxon:3712"
/clone="BOHKU78"
/note="Vector: pHOSt; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOSt using BstXI linkers"

ORIGIN

Query Match 0.6%; Score 25; DB 9; Length 793;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1788 AATGCTTAATCATTAATAAATAAG 1812

Db 609 AATGCTTAATCATTAATAAATAAG 633

RESULT 37

CW949303 798 bp DNA linear GSS 20-DEC-2004

LOCUS TCB33.4.F02.T7 Tribolium BAC library Tribolium castaneum genomic,

DEFINITION genomic survey sequence.

ACCESSION CW949303

VERSION CW949303.1 GI:56731923

KEYWORDS GSS.

SOURCE Tribolium castaneum (red flour beetle)

ORGANISM Tribolium castaneum

REFERENCE Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;

Tenebrionidae; Tribolium.

1 (bases 1 to 798)

Savard, J. and Tautz, D.

Tribolium castaneum BAC-ends sequencing project

Unpublished (2003)

Contact: Savard, J.

Abteilung fur Evolutionsgenetik, AG Tautz

Institut fur Genetik, Universitat zu Koln

Meyertal 121, 50931 Koln, Germany

Tel: 49 221 470 6911

Fax: 49 221 470 5975

Email: savard@uni-koeln.de

Class: BAC ends.

Location/Qualifiers

1..798

/organism="Tribolium castaneum"

/mol_type="genomic DNA"

/strain="GA-2"

/db_xref="taxon:7070"

/clone_lib="Tribolium BAC library"

/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;

Library constructed by Exelixis Inc."

RESULT 38

AG409273

LOCUS

DEFINITION

sequence.

ACCESSION AG409273

VERSION AG409273.1 GI:48051959

KEYWORDS GSS.

SOURCE Mus musculus molossinus (Japanese wild mouse)

ORGANISM Mus musculus molossinus

REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

Sciurognathi; Muridae; Murinae; Mus.

1

Abe, K., Noguchi, H., Tagawa, K., Yuzurina, M., Toyoda, A., Kojima, T.,

Ezawa, K., Saitou, N., Hattori, M., Sakaki, Y., Moriaki, K. and

Shiroishi, T.

Contribution of Asian mouse subspecies Mus musculus molossinus to

genomic constitution of strain C57BL/6J, as defined by BAC-end

sequence-SNP analysis

Genome Res. 14 (12), 2439-2447 (2004)

2 (bases 1 to 860)

Hattori, M., Toyoda, A., Noguchi, H., Kojima, T. and Sakaki, Y.

Direct Submission

Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical

and Chemical Research (RIKEN), Genomic Sciences Center (GSC);

1-7-22 Suenho-chou, Tsukumi-ku, Yokohama, Kanagawa, 230-0045, Japan

(E-mail: hattori@gsc.riken.jp, URL: http://hgp.gsc.riken.go.jp/).

Tel: 81-45-503-9111, Fax: 81-45-503-9170

Libraries are derived from the mouse BAC library MSMG01. For BAC

library availability, please contact Kunya Abe (abe@rc.riken.jp).

Tsukuba Institute, Bio Resource Center,

The Institute of Physical and Chemical Research (RIKEN) 3-1-1

Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199

e-mail: abe@rc.riken.jp

PRIMERS

Sequencing: T7

LIBRARY

Vector: pBAC3.6

R.Site 1: EcoRI

R.Site 2: EcoRI

Location/Qualifiers

1..860

/organism="Mus musculus molossinus"

/mol_type="genomic DNA"

/sub_species="molossinus"

/db_xref="taxon:57486"

/clone="MSMG01-269A12.T7"

/sex="male"

/tissue_type="mixture of kidney and spleen"

/clone_lib="MSMG01 Mouse Male BAC library"

ORIGIN

Query Match 0.6%; Score 25; DB 10; Length 860;

Best Local Similarity 100.0%; Pred. No. 31;

Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 GCCTAATAGCACTCATATAGGAG 45

Db 10 GCCTAATAGCACTCATATAGGAG 34

RESULT 39

CW940939/c

LOCUS

DEFINITION

genomic survey sequence.

ACCESSION CW940939

VERSION CW940939.1 GI:56723552

898 bp DNA linear GSS 20-DEC-2004

TCB22.1.A08.T7 Tribolium BAC library Tribolium castaneum genomic,

KEYWORDS
SOURCE
ORGANISM
 Tribolium castaneum (red flour beetle)

REFERENCE
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.
 1 (bases 1 to 898)

AUTHORS
 Savard,J. and Tautz,D.
TITLE
 Tribolium castaneum BAC-ends sequencing project
JOURNAL
 Unpublished (2003)

COMMENT
 Contact: Savard, J.
 Abteilung fur Evolutionsgenetik, AG Tautz
 Institut fur Genetik, Universitat zu Koln
 Weyertal 121, 50931 Koln, Germany
 Tel: 49 221 470 6911
 Fax: 49 221 470 5975
 Email: savard@uni-koeln.de
 Class: BAC ends.

FEATURES
source
 1..898
 /organism="Tribolium castaneum"
 /mol_type="genomic DNA"
 /strain="GA-2"
 /db_xref="taxon:7070"
 /clone_lib="Tribolium BAC library"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Library constructed by Exelixis Inc."

ORIGIN
 Query Match 0.6%; Score 25; DB 10; Length 898;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 24 TAATACGACTCCTATAGGAGCTC 48
 |||||||
 64 TAATACGACTCCTATAGGAGCTC 40

Db

RESULT 40
 AG400158 924 bp DNA linear GSS 21-DEC-2004
 LOCUS AG400158 Mus musculus molossinus DNA, clone:MSMg01-234D03.T7, genomic survey
 DEFINITION
 AG400158
 VERSION AG400158.1 GI:48041813
 KEYWORDS GSS.
 SOURCE Mus musculus molossinus (Japanese wild mouse)
 ORGANISM Mus musculus molossinus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1
 Abe,K., Noguchi,H., Tagawa,K., Yuzuriha,M., Toyoda,A., Kojima,T., Ezawa,K., Saitou,N., Hattori,M., Sakaki,Y., Moriwaiki,K. and Shitoinshi,T.
TITLE
 Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/6J, as defined by BAC-end sequence-SNP analysis
JOURNAL
 Genome Res. 14 (12), 2439-2447 (2004)
 15574823
 2 (bases 1 to 924)
 Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
 Direct Submision
 Submitted (17-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), The Institute of Physical and Chemical Research (RIKEN), Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@sc.riken.jp, URL:http://hsp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
 Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@tc.riken.jp).
 Tsukuba Institute, Bio Resource Center,
 The Institute of Physical and Chemical Research (RIKEN) 3-1-1
 Koyadai, Tsukuba, 305-0074 Japan

phone: 81-298-36-9189, fax: 81-298-36-9199
 e-mail: abe@tc.riken.jp

PRIMERS
 Sequencing : T7
LIBRARY
 Vector : pBAC3.6
 R.Site 1 : EcoRI
 R.Site 2 : EcoRI.

FEATURES
source
 1..924
 /organism="Mus musculus molossinus"
 /mol_type="genomic DNA"
 /sub_species="molossinus"
 /db_xref="taxon:57486"
 /clone="MSMg01-234D03.T7"
 /sex="male"
 /tissue type="mixture of kidney and spleen"
 /clone_lib="MSMg01 Mouse Male BAC Library"

ORIGIN
 Query Match 0.6%; Score 25; DB 10; Length 924;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 21 GCCATATACGACTCCTATAGGAG 45
 |||||||
 80 GCTTATATACGACTCCTATAGGAG 104

Db

RESULT 41
 CM937215/c 1036 bp DNA linear GSS 20-DEC-2004
 LOCUS CM937215 TcB16.1_F06.T7 Tribolium BAC library Tribolium castaneum genomic, genomic survey sequence.
 DEFINITION
 CM937215
 VERSION CM937215.1 GI:56719828
 KEYWORDS GSS.
 SOURCE Tribolium castaneum (red flour beetle)
 ORGANISM Tribolium castaneum
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia; Tenebrionidae; Tribolium.
 1 (bases 1 to 1036)
 Savard,J. and Tautz,D.
TITLE
 Tribolium castaneum BAC-ends sequencing project
JOURNAL
 Unpublished (2003)
COMMENT
 Contact: Savard, J.
 Abteilung fur Evolutionsgenetik, AG Tautz
 Institut fur Genetik, Universitat zu Koln
 Weyertal 121, 50931 Koln, Germany
 Tel: 49 221 470 6911
 Fax: 49 221 470 5975
 Email: savard@uni-koeln.de
 Class: BAC ends.

FEATURES
source
 1..1036
 /organism="Tribolium castaneum"
 /mol_type="genomic DNA"
 /strain="GA-2"
 /db_xref="taxon:7070"
 /clone_lib="Tribolium BAC library"
 /note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
 Library constructed by Exelixis Inc."

ORIGIN
 Query Match 0.6%; Score 25; DB 10; Length 1036;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
 24 TAATACGACTCCTATAGGAGCTC 48
 |||||||
 66 TAATACGACTCCTATAGGAGCTC 42

Db

```

RESULT 42
CK121482/c      161 bp      mRNA      linear      EST 01-JUN-2004
DEFINITION      202020.p1 AWM1 Arabidopsis thaliana cDNA clone MPMGP2011020202
5-PRIME, mRNA sequence.
ACCESSION      CK121482
VERSION        CK121482.1  GI:47831798
KEYWORDS
SOURCE
ORGANISM        Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 161)
Feilner,T., Immlink,R.G.H., Cahill,D.J. and Kersten,B.
Generation of a cDNA expression library from Arabidopsis
inflorescence meristem
Unpublished (2003)
JOURNAL
COMMENT          Contact: Birgit Kersten
Plant Protein Chip Group, Department Lehrach
Max-Planck-Institute for Molecular Genetics
Inmestr. 73, D-14195 Berlin, Germany
Tel: +49(0)30/84131648
Fax: +49(0)30/84131128
Email: Kersten@molgen.mpg.de
Insert Length: 161      Std Error: 0.00
Plate: 202      row: 0      column: 20
Seq primer: POE65.
Location/Qualifiers
1. 161
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/ecotype="Columbia"
/db_xref="GABI:951967"
/db_xref="taxon:3702"
/clone="MPMGP2011020202"
/issue_type="inflorescence meristem"
/dev_stage="about one week after bolting"
/lab_host="E. coli SCS-1/pSE111"
/clone_1lb="Atm1"
/note="Vector: POE-30NAST-actB (AY386205); Site 1: SalI;
Site 2: NotI; About 1 week after bolting, cDNA synthesis
using SuperscriptTM-system (Invitrogen) with an
oligo(dT)-primer containing NotI restriction site and a
SalI adapter. The main library (plate numbers begin with
1) of 38,000 clones was rearrayed into the sublibrary
(plate numbers begin with 201) containing 5,000 putative
expression clones. Average insert size is 1 kb. Note: The
rearrayed sublibrary (plate numbers begin with 201) was
sequenced. Library generation and sequencing was granted
in context of GABI-LAPP; data are also accessible at
https://gabi.rzp.de"

ORIGIN
Query Match      0.6%; Score 24; DB 7; Length 161;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      24  TAATAGCACTCATTAGGGAGCT 47
Db      111 TAATAGCACTCATTAGGGAGCT 88

RESULT 43
AQ955990/c      191 bp      DNA      linear      GSS 28-JAN-2000
LOCUS          LERRA118TR LERRA Arabidopsis thaliana genomic clone LERRA118, genomic
survey sequence.
ACCESSION      AQ955990
VERSION        AQ955990.1  GI:6783819
KEYWORDS
SOURCE          Arabidopsis thaliana (thale cress)

```

```

ORGANISM        Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 191)
Buell,C.R., Lin,X., Pal,G., Barnstead,M., Bowman,C., Uterbach,T.,
Feldbljum,T., Liang,F., Creasy,T. and Frazer,C.M.
Genomic survey sequencing of landsberg erecta ecotype of
Arabidopsis thaliana and identification of sequence-based
polymorphisms
Unpublished (2000)
JOURNAL
COMMENT          Contact: Xiaoying Lin
The Institute for Genomic Research
912 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: atc@igr.org
For additional information, see http://www.tigr.org/cdb/ac/at.html
Seq primer: TR
Class: shotgun.
Location/Qualifiers
1. 191
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Landsberg erecta"
/db_xref="taxon:3702"
/clone="LERRA118"
/note="Organ: Leaf; Vector: pHOSt; Total genomic DNA was
sheared to 0.9-1 Kbp before ligation."

ORIGIN
Query Match      0.6%; Score 24; DB 9; Length 191;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22  CCTAATACGACTCATTAGGGGAG 45
Db      79  CCTAATACGACTCATTAGGGGAG 56

RESULT 44
CK573161      278 bp      mRNA      linear      EST 01-MAR-2004
LOCUS          1172 Plasmodium yoelii liver stage LCM cDNA library Plasmodium
yoelii cDNA, mRNA sequence.
ACCESSION      CK573161
VERSION        CK573161.1  GI:44827251
KEYWORDS
SOURCE          EST.
ORGANISM        Plasmodium yoelii
Plasmodium yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 278)
Sacci,J.B. Jr., Ribeiro,J.M.C., Huang,F., Alam,U., Russell,J.A.,
Blair,P.L., Witney,A., Carnucci,D.J., Azad,A.F. and Aguiar,J.C.
Transcriptional analysis of in vivo Plasmodium yoelii liver stage
gene expression
Mol. Biochem. Parasitol. 142 (2), 177-183 (2005)
15876462
JOURNAL
COMMENT          Contact: Sacci JB
Department of Microbiology and Immunology
University of Maryland School of Medicine
BRB 13-009, 655 W. Baltimore Street, Baltimore, MD 21201, USA
Tel: 410 706 4071
Email: jsacc001@umaryland.edu
POLYA=Yes.
Location/Qualifiers
1. 278
/organism="Plasmodium yoelii"
/mol_type="mRNA"
/strain="17X NL"
/db_xref="taxon:5861"
/dev_stage="40 hour liver schizont"

```

/clone_lib="Plasmodium yoelii liver stage LCM cDNA library"
 /note="Vector: pTrioEx2, Plasmodium yoelii liver stage parasites were harvested by laser capture microdissection, from infected Balb/c mouse liver cryosections, 40 hours after inoculation with sporozoites. Total RNA was then isolated using the Strataprep Total RNA microprep kit from Stratagene."

ORIGIN

Query Match 0.6%; Score 24; DB 7; Length 278;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAGTTTCAT 3494
 DB 183 AAAAAAAAAAGTTTCAT 206

RESULT 45 DR973784 278 bp mRNA linear EST 03-AUG-2005
 LOCUS CHUT008f12.b1 Primary Chick Utricle Subtraction Gallus gallus cDNA
 DEFINITION 3, mRNA sequence.

ACCESSION DR973784 GI:71775897
 VERSION DR973784.1
 KEYWORDS Gallus gallus (chicken)
 SOURCE Gallus gallus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE 1 (bases 1 to 278)
 Lovett, M., Clifton, S., Page, D., Hillier, L., Martin, J., Wylie, T., Danc, M., Theising, B., Bowers, Y., Gibbons, M., Rutter, E., Bennett, J., Ronko, I., Teagarehvil, R., Kennedy, S., Waterston, R. and Wilson, R.
 WASHU Chicken EST Project
 UNPUBLISHED (2003)
 CONTACT: Mike Lovett
 WASHINGTON UNIVERSITY SCHOOL OF MEDICINE
 Email: lovett@genetics.wustl.edu
 DNA sequencing by: Washington University Genome Sequencing Center
 For information on obtaining a clone please contact: Mike Lovett (lovett@genetics.wustl.edu) This library was directionally cloned.
 Location/Qualifiers

FEATURES

source

1..278
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /db_xref="taxon:9031"
 /lab_host="DH5alpha"
 /clone_lib="Primary Chick Utricle Subtraction"
 /note="Vector: PAMPI; 1st strand of cDNA was synthesized with reverse transcriptase and oligo(dT) beads, then cDNA was amplified by PCR using modified SMART primers. The final cDNA was cloned in PAMPI vector in annealing reaction with Utricle DNA Glycosylase (UDG)."

ORIGIN

Query Match 0.6%; Score 24; DB 8; Length 278;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAATACGACTCACTATAGGAGC 46
 DB 217 CTAATACGACTCACTATAGGAGC 194

RESULT 46 A0955989 310 bp DNA linear GSS 28-JAN-2000
 LOCUS LERAI18TF LERA Arabidopsis thaliana genomic clone LERAI18, genomic
 DEFINITION

survey sequence.

ACCESSION A0955989
 VERSION A0955989.1 GI:6783818
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE 1 (bases 1 to 310)
 Buell, C.R., Lin, X., Pai, G., Barnstead, M., Bowman, C., Utebach, T., Feldlym, T., Liang, F., Creasy, T. and Fraser, C.M.
 Genomic survey sequencing of Landsberg erecta ecotype of Arabidopsis thaliana and identification of sequence-based polymorphisms
 UNPUBLISHED (2000)
 CONTACT: Xiaoying Lin
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: atc@tigr.org
 For additional information, see <http://www.tigr.org/tdb/at.html>
 Seq primer: TP
 Class: shotgun.

JOURNAL

COMMENT
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: atc@tigr.org
 For additional information, see <http://www.tigr.org/tdb/at.html>
 Seq primer: TP
 Class: shotgun.

FEATURES
 source
 Location/Qualifiers

1..310
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="Landsberg erecta"
 /db_xref="taxon:3702"
 /clone_lib="LERAI18"
 /note="Organ: Leaf; Vector: pHOS1; Total genomic DNA was sheared to 0.9-1 Kbp before ligation."

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 310;
 Best Local Similarity 100.0%; Pred. No. 91;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CTAATACGACTCACTATAGGAGC 45
 DB 9 CTAATACGACTCACTATAGGAGC 32

FEATURES

source

BH451271 318 bp DNA linear GSS 12-DEC-2001
 BOGNN77TF BOGN Brassica oleracea genomic clone BOGNN77, genomic survey sequence.

ACCESSION BH451271
 VERSION BH451271.1 GI:17636982

KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea

REFERENCE 1 (bases 1 to 318)
 Ayala, M., Haas, B.J., Kumar, N., Wu, H., Xiao, Y., Van Aken, S., Utebach, T.R., Wortman, J.R., White, O.R. and Town, C.D.
 Whole genome shotgun sequencing of Brassica oleracea and its application to gene discovery and annotation in Arabidopsis
 Genome Res. 15 (4), 487-495 (2005)

JOURNAL PUBMED 15805490

COMMENT Other_GSSs: BOGNN77TR

CONTACT: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org

DNA is from a doubled haploid provided by Tom Osborn.
 Seg primer: TP
 Class: sheared ends.

FEATURES
 source
 Location/Qualifiers
 1..318

/organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="T01000DH3"
 /db_xref="taxon:3712"
 /clone="BOGNN77"
 /clone_lib="BOGN"
 /note="Vector: PHOS1, Site 1: BstXI, 2-3 kb sheared
 genomic DNA inserted into PHOS1 using BstXI linkers"

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 318;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1310 ATCATACCAAAATCAAGGAGG 1333
 Db 25 ATCATACCAAAATCAAGGAGG 48

RESULT 48
 CV263561/c 320 bp mRNA linear EST 22-SEP-2004
 LOCUS WS02022.B21_C24 PTXN-IB-N-A-11 Populus trichocarpa x Populus nigra
 DEFINITION cDNA clone WS02022_C24 3', mRNA sequence.
 ACCESSION CV263561
 VERSION CV263561.1 GI:52516536

KEYWORDS
 SOURCE
 ORGANISM
 Populus trichocarpa x Populus nigra
 Populus trichocarpa x Populus nigra
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.

REFERENCE
 AUTHORS
 1 (bases 1 to 320)
 Ralph,S., Cooper,D., Kolosova,N., Oddy,C., Butterfield,Y.,
 Kirpatrick,R., Liu,Y., Palamquist,D., Stott,J., Barber,S., Yang,G.,
 Babakaitis,R., Brown-John,M., Chand,S., Featherstone,R., Mason,A.,
 Mayo,M., Moran,J., Olson,T., Wong,D., Ritzland,C.E., Siddiqui,A.,
 Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C., Ritzland,K. and
 Bohlmann,J.

TITLE
 The poplar transcripome: Analysis of expressed sequence tags from
 multiple cDNA libraries
 JOURNAL
 COMMENT
 Unpublished (2004)
 Contact: Joerg Bohlmann
 Genome BC forest genomics program
 University of British Columbia
 Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
 Vancouver, British Columbia, Canada, V6T 1Z3
 Tel: 1-604-822-0282
 Fax: 1-604-822-2114
 Email: bohlmann@mel.ubc.ca
 Plate: WS02022 row: C column: 24
 High quality sequence scop: 320
 POLYA=Yes.

FEATURES
 source
 Location/Qualifiers
 1..320

/organism="Populus trichocarpa x Populus nigra"
 /mol_type="mRNA"
 /cultivar="NXM6"
 /db_xref="taxon:293756"
 /clone="WS02022_C24"
 /sex="Male"
 /lab_host="R. coli DH10B T1 phage resistant cells"
 /clone_lib="PTXN-IB-N-A-11"
 /note="Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5'
 end of cDNA); Site 2: XhoI (3' end of cDNA); Sapling trees
 two metres in height and grown under greenhouse conditions
 were exposed to continuous feeding by Cryptorhynchus
 lapathi (poplar and willow borer) adults caged on the

sapling using mesh bags. Bark (with phloem and cambium
 attached) from within the caged region was harvested 2
 hours, 6 hours and 48 hours after the onset of treatment.
 mRNA was isolated from each tissue source independently
 and equal quantities of mRNA from each tissue were then
 pooled. cDNA was prepared from 5 micrograms of mRNA and
 directionally ligated into the pBluescript II SK (+) XR
 vector using the pBluescript II XR cDNA library
 construction kit according to manufacturer's instructions
 with modifications (Stratagene). Plasmid DNA was then
 transformed by electroporation into DH10B cells
 (Invitrogen) for propagation. Normalization was applied
 according to published methods [Bonaldi M.F. et al. (1996)
 Genome Research 6(9):791] in order to reduce the abundance
 of highly expressed transcripts."

ORIGIN

Query Match 0.6%; Score 24; DB 7; Length 320;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3909 GAAAAATAAAAATAAATAAAGT 3932
 Db 303 GAAAAATAAAAATAAATAAAGT 280

RESULT 49
 CE127892 339 bp DNA linear GSS 25-SEP-2003
 LOCUS tigr-gss-dog-17000326042655 Dog Library Canis familiaris genomic,
 DEFINITION genomic survey sequence.
 ACCESSION CE127892
 VERSION CE127892.1 GI:35224637

KEYWORDS
 SOURCE
 ORGANISM
 GSS.
 Canis familiaris (dog)
 Canis familiaris
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 Canis.

REFERENCE
 AUTHORS
 1 (bases 1 to 339)
 Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,
 Ruesch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 JOURNAL
 COMMENT
 Science 301 (5641), 1898-1903 (2003)
 14512627
 Contact: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.

FEATURES
 source
 Location/Qualifiers
 1..339

/organism="Canis familiaris"
 /mol_type="genomic DNA"
 /strain="Standard Poodle"
 /db_xref="taxon:9615"
 /clone_lib="Dog Library"
 /note="Site 1: BstXI, Libraries were prepared from
 peripheral blood"

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 339;
 Best Local Similarity 100.0%; Pred. No. 90;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3910 AAAAAATAAAAATAAATAAAGTA 3933
 Db 170 AAAAAATAAAAATAAATAAAGTA 193

RESULT 50
BM163414
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BM163414 349 bp mRNA linear EST 04-DEC-2001
E57565948 PyBS Plasmodium yoelii yoelii cDNA clone PYCLB94.5' end,
mRNA sequence.
BM163414
BM163414.1 GI:17309106
EST.
Plasmodium yoelii yoelii
Plasmodium yoelii yoelii
Eukaryote; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 349)
Carlton J.M., Daly T.M., Long C.A., Bergman, L.W., Valdiva A.B.,
Fraser, C.M. and Carucci, D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@igr.org
For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mrg.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
source
Location/Qualifiers
1..349
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
/strain="17XL"
/db_species="yoelii"
/db_xref="taxon:73239"
/clone="PYCLB94"
/dev_stage="Asexual blood stages"
/lab_host="E. coli XL-1 Blue"
/clone_id="PyBS"
/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
collected from BALB/CBYJ mice infected with Py17XL
parasites, and leukocytes removed by passage over
microcyretaline cellulose columns. Total RNA was
isolated using the guanidium isothiocyanate method, and
mRNA isolated using oligo(dT)-cellulose chromatography.
First strand cDNA synthesis was completed using a 50-base
primer and reverse transcriptase in the presence of
5-methyl dCTP. After second strand synthesis, uneven
termini were treated with Pfu DNA polymerase and EcoRI
adaptors ligated to the blunt ends. The sample was cleaved
with XhoI and separated on a Sephacryl S-500 column.
Size-fractionated cDNA was precipitated and ligated to
HydriZAP arms directionally using EcoRI-XhoI cleaved arms.
After packaging, the phagemid vector (PAD-GAL4) was
excised from the HydriZAP vector and plasmid DNA
isolated."

ORIGIN
Query Match 0.6%; Score 24; DB 3; Length 349;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAGTTTCAAT 3494
Db 81 AAAAAAAAAAGTTTCAAT 104

RESULT 51
AG229188/c
LOCUS
DEFINITION
ACCESSION

AG229188 350 bp DNA linear GSS 19-JUL-2003
Lotus corniculatus var. japonicus DNA, clone:ljB17K01_f, genomic
survey sequence.
AG229188

VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AG229188.1 GI:26539812
GSS.
Lotus corniculatus var. japonicus (Lotus japonicus)
Lotus corniculatus var. japonicus
Lotus corniculatus var. japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; euroside I; Fabales; Fabaceae; Papilionoideae; Lotaeae;
Lotus.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Sato, S., Nakamura, Y. and Tabata, S.
Lotus japonicus BAC End sequences
Published Only in Database (2002)
2 (bases 1 to 350)
Sato, S.
Direct Submission
Submitted (20-NOV-2002) Shusei Sato, Kazusa DNA Research Institute,
The First Laboratory for Plant Gene Research; 2-6-7
Kazusa-kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail: ssato@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/,
Tel: 81-438-52-3935 (ex. 2336), Fax: 81-438-52-3934)
Location/Qualifiers
1..350
/organism="Lotus corniculatus var. japonicus"
/mol_type="genomic DNA"
/strain="Miyakojima MG-20"
/variety="japonicus"
/db_xref="taxon:34305"
/clone="LjB17K01_f"
/clone_id="genomic BAC library"
/note="VECTOR: pBelosBAC11
synonym: Lotus japonicus"

ORIGIN
Query Match 0.6%; Score 24; DB 10; Length 350;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3554 TGATTGCAAGTTGCAACAGATG 3577
Db 160 TGATTGCAAGTTGCAACAGATG 137

RESULT 52
BZ239509/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

BZ239509 390 bp DNA linear GSS 12-OCT-2002
CH230-456M24.TVB CHORI-230 Segment 2 Rattus norvegicus genomic
clone CH230-456M24, genomic survey sequence.
BZ239509
BZ239509.1 GI:23899773
GSS.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Rattus.
1 (bases 1 to 390)
Zhao, S., Shetty, J., Shatman, S., Teague, G., Geer, K.,
Shwartsbeyn, A., Gebregeorgis, E., Overton, L., Russell, D., Chen, D.,
Riggs, F., de Jong, P. and Fraser, C.M.
Rat BAC End Sequences from Library CHORI-230 MboI segment
Unpublished (1999)
Other GSSs: CH230-456M24.TVB
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: szhao@igr.org
Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@mail.cho.org).
Clones may be purchased from BACPAC Resources

QY 22 CCTAATGAGCTGACTATAGGAG 45
 |||||
 DB 4 CCTAATGAGCTGACTATAGGAG 27

RESULT 55
 LOCUS BM163834
 DEFINITION EST566357 PyBS Plasmodium yoelii yoelii cDNA clone PYCLK30 5' end.
 mRNA sequence.
 ACCESSION BM163834
 VERSION BM163834.1 GI:17309515
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 1 (bases 1 to 398)
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Valdiva,A.B.,
 Frazer,C.M. and Carnuci,D.J.
 Plasmodium yoelii EST project at TIGR
 Unpublished (2001)
 TITLE
 JOURNAL
 COMMENT
 Contact: Jane Carlton
 Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208
 Email: carlton@tigr.org
 For clone info, please contact the Malaria Research and Reference
 Reagent Resource Center, ATCC
 http://www.malaria.mr4.org/mr4pages/index.html
 Seq primer: ADF.

FEATURES
 source
 Location/Qualifiers
 1..398
 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
 /strain="7XL"
 /sub_species="yoelii"
 /db_xref="taxon:73239"
 /clone="PYCLK30"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /clone_lib="PyBS"

/note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adapters ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybriZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (PAD-GAL4) was excised from the HybriZAP vector and plasmid DNA isolated."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 398;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAAGTTTCAAT 3494
 |||||
 DB 312 AAAAAAAAAAAGTTTCAAT 335

RESULT 56
 BM966009

LOCUS BM966009 399 bp mRNA linear EST 20-MAR-2002
 h020f03.y1 Toxocara canis adult PAMPI v1 Toxocara canis cDNA 5'
 PARTIAL LACZ GENE ; mRNA sequence.
 ACCESSION BM966009
 VERSION BM966009.1 GI:19558726
 KEYWORDS
 SOURCE
 ORGANISM

REFERENCE
 1 (bases 1 to 399)
 Ascarididae; Toxocaridae; Toxocara.
 McCarter,J., Clifton,S., Chiappelli,B., Pape,D., Martin,J.,
 Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,
 Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Franklin,C.,
 Tsagarashvili,I., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,
 Underwood,K., Steptoe,M., Allen,M., Person,B., Shaller,T.,
 Harvey,N., Schurk,R., Kohn,S., Shih,T., Jackson,Y., Cardenas,M.,
 McCann,R., Wareston,R. and Wilson,R.
 The Washington Univ. Nematode EST Project, 1999
 Unpublished (1999)
 TITLE
 JOURNAL
 COMMENT
 Contact: McCarter JP
 The Washington Univ. Nematode EST Project, 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: est@wustl.wustl.edu
 The library was constructed by Claire Murphy and Dr. James McCarter
 at Washington University, St. Louis. DNA Sequencing by: Washington
 University Genome Sequencing Center
 High quality sequence stop: 118.

FEATURES
 source
 Location/Qualifiers
 1..399
 /organism="Toxocara canis"
 /mol_type="mRNA"
 /db_xref="taxon:6265"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="Toxocara canis adult PAMPI v1"
 /note="Vector: PAMPI (Gibco); Site 1: NotI; Site 2: SalI;
 The library was constructed by Claire Murphy and Dr. James
 McCarter at Washington University, St. Louis. The cDNA was
 made by using Dynabead oligo-dT priming (Dynal). PCR based
 library using a modified protocol from the SMART PCR cDNA
 Synthesis Kit from Clontech. Directionally cloned into the
 UNO sites of PAMPI. Adult nematodes were collected from
 infected dogs and provided by Dr. Prema Arasu of North
 Carolina State University, Raleigh, NC
 (Prema_Arasu@ncsu.edu)."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 399;
 Best Local Similarity 100.0%; Pred. No. 89;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CCTATGAGCTGACTATAGGAGC 46
 |||||
 DB 11 CCTATGAGCTGACTATAGGAGC 34

RESULT 57
 LOCUS CR057094/c 418 bp DNA linear GSS 05-JUL-2004
 DEFINITION Forward strand read from insert in 5'HPT insertion targeting and
 chromosome engineering clone MHPN70n09, genomic survey sequence.
 ACCESSION CR057094
 VERSION CR057094.1 GI:49790240
 KEYWORDS GSS; genome survey sequence; WICER.
 SOURCE Mus musculus (house mouse)
 ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

REFERENCE 1 (bases 1 to 418)
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L.,
 Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
 Rogers,J. and Bradley,A.
 TITLE Direct Submission
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>

FEATURES
 source
 1..418
 /organism="Mus musculus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10090"
 /clone="MHPN70n09"
 /clone_1lb="MHPN"

ORIGIN
 Query Match 0.6%; Score 24; DB 11; Length 418;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAAAATTAATAAGTAAAGAAA 3939
 ||||||||||||||||||||||||||||
 Db 309 AAAAAATTAATAAGTAAAGAAA 286

RESULT 58
 LOCUS AZ301311 423 bp DNA linear GSS 29-DEC-2000
 DEFINITION UP_315-19A T7 RPlC11 Human Male BAC Library Homo sapiens genomic
 clone RPl1-315A19, genomic survey sequence.
 ACCESSION AZ301311
 VERSION AZ301311.2 GI:11996067
 KEYWORDS GSS.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
 Homiidae; Homo.
 1 (bases 1 to 423)
 1 (bases 1 to 423)
 Chang,Y.G., Dailymple,H.L., Narasimhan,S., Watts,J., Schuler,G.,
 Raap,A.K., Morley,M. and Bruzel,A.
 A resource of mapped human bacterial artificial chromosome clones
 Genome Res. 9 (10), 989-993 (1999)
 10525327
 On Dec 29, 2000 this sequence version replaced gi:9795907.
 Contact: Arcaro MA, Morley M, Burdick J, Cheung VG
 Department of Pediatrics
 University of Pennsylvania
 3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, USA
 Tel: 215 590 2664
 Fax: 215 590 3709
 Email: mlennox@mail.med.upenn.edu
 Plate: 315 row: A column: 19
 Seg primer: T7
 Class: BAC ends.

FEATURES
 source
 1..423
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="RPl1-315A19"
 /sex="Male"
 /cell_type="lymphocytes"
 /clone_1lb="RPlC11 Human Male BAC Library"
 /note="Vector: pBACe3.6; RPlC11 Human Male BAC Library"

ORIGIN
 Query Match 0.6%; Score 24; DB 9; Length 423;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45

Db 5 CCTAATACGACTCATTATAGGAG 28
 |||||||||||||||||||||||||

RESULT 59
 LOCUS AQ959559 429 bp DNA linear GSS 28-JAN-2000
 DEFINITION LEREL477F LERE Arabidopsis thaliana genomic clone LEREL47, genomic
 survey sequence.
 ACCESSION AQ959559
 VERSION AQ959559.1 GI:6787260
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 429)
 Buell,C.R., Lin,X., Pal,G., Barnstead,M., Bowman,C., Utterbach,T.,
 Feldblyum,T., Liang,F., Creasy,T. and Fraser,C.M.
 Genomic survey sequencing of landberg erecta ecotype of
 Arabidopsis thaliana and identification of sequence-based
 polymorphisms
 Unpublished (2000)
 Contact: Xiaoying Lin
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 838 0200
 Fax: 301 838 0208
 Email: atc@igr.org
 For additional information, see <http://www.tigr.org/cdb/at/c.html>
 Seg primer: TP
 Class: shotgun.

FEATURES
 source
 1..429
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /ecotype="landberg erecta"
 /db_xref="taxon:3702"
 /clone="LEREL47"
 /clone_1lb="LERE"
 /note="Organ: leaf; Vector: pUC19UK; Total genomic DNA was
 sheared to 0.6-0.8 Kbp before ligation."

ORIGIN
 Query Match 0.6%; Score 24; DB 9; Length 429;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATAGGAG 45
 |||||||||||||||||||||||||

Db 13 CCTAATACGACTCATTATAGGAG 36

RESULT 60
 LOCUS BM171421 440 bp mRNA linear EST 04-DEC-2001
 DEFINITION EST573944 PyBS Plasmodium yoelii yoelii CDNA clone PYCQV44 5' end,
 mRNA sequence.
 ACCESSION BM171421
 VERSION BM171421.1 GI:17304653
 KEYWORDS EST.
 SOURCE Plasmodium yoelii yoelii
 ORGANISM Plasmodium yoelii yoelii
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 440)
 Carlson,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
 Fraser,C.M. and Garucci,D.J.
 Plasmodium yoelii EST project at TIGR
 Unpublished (2001)
 Contact: Jane Carlson
 Parasite Genomics Group
 The Institute for Genomic Research

9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@tigr.org

For clone info, please contact the Malaria Research and Reference
Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html

Seq primer: ADP.

FEATURES

source

Location/Qualifiers

1..440

/organism="Plasmodium yoelii yoelii"

/mol_type="mRNA"

/strain="17XL"

/sub_species="yoelii"

/db_xref="taxon:73239"

/clone="PYC044"

/dev_stage="Asexual blood stages"

/lab_host="E. coli XL-1 Blue"

/clone_1lb="PyBS"

/note="Vector: pMD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cByJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcrystalline cellulose columns. Total RNA was isolated using the guanidium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybridAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pMD-GAL4) was excised from the HybridAP vector and plasmid DNA isolated."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 440;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAAGTTTCAAT 3494

Db 139 AAAAAAAAAAAGTTTCAAT 162

RESULT 61

AQ959560/c 444 bp DNA linear GSS 28-JAN-2000

LOCUS LEREL477R LERE Arabidopsis thaliana genomic clone LEREL47, genomic

DEFINITION survey sequence.

ACCESSION AQ959560

VERSION AQ959560.1 GI:6787261

KEYWORDS GSS.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1 (bases 1 to 444)

Buell,C.R., Lin,X., Pal,G., Barnstead,M., Bowman,C., Uterbach,T.,
Feldblum,T., Liang,F., Creasy,T. and Fraser,C.M.

Genomic survey sequencing of Landsberg erecta ecotype of

Arabidopsis thaliana and identification of sequence-based

polymorphisms

polymorphisms

unpublished (2000)

CONTACT: Xiaoying Lin

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: at@tigr.org

For additional information, see <http://www.tigr.org/cdb/at/at.html>
Seq primer: TR

Class: shotgun.

FEATURES

Location/Qualifiers

1..444

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/ecotype="Landsberg erecta"

/db_xref="taxon:3702"

/clone="LEREL47"

/note="Organ: Leaf; Vector: pUC19JK; Total genomic DNA was

sheared to 0.6-0.8 kbp before ligation."

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 444;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 CCTAATACGACTCATTATGGGAG 45

Db 425 CCTAATACGACTCATTATGGGAG 402

RESULT 62

AQ028235/c 454 bp DNA linear GSS 30-JUN-1998

LOCUS CIT-HSP-2325L11.TR CIT-HSP Homo sapiens genomic clone 2325L11,

DEFINITION genomic survey sequence.

ACCESSION AQ028235

VERSION AQ028235.1 GI:3268457

KEYWORDS GSS.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;

Hominidae; Homo.

1 (bases 1 to 454)

Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Baas,S., Linher,K.,

Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,

Simon,M. and Venter,J.C.

Use of a random BAC End Sequence Database for Sequence-Ready Map

Building (1998)

unpublished (1998)

CONTACT: Mark Adams

Department of Eukaryotic Genomics

The Institute for Genomic Research

9712 Medical Center Dr., Rockville, MD 20850, USA

Tel: 301 838 0200

Fax: 301 838 0208

Email: mdadams@tigr.org

Clones are available from Research Genetics (info@resgen.com). BAC

end search page: http://www.tigr.org/cdb/humgen/bac_end_search/bac_end_search.html.

Seq primer: M13 Reverse

Class: BAC ends.

Location/Qualifiers

1..454

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/clone="2325L11"

/sex="Male"

/cell_type="Sperm"

/clone_1lb="CIT-HSP"

/note="Vector: pBelOBAC11, Site_1: HindIII, Site_2:

HindIII"

ORIGIN

Query Match 0.6%; Score 24; DB 9; Length 454;

Best Local Similarity 100.0%; Pred. No. 88;

Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3470 CAAAAAAAAAAGTTTCA 3493
 |||||
 Db 254 CAAAAAAAAAAGTTTCA 231

RESULT 63
 BM166570 469 bp mRNA linear EST 04-DEC-2001
 LOCUS EST569093 PyBS Plasmodium yoelii yoelii cDNA clone PYCNT81 5' end,
 DEFINITION mRNA sequence.
 BM166570
 ACCESSION BM16570.1 GI:17299802
 VERSION EST.
 KEYWORDS Plasmodium yoelii yoelii
 SOURCE Plasmodium yoelii yoelii
 ORGANISM Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 REFERENCE 1 (bases 1 to 469)
 Carlton,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Valdiva,A.B.,
 Fraser,C.M. and Carucci,D.J.
 Plasmodium yoelii EST project at TIGR
 COMMENT Unpublished (2001)
 TITLE Contact: Jane Carlton
 JOURNAL Parasite Genomics Group
 COMMENT The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208
 Email: carlton@tigr.org
 For clone info, please contact the Malaria Research and Reference
 Reagent Resource Center, ATCC
 http://www.malaria.mt4.org/mr4pages/index.html
 Seq primer: ADP.

FEATURES
 source Location/Qualifiers

1..469
 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
 /strain="17XL"
 /sub_species="yoelii"
 /db_xref="taxon:73239"
 /clone="PYCNT81"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
 collected from BALB/cByJ mice infected with Pyl7XL
 parasites, and leukocytes removed by passage over
 microcrystalline cellulose columns. Total RNA was
 isolated using the guanidium thiocyanate method, and
 mRNA isolated using oligo(dT)-cellulose chromatography.
 First strand cDNA synthesis was completed using a 50-base
 primer and reverse transcriptase in the presence of
 5-methyl dCTP. After second strand synthesis, uneven
 termini were treated with Pfu DNA polymerase and EcoRI
 adaptors ligated to the blunt ends. The sample was cleaved
 with XhoI and separated on a Sephacryl S-500 column.
 Size-fractionated cDNA was precipitated and ligated to
 HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
 After packaging, the phagemid vector (PAD-GAL4) was
 excised from the HybridZAP vector and plasmid DNA
 isolated."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 469;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3471 AAAAAAAAAAAGTTTCAAT 3494
 |||||
 Db 139 AAAAAAAAAAAGTTTCAAT 162

RESULT 64
 BU303919/c

LOCUS BU303919 478 bp mRNA linear EST 27-NOV-2002
 DEFINITION 603737371F1 CSEQCHN56 Gallus gallus cDNA clone CHEST629m18 5', mRNA
 sequence.
 BU303919
 ACCESSION BU303919.1 GI:25753631
 VERSION EST.
 KEYWORDS Gallus gallus (chicken)
 SOURCE Gallus gallus
 ORGANISM Gallus gallus

REFERENCE 1 (bases 1 to 478)
 Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
 Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
 A Comprehensive Collection of Chicken cDNAs
 Curr. Biol. 12 (22), 1965-1969 (2002)
 CONTACT: Simon Hubbard
 12445392
 JOURNAL Department of Biomolecular Sciences
 University of Manchester Institute of Science and Technology
 (UMIST)
 COMMENT PO Box 88, Manchester, M60 1QD, UK
 Tel: 01612008930
 Fax: 01612360409
 Email: Simon.Hubbard@umist.ac.uk.

FEATURES
 source Location/Qualifiers

1..478
 /organism="Gallus gallus"
 /mol_type="mRNA"
 /strain="Compton line 151"
 /db_xref="taxon:9031"
 /clone="CHEST629m18"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /clone_lib="CSEQCHN56"
 /note="Organ: small intestine; Vector: pBluescript II
 KS(+); Site 1: EcoRI; Site 2: NotI; This normalized
 library was constructed from 1 million independent clones.
 cDNA synthesis was initiated using an oligo(dT) primer,
 using methylated C in the first strand synthesis reaction.
 Following this first strand reaction, double-stranded cDNA
 was blunt-ended, ligated to NotI adaptors, digested with
 EcoRI, size-selected, and cloned into the NotI and EcoRI
 compatible sites of a custom modified MCS of the
 pBluescript (KS+) vector. The library was normalized in 2
 rounds using conditions adapted from Soares et al., PNAS
 (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
 (1996): 791, except that a significantly longer
 reannealing hybridization was used."

ORIGIN

Query Match 0.6%; Score 24; DB 5; Length 478;
 Best Local Similarity 100.0%; Pred. No. 87;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2073 AAATCGAAAACATTTT TTTT 2096
 |||||
 Db 442 AAATCGAAAACATTTT TTTT 419

RESULT 65

BU396654/c 478 bp mRNA linear EST 27-NOV-2002
 LOCUS BU396654 603533803F1 CSEQCHN58 Gallus gallus cDNA clone CHEST492e2 5', mRNA
 DEFINITION sequence.
 BU396654
 ACCESSION BU396654.1 GI:25765710
 VERSION EST.
 KEYWORDS Gallus gallus (chicken)
 SOURCE Gallus gallus
 ORGANISM Gallus gallus

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
COMMENT

Phasianinae; Gallus.
1 (bases 1 to 478)
Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,
Fong, M.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.
A Comprehensive Collection of Chicken CDNAs
Curr. Biol. 12 (22), 1965-1969 (2002)
12445392
Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology
(UMIST)
PO Box 88, Manchester, M60 10D, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.
Location/Qualifiers

FEATURES
SOURCE

```
1. 478
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="Compton Line 151"
/db_xref="taxon:9031"
/clone="CNE5192e2"
/sex="Female"
/dev_stage="adult"
/lab_host="DH10B"
/clone_1lb="CSECHN58"
/note="Organ: small intestine; Vector: pBluescript II
KS(+); Site_1: EcoRI; Site_2: NotI; This normalized
library was constructed from 1 million independent clones.
cDNA synthesis was initiated using an oligo(dT) primer.
Following methylation C in the first strand synthesis reaction,
this first strand reaction, double-stranded cDNA
was bluntended, ligated to NotI adapters, digested with
EcoRI, size-selected, and cloned into the NotI and EcoRI
compatible sites of a custom modified MCS of the
pBluescript (KS+) vector. The library was normalized in 2
rounds using conditions adapted from Soares et al., PNAS
(1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
(1996): 791, except that a significantly longer
reannealing hybridization was used."
```

ORIGIN

Query Match 0.64; Score 24; DB 5; Length 478;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2073 AAATCGAAACATTTT TTTT 2096
|||||
Db 442 AAATCGAAACATTTT TTTT 419

RESULT 66
BF558277/c 487 bp mRNA linear EST 12-DEC-2000
LOCUS
DEFINITION
UI-R-A1-eo-c-08-0-UI-r1 UI-R-A1 Rattus norvegicus cDNA clone
BF558277
BF558277
BF558277.1 GI:11668007
EST.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Rattus.
1 (bases 1 to 487)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
PUBMED
COMMENT
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa

375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: Bento-soares@uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone Distribution:
clones will be available through Research Genetics (www.regen.com)
LNL (info@image.lnl.gov). IMAGE ID= 1778863
Seq primer: M13 forward.
Location/Qualifiers

FEATURES
SOURCE

```
1. 487
/organism="Rattus norvegicus"
/mol_type="mRNA"
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-A1-eo-c-08-0-UI"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/clone_1lb="UI-R-A1"
/note="Vector: p773D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-A1
library is a subtracted library derived from the UI-R-A0
library. The UI-R-A0 library consisted of a mixture of
individually tagged normalized libraries constructed from
rat placenta, adult lung, brain, liver, kidney, heart,
spleen, ovary, and muscle. The tag is a string of 3-5
nucleotides present between the Not I site and the
oligo-dT track which allows identification of the library
of origin of a clone within the mixture. The subtracted
library (UI-R-A1) was constructed as follows: PCR
amplified cDNA inserts from a pool of approximately 3,840
UI-R-A0 clones from which 3,818 had been derived was
used as a driver in a hybridization with the UI-R-A0
library in the form of single-stranded circles. The
remaining single-stranded circles (subtracted library) was
purified by hydroxyapatite column chromatography,
converted to double-stranded circles and electroporated
into DH10B bacteria (Life Technologies) to generate the
UI-R-A1 library. This procedure has been previously
described (Bonaldo, Lennon and Soares, Genome Research 6:
791-806, 1996) "
```

ORIGIN

Query Match 0.64; Score 24; DB 2; Length 487;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3461 TTCTTAGCACAACAAAAA 3484
|||||
Db 33 TTCTTAGCACAACAAAAA 10

RESULT 67
AL720059/c 511 bp mRNA linear EST 18-APR-2002
LOCUS
DEFINITION
UI-R-A1-eo-c-08-0-UI-r1 UI-R-A1 Rattus norvegicus cDNA clone
AL720059
AL720059
AL720059.1 GI:20184663
EST.
Rattus norvegicus (zebrafish)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 511)
Coimbra, R., Weil, D., Broctier, P., Blanchard, S., Levi, M.,
Hardelin, J.P., Weissenbach, J. and Petit, C.
A subtracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
JOURNAL
PUBMED
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1. 511
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA044ZD11"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_1lb="Danio rerio embryonic inner ear substracted
cDNA"
/note="substracted cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 511;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAAATTAATAAAGTAAGAAA 3939

Db 342 AAAAATTAATAAAGTAAGAAA 319

RESULT 68
AL720155 523 bp mRNA linear EST 18-APR-2002
LOCUS AL720155
DEFINITION Danio rerio embryonic inner ear substracted cDNA Danio
xerio cDNA clone BN0AA044ZD11 3', mRNA sequence.
AL720155
VERSION AL720155.1 GI:20184759
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio

REFERENCE
AUTHORS Hardelin,J.P., Weissenbach,U. and Petit,C.
A substracted cDNA library from the zebrafish (Danio rerio)
embryonic inner ear
Unpublished (2002)
CONTACT Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr.

FEATURES

source

1. 523
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA044ZD11"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_1lb="Danio rerio embryonic inner ear substracted
cDNA"
/note="substracted cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 523;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAAATTAATAAAGTAAGAAA 3939

Db 182 AAAAATTAATAAAGTAAGAAA 205

RESULT 69
AL715025 525 bp mRNA linear EST 18-APR-2002
LOCUS AL715025
DEFINITION Danio rerio embryonic inner ear substracted cDNA Danio

rerio cDNA clone BN0AA009ZE06 5', mRNA sequence.

AL715025
AL715025.1 GI:20179628

FEATURES

source

1. 525
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA009ZE06"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_1lb="Danio rerio embryonic inner ear substracted
cDNA"
/note="substracted cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAAATTAATAAAGTAAGAAA 3939

Db 332 AAAAATTAATAAAGTAAGAAA 309

RESULT 70
DR576414 529 bp mRNA linear EST 08-JUL-2005
LOCUS DR576414/c
DEFINITION MS00743_C21_F18 MS-PS-N-A-8 Picea glauca cDNA clone MS00743_F18 3,
mRNA sequence.
DR576414
VERSION DR576414.1 GI:70641131
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Picea glauca

REFERENCE
AUTHORS Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea.
1 (bases 1 to 529)
Ralph,S., Kolosova,N., Oddy,C., Cooper,D., Butterfield,Y.,
Kirkpatrick,R., Liu,J., Palmquist,D., Stolt,J., Barber,S., Yang,G.,
Babakoff,R., Brown-John,M., Chand,S., Featherstone,R., Mason,A.,
Mayo,M., Moran,J., Olson,T., Wong,D., Friedmann,M.F., Ritland,C.E.,
Siddiqui,A., Holt,R., Jones,S., Marra,M., Ellis,B.E., Douglas,C.,
Ritland,K. and Bohlmann,J.
The spruce transcriptome: Analysis of expressed sequence tags from
multiple cDNA libraries
Unpublished (2005)
Contact: Joerg Bohlmann
Genome BC forest genomics program
University of British Columbia
Michael Smith Laboratories, 6174 University Boulevard, Rm. 237,
Vancouver, British Columbia, Canada, V6T 1Z3
Tel: 1-604-822-0282
Fax: 1-604-822-2114
Email: bohlmann@mel.ubc.ca
Plate: MS00743 row: F column: 18
High quality sequence stop: 529

FEATURES

source

1. 525
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BN0AA009ZE06"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_1lb="Danio rerio embryonic inner ear substracted
cDNA"
/note="substracted cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 525;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3916 AAAAATTAATAAAGTAAGAAA 3939

Db 332 AAAAATTAATAAAGTAAGAAA 309

RESULT 70
DR576414 529 bp mRNA linear EST 08-JUL-2005
LOCUS DR576414/c
DEFINITION MS00743_C21_F18 MS-PS-N-A-8 Picea glauca cDNA clone MS00743_F18 3,
mRNA sequence.
DR576414
VERSION DR576414.1 GI:70641131
KEYWORDS EST.
SOURCE Picea glauca (white spruce)
ORGANISM Picea glauca

FEATURES
source

POLYA=yes.
Location/Qualifiers
1. 529
/organism="Picea glauca"
/mol_type="mRNA"
/cultiivar="PG-29"
/db_xref="taxon:3330"
/clone="WS00743 P18"
/sex="Hermaphrodite"
/tissue_type="Pushing buds harvested May 16th, young shoots harvested June 15th, and mature shoots harvested June 15th"
/lab_host="E. coli DH10B cells"
/clone_lib="WS-PS-N-A-8"
/note="Organ: Foliage from 25 year old trees harvested at Kalamalka Research Station in Vernon, British Columbia in 2001; Vector: pBluescript II SK (+) XR; Site 1: EcoRI (5' end of cDNA); Site 2: XhoI (3' end of cDNA); mRNA was isolated from each tissue source independently and equal quantities of mRNA from each tissue were then pooled. cDNA was prepared from 5 micrograms of mRNA and directionally ligated into the pBluescript II SK (+) XR vector using the pBluescript II XR cDNA Library Construction Kit according to manufacturer's instructions with modifications (Stratagene). Plasmid DNA was then transformed by electroporation into DH10B cells (Invitrogen) for propagation. Normalization was applied according to published methods [Bonaldo M.F. et al. (1996) Genome Research 6(9):791] in order to reduce the abundance of highly expressed transcripts."

ORIGIN

Query Match 0.6%; Score 24; DB 8; Length 529;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3470 CAAAAAAAAAAGTTTCAA 3493
|||||
Db 182 CAAAAAAAAAAGTTTCAA 159

RESULT 71
AL723652 540 bp mRNA linear EST 18-APR-2002
LOCUS AL723652 Danio rerio embryonic inner ear subcloned cDNA Danio
DEFINITION rerio cDNA clone BND0A0672A07 5', mRNA sequence.
ACCESSION AL723652
VERSION AL723652.1 GI:20188256
KEYWORDS EST.
SOURCE Danio rerio (zebrafish)
ORGANISM Danio rerio
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.
1 (bases 1 to 540)
Colomba.R., Well.D., Broctier.P., Blanchard.S., Levi.M., Hardekin.J.P., Weissenbach.J. and Petit.C.
A subcloned cDNA library from the zebrafish (Danio rerio) embryonic inner ear
Unpublished (2002)
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
Location/Qualifiers
1. 540
/organism="Danio rerio"
/mol_type="mRNA"
/db_xref="taxon:7955"
/clone="BND0A0672A07"
/tissue_type="inner ear"
/dev_stage="embryonic"
/clone_lib="Danio rerio embryonic inner ear subcloned

FEATURES
source

CDNA"
/note="subcloned cDNA library"

ORIGIN

Query Match 0.6%; Score 24; DB 1; Length 540;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 3916 AAAAAATTAATTAAGTTAAGAA 3939
|||||
Db 171 AAAAAATTAATTAAGTTAAGAA 194

RESULT 72
AL723652 564 bp mRNA linear EST 04-DEC-2001
LOCUS AL723652 564 bp mRNA linear EST 04-DEC-2001
DEFINITION EST570709 PyBS Plasmodium yoelii yoelii cDNA clone PYCOM73 5' end, mRNA sequence.
ACCESSION BM168186
VERSION BM168186.1 GI:17301418
KEYWORDS EST.
SOURCE Plasmodium yoelii yoelii
ORGANISM Plasmodium yoelii yoelii
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
1 (bases 1 to 564)
Carlton,T.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B., Fraser,C.M. and Carucci,D.J.
Plasmodium yoelii EST project at TIGR
Unpublished (2001)
Contact: Jane Carlton
Parasite Genomics Group
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-530-9319
Fax: 301-838-0208
Email: carlton@igr.org
For clone info, please contact the Malaria Research and Reference Reagent Resource Center, ATCC
http://www.malaria.mr4.org/mr4pages/index.html
Seq primer: ADF.

FEATURES
source

Location/Qualifiers
1. 564
/organism="Plasmodium yoelii yoelii"
/mol_type="mRNA"
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/db_xref="taxon:73239"
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/clone_lib="PyBS"
/note="Vector: pAD-GAL4; At 20-25% parasitemia, blood was collected from BALB/cBYJ mice infected with Py17XL parasites, and leukocytes removed by passage over microcytalline cellulose columns. Total RNA was isolated using the guanidinium isothiocyanate method, and mRNA isolated using oligo(dT)-cellulose chromatography. First strand cDNA synthesis was completed using a 50-base primer and reverse transcriptase in the presence of 5-methyl dCTP. After second strand synthesis, uneven termini were treated with Pfu DNA polymerase and EcoRI adaptors ligated to the blunt ends. The sample was cleaved with XhoI and separated on a Sephacryl S-500 column. Size-fractionated cDNA was precipitated and ligated to HybridZAP arms directionally using EcoRI-XhoI cleaved arms. After packaging, the phagemid vector (pAD-GAL4) was excised from the HybridZAP vector and plasmid DNA isolated."

ORIGIN

Query Match 0.6%; Score 24; DB 3; Length 564;
Best Local Similarity 100.0%; Pred. No. 86;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAAGTTTCAAT 3494
 DB 89 AAAAAAAAAAAGTTTCAAT 112

RESULT 73
 LOCUS BZ293554 581 bp DNA linear GSS 31-OCT-2002
 DEFINITION CG0392.r1 Candida glabrata Random Genomic Library Candida glabrata
 ACCESSION BZ293554
 VERSION BZ293554
 KEYWORDS BZ293554.1 GI:24433641
 SOURCE GSS.
 ORGANISM Candida glabrata
 BUKARYOTA; FUNGI; ASCOMYCOTA; SACCHAROMYCOTINA; SACCHAROMYCETES;
 SACCHAROMYCETALES; MITOSPORIC SACCHAROMYCETALES; CANDIDA.
 1 (bases 1 to 581)
 Wong,S., Fares,M.A., Zimmermann,W., Butler,G. and Wolfe,K.H.
 Evidence from comparative genomics for a complete sexual cycle in
 the 'asexual' pathogenic yeast Candida glabrata
 Genome Biol. 4 (2), R10 (2003)
 12620120
 CONTACT: Wong S
 Department of Genetics, Smurfit Institute
 Trinity College Dublin
 Dublin 2, Ireland
 Tel: 353 1 6082319
 Fax: 353 1 6798558
 Email: swong@tcd.ie
 Class: plasmid ends.
 Location/Qualifiers
 1..581
 /organism="Candida glabrata"
 /mol_type="genomic DNA"
 /strain="CBS 138"
 /db_xref="taxon:5478"
 /clone="CG0392"
 /clone_1lb="Candida glabrata Random Genomic Library"

ORIGIN
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 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3096 CTTTATGAACCTCTGTAGTTT 3119
 DB 526 CTTTATGAACCTCTGTAGTTT 549

RESULT 74
 LOCUS BM170115 631 bp mRNA linear EST 04-DEC-2001
 DEFINITION EST512628 PyBS Plasmodium yoelii yoelii cDNA clone PYCGB42 5' end,
 mRNA sequence.
 BM170115
 BM170115.1 GI:17303347
 EST.
 Plasmodium yoelii yoelii
 Plasmodium yoelii yoelii
 Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 1 (bases 1 to 631)
 Carlson,J.M., Daly,T.M., Long,C.A., Bergman,L.W., Vaidya,A.B.,
 Frazer,C.M. and Carucci,D.J.
 Plasmodium yoelii EST project at TIGR
 Unpublished (2001)
 CONTACT: Jane Carlson
 Parasite Genomics Group
 The Institute for Genomic Research
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-530-9319
 Fax: 301-838-0208

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

Email: carlton@tigr.org
 For clone info, please contact the Malaria Research and Reference
 Reagent Resource Center, ATCC
 http://www.malaria.mr4.org/mr4pages/index.html
 Seq primer: ADF.
 Location/Qualifiers
 1..631
 /organism="Plasmodium yoelii yoelii"
 /mol_type="mRNA"
 /strain="17XL"
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 /db_xref="taxon:73239"
 /clone="PYCGB42"
 /dev_stage="Asexual blood stages"
 /lab_host="E. coli XL-1 Blue"
 /clone_1lb="PyBS"
 /note="Vector: PAD-GAL4; At 20-25% parasitemia, blood was
 collected from BALB/cBYJ mice infected with Py17XL
 parasites, and leukocytes removed by passage over
 microcrystalline cellulose column. Total RNA was
 isolated using the guanidium isothiocyanate method, and
 mRNA isolated using oligo(dT)-cellulose chromatography.
 First strand cDNA synthesis was completed using a 50-base
 primer and reverse transcriptase in the presence of
 5-methyl dCTP. After second strand synthesis, uneven
 termini were treated with Pfu DNA polymerase and EcoRI
 adaptors ligated to the blunt ends. The sample was cleaved
 with XhoI and separated on a Sephacryl S-500 column.
 Size-fractionated cDNA was precipitated and ligated to
 HybridZAP arms directionally using EcoRI-XhoI cleaved arms.
 After packaging, the phagemid vector (PAD-GAL4) was
 excised from the HybridZAP vector and plasmid DNA
 isolated."

ORIGIN
 Query Match 0.6%; Score 24; DB 3; Length 631;
 Best Local Similarity 100.0%; Pred. No. 86;
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3471 AAAAAAAAAAAGTTTCAAT 3494
 DB 139 AAAAAAAAAAAGTTTCAAT 162

RESULT 75
 LOCUS CE784932 637 bp DNA linear GSS 30-SEP-2003
 DEFINITION tigr-gss-dog-17000330840001 Dog library Canis familiaris genomic,
 genomic survey sequence.
 CE784932
 CE784932.1 GI:37125695
 GSS.
 Canis familiaris (dog)
 SOURCE
 ORGANISM Canis familiaris
 BUKARYOTA; METAZOA; CHORDATA; CRANIATA; VERTEBRATA; EURELOSTOMI;
 MAMMALIA; EUTHERIA; LAURASTHERIA; CARNIVORA; FISSIPEDIA; CANIDAE;
 Canis.
 1 (bases 1 to 637)
 Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.M. and
 Venter,J.C.
 The dog genome: survey sequencing and comparative analysis
 Science 301 (5641), 1898-1903 (2003)
 14512627
 CONTACT: Kirkness EF
 The Institute for Genomic Research
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
 Rockville, MD 20850, USA
 Tel: 301-838-0200
 Fax: 301-838-0208
 Email: ekirknes@tigr.org
 Class: shotgun.
 Location/Qualifiers

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT


```

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                 /mol_type="genomic DNA"
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ORIGIN
Query Match      0.6%; Score 24; DB 10; Length 637;
Best local Similarity 100.0%; Pred. No. 86;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      84 GTGTGTGTGTGTGTTTAACTCA 107
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Db      167 GTGTGTGTGTGTGTTTAACTCA 190

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Job time : 10442 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 20:21:42 ; Search time 13879 Seconds
(without alignments)
17316.385 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgactctcgcctcactg.....agaaccacaaagaacc 4228

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 0

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 100 summaries

Database :

GenEmbl:*
1: gb_ba:*
2: gb_in:*
3: gb_env:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pr:*
9: gb_ro:*
10: gb_scs:*
11: gb_sy:*
12: gb_un:*
13: gb_vl:*
14: gb_hcs:*
15: gb_pl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4228	100.0	4228	6	BD274517
2	4228	100.0	4228	6	AR316368
3	4228	100.0	4228	6	AR427902
4	2619	61.9	110766	15	ATT28119
5	2619	61.9	198493	15	ATCRIV88
6	366	8.7	371	15	ATH531085
7	366	8.7	371	15	ATH531085
8	268	6.3	2148	6	BD274516
9	268	6.3	2148	6	AR316367
10	268	6.3	2148	6	AR427901
11	268	6.3	2148	15	ATU40256
12	155	3.7	2056	15	AY080706
13	57	1.3	20125	11	XXU02426
14	55	1.3	1421	9	AF121976
15	55	1.3	2408	6	AR059581
16	55	1.3	2408	6	AR059581
17	55	1.3	2408	6	AR059581
18	55	1.3	2408	6	AR370418

19	55	1.3	3049	6	AX430197	AX430197 Sequence
20	55	1.3	3049	6	AX449167	AX449167 Sequence
21	55	1.3	3869	15	AB026549	AB026549 Arabidops
22	55	1.3	5651	4	RABAMTA	RABAMTA
23	55	1.3	8072	8	AB031009	AB031009 Homo sapi
24	55	1.3	11716	6	CS070402	CS070402 Sequence
25	55	1.3	13701	15	AB124593	AB124593 Oryza sat
26	55	1.3	27078	6	CS070389	CS070389 Sequence
27	53	1.3	1955	15	ATU44028	U44028 Arabidopsis
28	46	1.1	4026	6	CS070390	CS070390 Sequence
29	45	1.1	13143	8	AB080913	AB080913 Homo sapi
30	44	1.0	1228	9	S4965452	S49657 Mus sp. spe
31	37	0.9	1905	15	ATU41339	U41339 Arabidopsi
32	33	0.8	2317	15	CASAP6G	Z30193 C.albicans
33	32	0.8	4162	6	AR029517	AR029517 Sequence
34	32	0.8	4162	6	AR098470	AR098470 Sequence
35	32	0.8	4162	6	AR494979	AR494979 Sequence
36	32	0.8	4162	6	AX441395	AX441395 Sequence
37	32	0.8	4162	6	AX453891	AX453891 Sequence
38	31	0.7	4165	6	I41430	I41430 Sequence
39	29	0.7	147619	6	AL512368	AL512368 Human DNA
40	29	0.7	177938	14	AL512455	AL512455 Homo sapi
41	29	0.7	204712	14	AC134627	AC134627 Rattus no
42	29	0.7	215429	14	AC123561	AC123561 Rattus no
43	29	0.7	276881	14	AC095481	AC095481 Rattus no
44	28	0.7	105	11	SYNLAMSH1	M37056 Cloning vec
45	28	0.7	3484	6	A91914	A91914 Sequence
46	28	0.7	3484	6	AR309120	AR309120 Sequence
47	28	0.7	3484	6	AR372694	AR372694 Sequence
48	28	0.7	3484	6	BD007602	BD007602 Nematoda-
49	28	0.7	140069	9	AL355005	AL355005 Mouse DNA
50	28	0.7	183958	14	BX530056	BX530056 Mus muscu
51	28	0.7	220894	9	AL732410	AL732410 Mouse DNA
52	27	0.6	374	6	CS088900	CS088900 Sequence
53	27	0.6	374	6	CS088904	CS088904 Sequence
54	27	0.6	374	6	CS088909	CS088909 Sequence
55	27	0.6	2912	11	CVGEM9ZFM	CVGEM9ZFM
56	27	0.6	5824	11	CVB311872	AJ311872 Cloning v
57	27	0.6	6063	11	CVB311873	AJ311873 Cloning v
58	27	0.6	7038	6	BD263403	BD263403 Compositi
59	27	0.6	8815	6	BD263400	BD263400 Compositi
60	27	0.6	14271	11	AY189825	AY189825 Hls-3 int
61	27	0.6	155363	14	AC157620	AC157620 Papio anu
62	27	0.6	183363	9	AC139294	AC139294 Mus muscu
63	27	0.6	230502	9	AC151836	AC151836 Mus muscu
64	26	0.6	38	6	BD272600	BD272600 Amplicifica
65	26	0.6	40	6	AX020362	AX020362 Sequence
66	26	0.6	43	6	CS122533	CS122533 Sequence
67	26	0.6	4151	11	AY720436	AY720436 Plant exp
68	26	0.6	4152	11	AY720435	AY720435 Plant exp
69	26	0.6	4152	11	AY720438	AY720438 Plant exp
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71	26	0.6	4153	11	AY720434	AY720434 Plant exp
72	26	0.6	4154	11	AY720437	AY720437 Plant exp
73	26	0.6	4156	11	AY720439	AY720439 Plant exp
74	26	0.6	4157	11	AY720440	AY720440 Plant exp
75	26	0.6	6337	6	BD235520	BD235520 Desaturas
76	26	0.6	65222	14	AC133631	AC133631 Homo sapi
77	26	0.6	119903	8	AC004662	AC004662 Homo sapi
78	26	0.6	152100	8	AL133332	AL133332 Human DNA
79	26	0.6	168496	9	AC157098	AC157098 Mus muscu
80	26	0.6	182662	8	AC023830	AC023830 Homo sapi
81	26	0.6	183838	8	AC104332	AC104332 Homo sapi
82	26	0.6	193965	9	AC158650	AC158650 Mus muscu
83	26	0.6	195156	14	AC019034	AC019034 Homo sapi
84	26	0.6	197792	14	AC021060	AC021060 Mus muscu
85	26	0.6	206021	8	AC012065	AC012065 Homo sapi
86	26	0.6	207961	14	AC013282	AC013282 Homo sapi
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ALIGNMENTS

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DEFINITION	Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant.				
ACCESSION	BD274517				
VERSION	BD274517.1	GI:33084285			
KEYWORDS	JP 2002534078-A/2.				
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.				
REFERENCE	1 (bases 1 to 4228) Fischer, R.L., and Mizukami, Y. Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant Patent: JP 2002534078-A 2 15-OCT-2002				
AUTHORS	THE REGENTS OF THE UNIVERSITY OF CALIFORNIA				
JOURNAL	OS Arabidopsis thaliana (thale cress) PN JP 2002534078-A/2 PD 15-OCT-2002 PF 07-JAN-2000 JP 2000592392 PR 08-JAN-1999 US 09/4227421 PI ROBERT L FISCHER, YUKIKO MIZUKAMI PC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC ANT				
COMMENT	Promoter FH Key Location/Qualifiers FT promoter (1)..(4228).				
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Qy	121	ACATGTGATATCAATATATATATTGAAATGGAATTCATTTAATAGATGATGAT	180		
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Qy	181	TAAATATATATAGCTGACATTAACAACCAATGTTTCTGTTTAAAGATGATGAT	240		
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Db	241	GTTGCACTTAT	300		

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Qy	361	ATGATTAATGAGATTTAAATCTTTTAAATTAATTAATTAATTAATTAATTAAT	420		
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Qy	421	ATATGTTAGTGTCTTCAAGTCTCACTGTTCAAGAAATTAATCTGTTATCTTGA	480		
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Qy	661	TATGATTTCAAGTACGATGATTAATTAACATTAACGATGATGATGATGATGAT	720		
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Qy	901	TATGTTAAGTCAATTAATTTCTTTAAGTGAATTTTAAAGTGAATTTTAAAGT	960		
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Qy	961	CTTGCAGGAGTATTAAGTCACTGATGATGATGATGATGATGATGATGATGAT	1020		
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Qy	1021	TCTGCTTAAGATATCTTCAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1080		
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Db	1201	AAATTCGAAAAAGAAAAAGAAAAAGCAAGAAATCTATTCGAAAAAGCATTAAT	1260		
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Qy	1321	AATCAAG	1380		
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QY 1381 CCCACATCCCTTTTCTTCCACAAATCATTCACACGAGAAATCTGTCTGATC 1440
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DEFINITION Sequence 3 from patent US 6559357.
ACCESSION AR316368
VERSION AR316368.1 GI:31711159
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE
1. (bases 1 to 4228)
Fischer, R.L. and Mizukami, Y.
Methods for altering mass and fertility in plants
Patent: US 6559357-A 3 06-MAY-2003;
The Regents of the University of California; Oakland, CA
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DEFINITION Sequence 3 from patent US 6639128.
ACCESSION AR427902
VERSION AR427902.1 GI:40186931
KEYWORDS
SOURCE Unknown.

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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4228)
AUTHORS Fischer, R.L., and Mizukami, Y.
TITLE Methods for altering organ mass, controlling fertility and
JOURNAL enhancing asexual reproduction in plants
PATENT: US 6639128-A 3 28-OCT-2003;
NATIONAL Science Foundation; Arlington, VA
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            Submitted (09-MAR-2000) MIPS, at the Max-Planck-Institut fuer
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            Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
            Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
            E-mail: michael.bevan@brc.ac.uk
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ATCHRIV88

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 VERSION AL161592.2 GI:7270751

KEYWORDS

ORGANISM Arabidopsis thaliana (thale cress)
 SOURCE Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE 1 (bases 1 to 23823)
AUTHORS Rose, M., Hempel, S., Entlian, K.-D., Mewes, H.W., Lemcke, K. and
Mayer, K.F.X.
JOURNAL Unpublished
REFERENCE 2 (bases 3704 to 114469)
AUTHORS Robben, J., Grynopmez, B., Volckaert, G., Mewes, H.W., Lemcke, K. and
Mayer, K.F.X.
JOURNAL Unpublished
REFERENCE 3 (bases 114416 to 198493)
AUTHORS Wedler, H., Kutzner, M., Wambutt, R., Mewes, H.W., Lemcke, K. and
Mayer, K.F.X.
JOURNAL Unpublished
REFERENCE 4 (bases 1 to 198493)
AUTHORS EU Arabidopsis sequencing project.
JOURNAL Direct Submision
TITLE Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:
lemcke@mips.biochem.mpg.de, mayer@mips.biochem.mpg.de Project
Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
Laboratory, John Innes Centre, Colney Lane, NR4 7UJ Norwich, UK,
E-mail: michael.bevan@bbsrc.ac.uk
COMMENT Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thai/>
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Db 39305 CATTAACCAATCAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAG 39364
Qy 1372 ACAAGTGTCTGCTATATCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTT 1431
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Qy 1492 TGTTTAATGATTAATTTGTATATATATATATATATATATATATATATATATATAT 1551

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Db 39545 ATAAATGATCTCTTCCT-CTTATCAATAATTACACCACTATGCTPATCAAGTAATA 39603
Qy 1612 ATTAACACCACTCTCTTATCAATAATTATGATATATTAATAAACAACGACTATAGGC 1671
Db 39604 ATTAACACCACTCTCTTATCAATAATTATGATATATTAATAAACAACGACTATAGGC 39663
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Qy 1732 ACACCTGGGGAAAAAATCCAGCTTAATGCTCATTTAAAGATATTTAAATG 1791
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Qy 2091 TTTTTCCTTGAATCTGTTTAAATTTCTCTGCTGCATATCTCGACGATTTTACCAACG 2150
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Db 40204 TATCTTTCCTTGTATTTATTTAGAAAAACAATATTTATCAGAAAAAAGCTTCTTC 40263
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Qy 3410 AGGTTAAGATCTGAAATTTTGTGTTTAAACCAAGTTTCAATTTCTCTTAGCA 3469
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Qy 3470 CAAAAAATAAATAAGTTTCAATTTTAAAGATCTAAATTTTGTGATCAAGTT 3529
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Qy 3590 CATATCAAAATGATGATCAAAATTAATTTGCTGCTTGAACAAGAAACGATGGAATA 3649
Db 41576 CATATCAAAATGATGATCAAAATTAATTTGCTGCTTGAACAAGAAACGATGGAATA 41635
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 QY 3950 AATAGAACACAGATCCCAACGATTCMAACAGCAAAATTTGTGCTTGTCTCTCTT 4009
 DB 41936 AATAGAACACAGATCCCAACGATTCMAACAGCAAAATTTGTGCTTGTCTCTCTT 41995
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RESULT 6
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 LOCUS 371 bp DNA linear PLN 29-MAR-2003
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 212A06.
 ACCESSION AJ530550
 VERSION AJ530550.1 GI:26798810
 KEYWORDS left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Brakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 1
 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)
 12446565
 2 (bases 1 to 371)
 Balzerque, S.
 Direct Submission
 Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 COMMENT

PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgip.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics

program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante.info.inbio.gen.fr>).
 Location/Qualifiers
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 left border"

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 Best Local Similarity 100.0%; Pred. No. 1,1e-148;
 Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2459 ATTCTCAGCAAAACGCGCGCTAGAGGTGTCTTATCTTACATTACAGCTGGGTGGCC 2518
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 QY 2579 GTTAGTCTCAGCTGTACAAACAAATCCAAATCGTATACATATATCAATATCTAC 2638
 DB 126 GTTAGTCTCAGCTGTACAAACAAATCCAAATCGTATACATATATCAATATCTAC 185
 QY 2639 TAGTACTAGATTACGCTACGTATACATCGCTTTTGCAGAAATTTCTAACTAATCTATAC 2698
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 DB 246 AACAACTTGAATCTTTGTAATTTATCTTAAACCAAGTTGATTTGCGATTG 305
 QY 2759 GGAAGTACACTAGTCCCTTTTCCCAAAATAATCTCTTACATGACCGGTTAAA 2818
 DB 306 GGAAGTACACTAGTCCCTTTTCCCAAAATAATCTCTTACATGACCGGTTAAA 365
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 DB 366 GATATT 371

RESULT 7
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 LOCUS 371 bp DNA linear PLN 29-MAR-2003
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence, left border, clone 225B08.
 ACCESSION AJ531085
 VERSION AJ531085.1 GI:26799345
 KEYWORDS left border; T-DNA flanking sequence.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Brakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsie.
 1
 Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., DeRose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.
 T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites
 EMBO Rep. 3 (12), 1152-1157 (2002)
 12446565
 2 (bases 1 to 371)
 Balzerque, S.
 Direct Submission
 Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue

COMMENT
Gaston Cremlieux, 91057 Evry cedex, FRANCE
PCR was performed on DNA from transformants of *Arabidopsis thaliana* plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobio.gen.fr>).
Location/Qualifiers
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/organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="225B08"
/clone_id="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Wassilewskija"
misc_feature
1. .371
/note="T-DNA flanking sequence
left border"

ORIGIN
Query Match 8.7%; Score 366; DB 15; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.1e-148; Mismatches 0; Indels 0; Gaps 0;
Matches 366; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2459 ATTCTTCAGCAAAACGCGCGCTGAGAGTGTCTTATCTTACATTACAGCTGGTTGGC 2518
DB 6 ATCTTCAGCAAAACGCGCGCTGAGAGTGTCTTATCTTACATTACAGCTGGTTGGC 65
QY 2519 AGACATCATGCGCTTACGTAATTTGAGCTTACGTAAGCTTTAACATATCTA 2578
DB 66 AGACATCATGCGCTTACGTAATTTGAGCTTACGTAAGCTTTAACATATCTA 125
QY 2579 GTTAGTTCACGTACAAACAAACAAATCCAAATCGTAACATATATCAAACTATAC 2638
DB 126 GTTAGTTCACGTACAAACAAACAAATCCAAATCGTAACATATATCAAACTATAC 185
QY 2639 TAGTACTAGATTACGCTACATATACGCTTTTCGCAAAATTTCTAACTATATAC 2698
DB 186 TAGTACTAGATTACGCTACATATACGCTTTTCGCAAAATTTCTAACTATATAC 245
QY 2699 AACAACTGATGTTGTTGTAATTTATCTTAAACAAAGTTTGAATTGTCATTG 2758
DB 246 AACAACTGATGTTGTTGTAATTTATCTTAAACAAAGTTTGAATTGTCATTG 305
QY 2759 GAGAGTACATCTAGTCCCTTTTTCGCAAAATATCTTCCTACATGACCGGTTAA 2818
DB 306 GAGAGTACATCTAGTCCCTTTTTCGCAAAATATCTTCCTACATGACCGGTTAA 365
QY 2819 GTATTT 2824
DB 366 GTATTT 371

RESULT 8
BD274516 2148 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant.
ACCESSION BD274516
VERSION BD274516.1 GI:33084284
KEYWORDS JP 2002534078-A/1.
SOURCE
ORGANISM Arabidopsis thaliana (thale cress)
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 2148)
AUTHORS Fischer,R.L. and Mizukami,Y.

TITLE
METHODS FOR MODIFYING WEIGHT OF ORGAN, CONTROLLING FERTILITY AND ENHANCING ASEXUAL REPRODUCTION IN PLANT
JOURNAL THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT Arabidopsis thaliana (thale cress)
OS JP 2002534078-A/1
PN 15-OCT-2002
PD 07-JAN-2000 JP 200592392
PR 08-JAN-1999 US 09/227421
PI ROBERT L FISCHER, YUKIKO MIZUKAMI
PC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC
A1NTEGUMENTA (ANT)
CC encodes first AP2 domain
CC encodes linker region
CC encodes second AP2 domain
FH Key Location/Qualifiers
FT CDS (269) . (1936)
FT misc_feature (1109) . (1339)
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Best Local Similarity 100.0%; Pred. No. 5.1e-106; Mismatches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AGATCCCAACGCAATTCACAGCAAAATTTGCTTTGCTTCTCTTATTAATATC 60
QY 4021 CTCTCAAAACCTCTCTATATCTCTTAAACCCCTCTCTGTTTCTTACCGCAA 4080
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QY 4081 CAAGAAAAACAAAGTTTGAGAAAAATGCTGTTCTTGTTGTAACAATGGGT 4140
DB 121 CAAGAAAAACAAAGTTTGAGAAAAATGCTGTTCTTGTTGTAACAATGGGT 180
QY 4141 TTAGCTTACTACTTGAGAGATTATTAAGAAAGAAAGATGATTAATAGAAAGA 4200
DB 181 TTAGCTTACTACTTGAGAGATTATTAAGAAAGAAAGATGATTAATAGAAAGA 240
QY 4201 AGAAGCAGAAACCAAAAAGAAAC 4228
DB 241 AGAAGCAGAAACCAAAAAGAAAC 268

RESULT 9
AR316367 2148 bp DNA linear PAT 12-JUN-2003
LOCUS
DEFINITION Sequence 1 from patent US 6559357.
ACCESSION AR316367
VERSION AR316367.1 GI:31711158
KEYWORDS
SOURCE
ORGANISM Unknown.
REFERENCE Unclassified.
1 (bases 1 to 2148)
AUTHORS Fischer,R.L. and Mizukami,Y.
TITLE Methods for altering mass and fertility in plants
JOURNAL Patent: US 6559357-A 1 06-MAY-2003;
The Regents of the University of California; Oakland, CA
LOCATION/Qualifiers
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/organism="unknown"
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QY 4021	CTCTCAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTGTTCTTACCGCA			4080
Db 61	CTCTCAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTGTTCTTACCGCA			120
QY 4081	CAAGAAAAAACAAGTTTGAGAAAAATGGGTGGTGGTGTGAACCAATGATGGGT			4140
Db 121	CAAGAAAAAACAAGTTTGAGAAAAATGGGTGGTGGTGTGAACCAATGATGGGT			180
QY 4141	TTTAGCTTACTACTTCGAGATTATTAAGAAAGAGTGAAGTACATTATAGAAAGA			4200
Db 181	TTTAGCTTACTACTTCGAGATTATTAAGAAAGAGTGAAGTACATTATAGAAAGA			240
QY 4201	AGAGAGCAGAAACCAAAAAAGAAACC 4228			
Db 241	AGAGAGCAGAAACCAAAAAAGAAACC 268			
RESULT 10				
LOCUS	AR427901	2148 bp	DNA	linear
DEFINITION	Sequence 1 from patent US 6639128.			
ACCESSION	AR427901			
VERSION	AR427901.1	GI:40166930		
KEYWORDS				
SOURCE	Unknown.			
ORGANISM	Unknown.			
REFERENCE	1. (bases 1 to 2148)			
AUTHORS	Flecher, R.L. and Mizukami, Y.			
TITLE	Methods for altering organ mass, controlling fertility and enhancing asexual reproduction in plants			
JOURNAL	Patent: US 6639128-A 1 28-OCT-2003;			
FEATURES	National Science Foundation; Arlington, VA			
SOURCE	location/Qualifiers			
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Best Local Similarity	100.0%	Pred. No. 5.1e-106		
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QY 4021	CTCTCAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTGTTCTTACCGCA			4080
Db 61	CTCTCAAAAACCCCTCTCTATATCTCTCTAAAGCCCCCTTCTGTGTTCTTACCGCA			120
QY 4081	CAAGAAAAAACAAGTTTGAGAAAAATGGGTGGTGGTGTGAACCAATGATGGGT			4140
Db 121	CAAGAAAAAACAAGTTTGAGAAAAATGGGTGGTGGTGTGAACCAATGATGGGT			180
QY 4141	TTTAGCTTACTACTTCGAGATTATTAAGAAAGAGTGAAGTACATTATAGAAAGA			4200
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QY 4201	AGAGAGCAGAAACCAAAAAAGAAACC 4228			
Db 241	AGAGAGCAGAAACCAAAAAAGAAACC 268			
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LOCUS	ATU40256	2148 bp	mRNA	linear	PLN 10-JAN-2005
DEFINITION	Arabidopsis thaliana ovule development protein (AINTGUMENTA) mRNA, complete cds.				
ACCESSION	U40256				
VERSION	U40256.1	GI:1209098			
KEYWORDS					
SOURCE	Arabidopsis thaliana (thale cress)				
ORGANISM	Arabidopsis thaliana				
REFERENCE	1 (bases 1 to 2148)				
AUTHORS	Klucher, K.M., Chow, H., Reiser, L. and Fischer, R.L.				
TITLE	The AINTGUMENTA gene of Arabidopsis required for ovule and female gametophyte development is related to the floral homeotic gene APTAL2				
JOURNAL	Plant Cell 8 8 (2), 137-153 (1996)				
PUBMED	8742706				
REFERENCE	2 (bases 1 to 2148)				
AUTHORS	Klucher, K.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-NOV-1995) L. Reiser, Plant Biology, UC Berkeley, 111 Koshland Hall, Berkeley, CA 94720, USA				
FEATURES	Location/Qualifiers				
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	/protein_id="AA91040.1"				
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	/translation="MKSFCDNDNNHNTNLGLFSLSNMMKMGGRGREATYSSSTSSAATSSVLPOLVAGDNTSNFGVCGSNPGGIYSHMSVPLRSLDGLCMEALNRSLSNNHODSSRYEDPFGTHNNTSHKEMDLSIDLPYNTTHERTPTTNPOFSEFNQNNHOSNRNQDISEALVETSVFETTTAAAKKRGDEVVVVGQKQIVRKS.IDTPGQRTQYRGTVRHRWTRKEALIMDNSFKGEHSKRGVYVAGYDMEKAARAYDLAAKYNGPSHTNFSAKENYOKELJEDKMMNTRQEVYVHLRKSFGFSRGSIIYGVTEHHQNGRQARIGVAGKNDLYLGRPGOEBAAEAYVAALKEFTGATVNFDIRDYDRLNSSLTSLSGELARRNNNSIVVRNTEBDGTALAAVYVSGSNKEVSTPERLSPALFALPQVNDMFGSNNMGNNSPWTSNPNAELTVALTLPPMPVFAAMADS"				
ORIGIN					
Query Match	6.3%; Score 268; DB 15; Length 2148;				
Best Local Similarity	100.0%; Pred. No. 5.1e-106; Indels 0; Gaps 0;				
Matches 268; Conservative	0; Mismatches 0;				
QY	3961 AGATCCCAAGCATTCACACGAAATTGCTGCTTGCCTCTCTCTTATTAATATC	4020			
Db	1 AGATCCCAAGCATTCACACGAAATTGCTGCTTGCCTCTCTCTTATTAATATC	60			
QY	4021 CTCTCAAAAACCTCTCTCTATATCTCTCTTAAAGCCCCCTTCTGTTTCTTACCGCAA	4080			
Db	61 CTCTCAAAAACCTCTCTCTATATCTCTCTTAAAGCCCCCTTCTGTTTCTTACCGCAA	120			
QY	4081 CAAAGAAAAACAAAGTTGAGAAAAAGTGCTGTTGCTGTGTAACCAATGATGGGT	4140			
Db	121 CAAAGAAAAACAAAGTTGAGAAAAAGTGCTGTTGCTGTGTAACCAATGATGGGT	180			
QY	4141 TTTAGCTTACTCTGAGAGATTATATAGAAAGAAAGAGTGAAGATACATTATAGAAAGA	4200			
Db	181 TTTAGCTTACTCTGAGAGATTATATAGAAAGAAAGAGTGAAGATACATTATAGAAAGA	240			
QY	4201 AGAAGACAGAAACCAAAAAAGAAACC	4228			

Db 241 AGAAGACAGAAAACCAAAAAGAACCC 268

RESULT 12
AY080706 2056 bp mRNA linear PLN 18-SEP-2002
LOCUS Arabidopsis thaliana putative ovule development protein
DEFINITION ainegumenta (At4g37750) mRNA, complete cds.

ACCESSION
AY080706
VERSION
AY080706.1 GI:19310586
KEYWORDS
FLI CDNA.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eustoids II; Brassicales; Brassicaceae; Arabidopsids.

REFERENCE
1 (bases 1 to 2056)
Yamada,K., Liu,S.X., Sakano,H., Pham,P.K., Banh,J., Chung,M.K.,
Goldsmith,A.D., Lee,J.M., Quach,H.L., Toriumi,M., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shim,P., Southwick,A., Shinozaki,K.,
Davis,R.W., Ecker,J.R. and Theologis,A.
Arabidopsis Full Length cDNA Clones
Unpublished

TITLE
JOURNAL
REFERENCE
AUTHORS
2 (bases 1 to 2056)
Yamada,K., Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M.,
Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L.,
Tang,C.C., Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L.,
Carninci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Ishida,J.,
Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B.,
Lin,J., Meyers,M.C., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J.,
Sakurai,T., Satou,M., Seki,M., Shim,P., Southwick,A.,
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Direct Submission
Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL cDNAs (RAFL cDNA: RIKEN
Arabidopsis Full-length cDNA.). Seki,M., Narusaka,M., Ishida,J.,
Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.,
Hayashizaki,Y. and Shinozaki,K.

TITLE
JOURNAL
COMMENT
The Salk, Stanford, PGEC (SSP) Consortium members carried out the
sequencing and annotation of the RAFL cDNAs: Yamada,K., Banh,J.,
Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M.,
Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C.C.,
Toriumi,M., Wu,H.C., Yamamura,Y., Yu,G., Bowser,L., Chen,H.,
Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C., Lam,B., Lin,J.,
Meyers,M.C., Miranda,M., Nguyen,M., Palm,C.J., Shim,P.,
Southwick,A., Davis,R.W., Ecker,J.R. and Theologis,A.
Yamada,K. (SSP/PGEC) and Seki,M. (RIKEN GSC) contributed equally to
this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSP/PGEC)
contributed equally to this work as PIs.

FEATURES
source
1..2056
/organism="Arabidopsis thaliana"
/mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="4"
/clone="RAFL06-86-F19 (RI1873)"
/ecotype="Columbia"
/note="This clone is in a modified pBluescript vector
(lambda ZAP) as a XhoI/SacI insert."
1..2056
/gene="At4g37750"
1..157
/gene="At4g37750"

gene
5'UTR

misc_difference 2
/gene="At4g37750"
/note="not present in genomic sequence"
158..1825
/gene="At4g37750"
/codon_start=1
/evidence=experimental
/product="putative ovule development protein ainegumenta"
/protein_id="AA185024.1"
/db_xref="GI:19310587"
/translation="MKSFCDDNDNHSNTTNLLGFSLSNMMKRGCGREAIYSSST
SSAATSSSVPPQLVVDNTSNFVCYGVSPNGGIYSNHSVMPLRSDGSLCLMEALNR
SSSHNHQDSFKVEDPFGTHHNTSHKEMDLSDLSFNTTDEPTNTNPFESF
POTRNHEETRYGNDPSSLTGGSGFVGVYGEFOQSLSLMSPGSQSSCTTGGSHHQ
NONNHQSTHNOHISALVETSGVPTTMAAKKRGQGVVGVGQDMEEKARAYDL
PGQRTSQRYGTVRHRRTGVYEAHLMDNSFKGSHKRGQGVYIGYDMEEKARAYDL
AALKRWGPSTHTNFSAEYTKETEDKKNTRQSYVAHLRKSSGFSRGSITYGTVTRH
HGHGQARIGVAGAKNDLYLTFGTQEEAAEYDVAAIKFRGTNAVTFDITRYDV
RIMSNTLLSGELARNNNSIVRVNTEDTALNAVVEGSSNKEVSTPERLSPPALFA
LPOVQKMGSGNMGNSPMTSNPNALKTVALTLTPQMEVFAMADS"
1826..2056
/gene="At4g37750"

ORIGIN
3'UTR
Query Match 3.7%; Score 155; DB 15; Length 2056;
Best Local Similarity 100.0%; Pred. No. 1.6e-56;
Matches 155; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4074 ACCGCAACAAAGAAAACAAAGTTTGAGAAAATGCTGTCTTCTGTAACCAATG 4133
DB 3 ACCGCAACAAAGAAAACAAAGTTTGAGAAAATGCTGTCTTCTGTAACCAATG 62

QY 4134 ATTGGGTTTACGTTCTCTCTCGAGAGATTATTAAGAAAGAGTGAATACATTAT 4193
DB 63 ATTGGGTTTACGTTCTCTCTCGAGAGATTATTAAGAAAGAGTGAATACATTAT 122

QY 4194 AGAAGACAGAAAGCAAGAAACCAAAAAGAACCC 4228
DB 123 AGAAGACAGAAAGCAAGAAACCAAAAAGAACCC 157

RESULT 13
XXU02426
LOCUS XXU02426 20125 bp DNA linear SYN 29-JAN-1997
DEFINITION Cloning vector lambda EMBL3 SP6/T7, left arm.
ACCESSION U02426
VERSION U02426.1 GI:413792
KEYWORDS
SOURCE Cloning vector lambda EMBL3 SP6/T7
ORGANISM Cloning vector lambda EMBL3 SP6/T7
REFERENCE
1 (bases 1 to 20125)
Other sequences; artificial sequences; vectors.

REFERENCE
Kites,P.A.
TITLE ClonteCH Vectors On Disc version 1.3
AUTHORS Kites,P.A.
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 20125)
TITLE ClonteCH Vectors On Disc version 1.3
AUTHORS Kites,P.A.
JOURNAL Unpublished

COMMENT
Direct Submission
Submitted (07-OCT-1993) Paul A. Kites, ClonteCH Laboratories, Inc.,
1020 East Meadow Circle, Palo Alto, CA 94303, USA
This sequence has been compiled from information in the sequence
databases, published literature and other sources. If you suspect
there is an error in this sequence, please contact ClonteCH's
Technical Service Department at (415) 424-8222 or (800) 662-2566,
extension 3 or E-mail TECH@CLONTECH.COM.
Location/Qualifiers
1..20125
/organism="Cloning vector lambda EMBL3 SP6/T7"
/mol_type="genomic DNA"
/db_xref="taxon:31784"

FEATURES
source
1..20125
/organism="Cloning vector lambda EMBL3 SP6/T7"
/mol_type="genomic DNA"
/db_xref="taxon:31784"

ORIGIN
Query Match 1.3%; Score 57; DB 11; Length 20125;

Best Local Similarity 100.0%; Pred. No. 6,6e-14;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACCTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATCCT 57
Db 20044 GTGACCTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATCCT 20100

RESULT 14
AF121976 1421 bp DNA linear ROD 07-DEC-1999
LOCUS Mus musculus odorant receptor S19 gene, complete cds.
DEFINITION AF121976
ACCESSION AF121976
VERSION AF121976.2 GI:6532000
KEYWORDS
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
REFERENCE 1 (bases 442 to 1421)
AUTHORS Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
TITLE Combinatorial receptor codes for odors
JOURNAL Cell 96 (5), 713-723 (1999)
PUBMED 10089886
REFERENCE 2 (bases 442 to 1421)
AUTHORS Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
TITLE Direct Subm1881on
JOURNAL Submitted (20-JUN-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
REFERENCE 3 (bases 1 to 1421)
AUTHORS Malnic,B., Hirono,J., Sato,T. and Buck,L.B.
TITLE Direct Subm1881on
JOURNAL Submitted (07-DEC-1999) Neurobiology, Harvard Medical School, 220
Longwood Avenue, Boston, MA 02115, USA
REMARK Sequence update by submitter
COMMENT On Dec 7, 1999 this sequence version replaced gi:4680261.
FEATURES
source location/Qualifiers
1..1421
/organism="Mus musculus"
/mol_type="genomic DNA"
/strain="BALB/C"
/db_xref="taxon:10090"
<291..>1310
/product="odorant receptor S19"
291..1310
/note="G-protein-coupled receptor"
/codon_start=1
/product="odorant receptor S19"
/protein_id="BAD7596.2"
/db_xref="GI:6532001"
/translation="MPEKMLSKLAVLLIESCRQALVKGRIIVDSRPHNPNTTH
YRELEDOHWIAIPFGSMYIALVGNCTIIYITIDRALHBPWYLFICLSITDVIYC
STTLPEKLAIFMLRSHVSYHGLCTOMFPAVATRSATILMAAPRYVALCRPLHY
TSILNAVVIKIGLACTRGILTFVFPVILIERLPFGCHITIPHTCEHGIACACA
SLIPNTYIGLVASVGMVLIATSYIILQAVLPLPSKQAFAPSTCGAHCIVY
LVEPYPAFSPFTHRGHNVPPQVHIIILAMLYLPLVPLVYGVINTKQIRILIDF
FVGR"

ORIGIN
Query Match 1.3%; Score 55; DB 9; Length 1421;
Best Local Similarity 100.0%; Pred. No. 1.1e-12;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
AR059581 2408 bp DNA linear PAT 29-SEP-1999
LOCUS AR059581
DEFINITION Sequence 69 from patent US 5840498.

ACCESSION AR059581
VERSION AR059581.1 GI:5986031
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.B. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5840498-A 69 24-NOV-1998;
FEATURES location/Qualifiers
1..2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACCTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACCTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

RESULT 16
AR063063 2408 bp DNA linear PAT 29-SEP-1999
LOCUS AR063063
DEFINITION Sequence 69 from patent US 5844072.
ACCESSION AR063063
VERSION AR063063.1 GI:5990754
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.B. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5844072-A 69 01-DEC-1998;
FEATURES location/Qualifiers
1..2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.6e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACCTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACCTCTAGGCTCACTGCGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

RESULT 17
193548 2408 bp DNA linear PAT 01-DEC-1998
LOCUS 193548
DEFINITION Sequence 69 from patent US 5731149.
ACCESSION 193548
VERSION 193548.1 GI:3938018
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsted,M.B. and Ouellette,A.J.
TITLE Antibiotic cryptidin peptides and methods of their use
JOURNAL Patent: US 5731149-A 69 24-MAR-1998;
FEATURES location/Qualifiers
1..2408
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.9e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

RESULT 18
AR370418 2408 bp DNA linear PAT 12-SEP-2003
LOCUS Sequence 69 from patent US 6300470.
DEFINITION AR370418
ACCESSION AR370418
VERSION AR370418.1 GI:34606949
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2408)
AUTHORS Selsled,M.E. and Ouellette,A.J.
TITLES Antibiotic cryptdin peptides and methods of their use
JOURNAL Patent: US 6300470-A 69 09-OCT-2001;
The Regents of the University of California; Oakland, CA
FEATURES
source 1..2408
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 2408;
Best Local Similarity 100.0%; Pred. No. 9.9e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

RESULT 19
AX430197 3049 bp DNA linear PAT 28-JUN-2002
LOCUS Sequence 4 from Patent EP1207204.
DEFINITION AX430197
ACCESSION AX430197
VERSION AX430197.1 GI:21655562
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLES Tissue-specific promoters from sugar beet
JOURNAL Patent: EP 1207204-A 4 22-MAY-2002;
KWS Saat AG (DE)
FEATURES
source 1..3049
/organism="Beta vulgaris"
/mol_type="unassigned DNA"
/db_xref="taxon:161934"
1..2998
2877..2883
TATA_signal
mRNA 2928..3049

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 666 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 720

Db 2656 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 2710

RESULT 20
AX449167 3049 bp DNA linear PAT 03-JUL-2002
LOCUS Sequence 4 from Patent WO0240687.
DEFINITION AX449167
ACCESSION AX449167
VERSION AX449167.1 GI:21697968
KEYWORDS
SOURCE Beta vulgaris
ORGANISM Beta vulgaris
REFERENCE 1
AUTHORS Hehl,R., Kloos,D. and Stahl,D.J.
TITLES Tissue specific promoters
JOURNAL Patent: WO 0240687-A 4 23-MAY-2002;
KWS Saat AG (DE)
FEATURES
source 1..3049
/organism="Beta vulgaris"
/mol_type="unassigned DNA"
/db_xref="taxon:161934"
1..2998
2877..2883
TATA_signal
mRNA 2928..3049

ORIGIN
Query Match 1.3%; Score 55; DB 6; Length 3049;
Best Local Similarity 100.0%; Pred. No. 8.9e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 55
Db 2656 GTGACTCTTAGGCTCACTGGCTTAATACGACTCACTATAGGAGCTCGAGATC 2710

RESULT 21
AB026549 3869 bp DNA linear PLN 24-OCT-2001
LOCUS Arabidopsis thaliana gene for neoxanthin cleavage enzyme, complete cds.
DEFINITION AB026549
ACCESSION AB026549
VERSION AB026549.1 GI:16416373
KEYWORDS neoxanthin cleavage enzyme.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1
AUTHORS Iuchi,S., Kobayashi,M. and Shinozaki,K.
TITLES Characterization of neoxanthin cleavage enzyme from Arabidopsis thaliana
JOURNAL Unpublished
AUTHORS Iuchi,S. and Shinozaki,K.
TITLES Direct Submision
JOURNAL Submitted (22-APR-1999) Satoshi Iuchi, RIKEN, Plant Mol. Bio.; 3-1-1 Kouyadai, Tsukuba 305-0074, Japan
(E-mail:iuchi@rtc.riken.go.jp, Tel:81-298-36-4359)
FEATURES
source 1..3869
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/ecotype="Columbia"
1831..3630
/codon_start=1
/product="neoxanthin cleavage enzyme"
/protein_id="BAB70609.1"

/db_xref="GI:16416374"
/translation="MASPTATRAVSGRWLGNTQPPRSSGSDLSYCSLPMASTV
TRKLVSSALHTPPALHPKQSSNSPALTIVVPRKESNTTKOMNLPORAAAALDAAG
FLVSHKRLHPKTPADPSVOIAGNFAPNVPKRLPEVVKLPDSIKGVVRGAP
LHBEVTHHPFDGDMYAVKFEHGSASYACRFTQTRFYERGLGHPVPPKAIGEHL
GHGTAIALMLFARAAGIYDPAHGTGVANGLVFNGLRLAMEDDLPOVOITPNG
DLKTVGFPDGGOLSESTMIAHPKVDPSGSLFALSYDVSKVLYKVRFPDGTGSD
VETLDQPTMWDPAITENRYVVPDOVPRFLPMIRIGSSPVYDKNKVARFGITLDT
AESDSNTKMDAPDCFCFHLNMANEBEPIDVNVIGSCMTPEDSIFNBSDEKSVLS
EIRLNLKTVGSTRPPIISNEDQVNLGAGVNRMLGRKTKFAYLALAEWPVKVSGFA
KVDLTJGEVKHLYGDNRYGGEPLFLPGEGGEDEGYILCFVHDEKTKWSLQIVNAV
SLVEATVTKLPSRVPGFHFICADLDLAKQV"

ORIGIN

Query Match 1.3%; Score 55; DB 15; Length 3869;
Best Local Similarity 100.0%; Pred. No. 8.3e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGACCTCTAGGCGCTCACTGGCCTTAATACGACTACTATAGGAGCTCGAGATC 55
Db 1 GTGACCTCTAGGCGCTCACTGGCCTTAATACGACTACTATAGGAGCTCGAGATC 55

RESULT 22

RABAMYA 5651 bp DNA linear MAM 27-APR-1993
LOCUS DEFINITION RABBIT serum amyloid A gene, exons 1, 2, 3, and 4.
ACCESSION M8536
VERSION M8536.1 GI:164769
KEYWORDS acute phase reactant; serum amyloid A.
SOURCE Oryctolagus cuniculus (rabbit)
ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha;
Leporidae; Oryctolagus.
1 (sites)

REFERENCE

1 (sites)

Ray, B.K. and Ray, A.
Complementary DNA cloning and nucleotide sequence of rabbit serum
amyloid A protein

JOURNAL Biochem. Biophys. Res. Commun. 178 (1), 68-72 (1991)
PUBMED 1712590

2 (bases 1 to 5651)

Ray, B.K. and Ray, A.
Rabbit serum amyloid A gene: cloning, characterization and sequence
analysis

JOURNAL Biochem. Biophys. Res. Commun. 180 (3), 1258-1264 (1991)
PUBMED 1953777

Original source text: Oryctolagus cuniculus (strain New Zealand)
liver DNA.

FEATURES

Location/Qualifiers

source

1. 5651

/organism="Oryctolagus cuniculus"

/mol_type="genomic DNA"

/db_xref="taxon:9986"

/tissue_type="liver"

TATA_signal

join(626..659,1089..1181,4322..4462,4904..5148)

mRNA

626..659

exon

/number=1

intron

660..1088

exon

/number=1

intron

1089..1181

exon

/number=2

intron

1182..4321

exon

/number=3

intron

4322..4462

exon

/number=3

intron

4463..4903

exon

/number=3

intron

4904..5148

exon

/number=4

polya_signal 5129..5134
ORIGIN

Query Match 1.3%; Score 55; DB 4; Length 5651;
Best Local Similarity 100.0%; Pred. No. 7.3e-13;
Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGACCTCTAGGCGCTCACTGGCCTTAATACGACTACTATAGGAGCTCGAGATC 55
Db 5651 GTGACCTCTAGGCGCTCACTGGCCTTAATACGACTACTATAGGAGCTCGAGATC 5597

RESULT 23

AB031009 8072 bp DNA linear PRI 19-FEB-2000
LOCUS DEFINITION Homo sapiens DNA, MHC class I CL region, 7.1 ancestral haplotype.
ACCESSION AB031009
VERSION AB031009.1 GI:7008034
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (sites)

Leelayuwat, C., Abraham, L.J., Tabarias, H., Christiansen, F.T. and
Dawkins, R.L.

Genomic organization of a polymorphic duplicated region centromeric
of HLA-B

Immunogenetics 36 (4), 208-212 (1992)
1353477

2 (bases 1 to 8072)

Dawkins, R.L., Gaudieri, S. and Leelayuwat, C.

Direct Submission

Submitted (12-AUG-1999) Silvana Gaudieri, University of Western

Australia, Centre for Molecular Immunology and Instrumentation;

Stirling Hwy, Nedlands, WA 6009, Australia

(E-mail:sgaudier@lab.nig.ac.jp, Tel:61-8-93464414,

Fax:61-8-93464578)

FEATURES

Location/Qualifiers

source

1. 8072

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/chromosome="6"

/map="6p21.3"

/haplotype="MHC 7.1 Ancestral Haplotype HLA-A3 HLA-B7

HLA-DR15"

/cell_type="B lymphoblastoid"

/dev_stage="Adult"

490..517

/note="AT-rich"

533..832

/rpt_family="AluSg"

complement(1825..1983)

/rpt_family="L2"

1984..2552

/rpt_family="MER61B"

2598..3373

/note="Haplospecific geometric element Homologous region"

2868..2962

/note="(GA)n"

complement(3005..3110)

/rpt_family="MERSA"

3871..3901

/note="AT-rich"

complement(4318..4388)

/rpt_family="7SIRNA"

complement(4551..4682)

/rpt_family="LIM3"

complement(4716..4939)

/rpt_family="L2"

5083..5286


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misc_feature      /rpt_family="L1ME1"
                  5569..6766
                  /note="PERB3 homologous region"
repeat_unit      5678..6090
                  /rpt_family="HERV16"
repeat_unit      6118..6573
                  /rpt_family="HERVL"
misc_feature      complement(6600..8072)
                  /note="PERB7 homologous region"
repeat_unit      6679..6893
                  /rpt_family="HERV16"
repeat_unit      6959..7040
                  /rpt_family="HERVL"
repeat_unit      7136..7464
                  /rpt_family="HERVL"
repeat_unit      7705..8072
                  /rpt_family="HERVL"

ORIGIN
Query Match      1.3%; Score 55; DB 8; Length 8072;
Best Local Similarity 100.0%; Pred.No.6.6e-13; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

Qy 1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 55
1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 55
Db 1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 55

RESULT 24
LOCUS      CS070402      11716 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION      Sequence 31 from Patent WO2001023541.
ACCESSION      CS070402
VERSION      CS070402.1 GI:63087970
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
              synthetic construct
              other sequences; artificial sequences.
REFERENCE      1
AUTHORS      Fodor, W.L. and Ramsondar, J.J.
TITLE      Compositions and methods for altering gene expression
              Patent: WO 2001023541-A 31 05-APR-2001;
              Alexion Pharmaceuticals, Inc. (US)
FEATURES
source      1..11716
              Location/Qualifiers
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="gene targeting vector"
              4852..4937
              /note="Nucleotides at positions 4852 to 4937 are n wherein
              n = nucleotides between the end of Intron 3 and beginning
              of Intron 4"

ORIGIN
Query Match      1.3%; Score 55; DB 6; Length 11716;
Best Local Similarity 100.0%; Pred.No.5.9e-13; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

Qy 1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 55
1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 55
Db 1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 55

RESULT 25
LOCUS      AB124593      13701 bp      DNA      linear      PLN 12-NOV-2004
DEFINITION      Oryza sativa (indica cultivar-group) DNA, endogenous rice tungro
              bacilliform virus-like sequence, clone:IR36-ERTBV3.
ACCESSION      AB124593
VERSION      AB124593.1 GI:46409013
KEYWORDS
SOURCE      Oryza sativa (indica cultivar-group)

```

```

ORGANISM      Oryza sativa (indica cultivar-group)
              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
              Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
              Ehrhartoideae; Oryzeae; Oryza.
REFERENCE      1
AUTHORS      Kunii, M., Kanda, M., Nagano, H., Uyeda, I., Kishima, Y. and Sano, Y.
TITLE      Reconstruction of putative DNA virus from endogenous rice tungro
              bacilliform virus-like sequences in the rice genome: implications
              for integration and evolution
JOURNAL      (er) BMC Genomics 5 (1), 80 (2004)
PUBMED      15488154
REFERENCE      2 (bases 1 to 13701)
AUTHORS      Kishima, Y. and Sano, Y.
TITLE      Direct Submission
JOURNAL      Submitted (17-OCT-2003) Yuji Kishima, Hokkaido University,
              Laboratory of Plant Breeding, Graduate School of Agriculture;
              Kita-ku Kita 9 Nishi 9, Sapporo, Hokkaido, 060-8589, Japan
              (E-mail:kishima@aps.egr.hokudai.ac.jp, Tel:81-11-706-2439,
              Fax:81-11-706-4934)
FEATURES
source      1..13701
              Location/Qualifiers
              /organism="Oryza sativa (indica cultivar-group)"
              /mol_type="genomic DNA"
              /cultivar="IR36"
              /db_xref="taxon:33946"
              /clone="IR36-ERTBV3"
              /clone_jib="EMBL3 etiolated shoots genomic DNA (CLONTECH,
              F110413)"
              158..5914
              /note="endogenous rice tungro bacilliform virus-like
              sequence"

ORIGIN
Query Match      1.3%; Score 55; DB 15; Length 13701;
Best Local Similarity 100.0%; Pred.No.5.6e-13; Indels 0; Gaps 0;
Matches 55; Conservative 0; Mismatches 0;

Qy 1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 55
1 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 13615
Db 13669 GTGACTCTAGGCTCACTGAGCTTAATACGACTCATATAGGAGCTCGAGATC 13615

RESULT 26
LOCUS      CS070389      27078 bp      DNA      linear      PAT 05-MAY-2005
DEFINITION      Sequence 18 from Patent WO2001023541.
ACCESSION      CS070389
VERSION      CS070389.1 GI:63087957
KEYWORDS
SOURCE      .
ORGANISM      Sus scrofa (pig)
              Sus scrofa
              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
              Sus.
REFERENCE      1
AUTHORS      Fodor, W.L. and Ramsondar, J.J.
TITLE      Compositions and methods for altering gene expression
              Patent: WO 2001023541-A 18 05-APR-2001;
              Alexion Pharmaceuticals, Inc. (US)
FEATURES
source      1..27078
              Location/Qualifiers
              /organism="Sus scrofa"
              /mol_type="unassigned DNA"
              /db_xref="taxon:9823"
              /note="porcine Gal alpha (1,3) galactosyl transferase
              gene"
              4852..4937
              /note="Nucleotides 4852 to 4937 are n wherein n =
              nucleotides within the Exon 4 region"
              11717..11752
              /note="Nucleotides 11717 to 11752 are n wherein n =
              nucleotides within the Exon 5 region"
              13748..13811
              misc_feature

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misc_feature /note="Nucleotides 13748 to 13811 are n wherein n = nucleotides within the Exon 6 region"
 misc_feature /note="Nucleotides 14359 to 14463 are n wherein n = nucleotides within the Exon 7 region"
 misc_feature /note="Nucleotides 21628 to 21765 are n wherein n = nucleotides within the Exon 8 region"
 misc_feature /note="Nucleotides 21628 to 21765 are n wherein n = nucleotides within the Exon 9 region"

ORIGIN

Query Match 1.3%; Score 55; DB 6; Length 27078;
 Best Local Similarity 100.0%; Pred. No. 4.5e-13;
 Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTCGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATGAGGAGCTCGAGGATC 55
 Db 1 GTCGACTCTAGGCGCTCACTGAGCTAATACGACTCACTATGAGGAGCTCGAGGATC 55

RESULT 27
 ATU44028 1955 bp mRNA linear PLN 30-JAN-1996
 LOCUS Arabidopsis thaliana transcription factor CKC mRNA, complete cds.
 DEFINITION U44028.1 GI:1171428
 VERSION
 KEYWORDS
 SOURCE Arabidopsis thaliana (chale crees)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; euroside II; Brassicales; Brassicaceae; Arabidopsia.

REFERENCE
 AUTHORS Vergani P., Morandini P. and Soave C.
 TITLE Direct Submission
 JOURNAL Submitted (29-DEC-1995) Paola Vergani, Dept. of Biology 'L. Gorini', University of Milan, Via Celoria 26, Milan, 20133, Italy

FEATURES
 source
 1..1955
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 76..1743
 /function="transcription factor; complements a yeast protein kinase C 1 mutant; Method: conceptual translation supplied by author."
 /codon_start=1
 /product="CKC"
 /protein_id="AA06281.1"
 /db_xref="GI:1171429"
 /translation="MKSFCNDNDNNHSTNTNLGFSLSNMWKKGRGGRATYSSTCSAATSSSVPCPLVNGSDNTSNRGVCSLMSVHNSMPLRSGSLCIMEALRSSHSHHODSSPKVEDFFGTHHNTSHKANDLSLDLFFNTTHETVTFNFOFESFPQRNHEETRNNGDNDLSLTHGSEFNVGEFQSLSPSSQSCITGSHHQNONQNHQOHQOISEALVETSVGFETTTMAAKKGOEDVVVVGQKIVHRKSIDT FQRTSGYRGVTRHRTGRYEAHLMDNSPKKEGSRGRGVYLGQYMERKAAYDL AALKYMGSPSTHNSAENYOKETEDMMRMROEVVAHLRRKSGSPSGASIDYGVTL HOGHGMARIGRAVAGKDYLGTCGQBEAAEAADVAAIKERGNATNTNDDIRYVD RHMSSNTLSGELARRNNNSIVRANTEDQTLNANVVGSGSKVEVTERLSPFALTRA LPVNMCFSGNMGGNMSPWTSNPAELKTVALTLPMVPFAAWADS"

CDS

1.3%; Score 53; DB 15; Length 1955;
 Best Local Similarity 100.0%; Pred. No. 7.7e-12;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN

Query Match 1.3%; Score 53; DB 15; Length 1955;
 Best Local Similarity 100.0%; Pred. No. 7.7e-12;
 Matches 53; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4176 AGAGTGAAGATACCTTATAGAAAGAGAGAAACCAAAAAAGAAACC 4228
 Db 23 AGAGTGAAGATACCTTATAGAAAGAGAGAAACCAAAAAAGAAACC 75

RESULT 28
 CS070390 4026 bp DNA linear PAT 05-MAY-2005
 LOCUS Sequence 19 from Patent WO2001023541.
 DEFINITION CS070390
 ACCESSION CS070390
 VERSION CS070390.1 GI:63087958
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1..4026
 /organism="synthetic construct"
 /mol_type="unassigned DNA"
 /db_xref="taxon:32630"
 /note="Gal alpha (1,3) galactosyl transferase gene"

ORIGIN

Query Match 1.1%; Score 46; DB 6; Length 4026;
 Best Local Similarity 100.0%; Pred. No. 7.1e-09;
 Matches 46; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 AGGCTCAGTGGCTTAATAGACTCACTATGAGGAGCTCGAGGATC 55
 Db 10 AGGCTCAGTGGCTTAATAGACTCACTATGAGGAGCTCGAGGATC 55

RESULT 29
 AB080913 13143 bp DNA linear PRI 05-FEB-2004
 LOCUS Homo sapiens gene for Fc-epsilon receptor I beta-chain, complete cds.
 DEFINITION
 ACCESSION AB080913
 VERSION AB080913.1 GI:29420482
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 PUBMED
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 FEATURES
 source
 1..13143
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 1383..1540
 join(1485..1540,2411..2540,3055..3189,5509..5565,6117..6275,6677..6775,8269..8367)
 /codon_start=1
 /product="Fc-epsilon receptor I beta-chain"
 /protein_id="BAC6486.1"
 /db_xref="GI:29420483"
 /translation="MDTESRANLALPOBSSVPAPEVLEISPOEVSGLTKSASSPLATWLTVAKEQEPFLGVQIITAMICLCFRTVCSVDLISHIEDIPSSPKAGYGF

1
 Akizawa Y., Nishiyama C., Hasegawa M., Maeda K., Nakahata T., Okumura K., Ra C. and Ogawa H.
 Regulation of human Fc epsilon RI beta chain gene expression by Oct-1 Int. Immunol. 15 (5), 549-556 (2003)
 2 (bases 1 to 13143)
 Nishiyama C. and Hasegawa M.
 Direct Submission
 Submitted (06-MAR-2002) Chiharu Nishiyama, Juntendo University School of Medicine, Allergy Research Center; 2-1-1 Hongo, Bunkyo-ku, Tokyo 113-8421, Japan
 (E-mail: chiharu@med.juntendo.ac.jp, Tel: 81-3-5802-1591, Fax: 81-3-3813-5512)
 Location/Qualifiers
 1..13143
 /organism="Homo sapiens"
 /mol_type="genomic DNA"
 /db_xref="taxon:9606"
 1383..1540
 join(1485..1540,2411..2540,3055..3189,5509..5565,6117..6275,6677..6775,8269..8367)
 /codon_start=1
 /product="Fc-epsilon receptor I beta-chain"
 /protein_id="BAC6486.1"
 /db_xref="GI:29420483"
 /translation="MDTESRANLALPOBSSVPAPEVLEISPOEVSGLTKSASSPLATWLTVAKEQEPFLGVQIITAMICLCFRTVCSVDLISHIEDIPSSPKAGYGF

exon 2411..2540
 exon 3055..3189
 exon 5509..5565
 exon 6117..6275
 exon 6677..6775
 exon 8269..11251
 ORIGIN

Query Match	1.1%;	Score 45;	DB 8;	Length 13143;
Best Local Similarity	100.0%;	Pred. No. 1,4e+08;		
Matches 45;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY	11	GGCTCACTGGCCCTAATACACTCACTATTAGGAGACTGAGAGATC	55	
Db	13143	GGCTCACTGGCCCTAATACACTCACTATTAGGAGACTGAGAGATC	13099	

RESULT	30
S4965AS2	
LOCUS	1328 bp DNA linear ROD_25-JAN-2005
DEFINITION	Mus sp. sperm mitochondria-associated cysteine-rich protein gene,
ACCESSION	5' UTR and complete cds.
VERSION	S49657.1 GI:259841
KEYWORDS	.
SEGMENT	2 OF 2
SOURCE	Mus sp.
ORGANISM	Mus sp.

REFERENCE	AUTHORS	TITLE
1 (pages 1 to 1228)	Karimipour, I., Cutler, M., Shih, D., Smith, J. and Kleene, K. C.	Sequence of the gene encoding the mitochondrial capsule

JOURNAL DNA Cell Biol. 11 (9), 693-699 (1992)

REMARK GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 118581] from the original journal article.

```

FEATURES
source
1. 1228

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MRNA
fold(S49654.1:<787..928.391..>842)

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5*UTR      join(S49654.1:<787.  .928,391.  .410)
CDS        411.  .842
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/product="sperm mitochondria-associated cysteine-rich
protein"
/protein_id="AAC08282.2"
/db_xref="GI:58126430"
/translation="MSPSKTNOCPPPCPCPPCCPPKCCPPKCCPPKCCPPKCCPPK
PCPCPPCCPPCCPPCCPPCCPLKCCPPKCCPPKCCPPKCCPPKCCPPKCCPPKCCPP
SSEKREKEDPDSGTLKGGDSPPSPGAGAGGNN"

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Query Match	1.0%;	Score 44;	DB 9;	Length 1228;
Best Local Similarity	100.0%;	Pred. No. 7.8e-08;		
Matches 44; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1 2	55
GCCCTACCTGGCCCTAATACGACTCATATGGGAGCTCGGAGATC		
DB	98	141
GCCCTACCTGGCCCTAATACGACTCATATGGGAGCTCGGAGATC		

RESULT	31
LOCUS	ATU41339
DEFINITION	Arabidopsis thaliana ANT (AINTSEGMENTA)
VERSION	U41339
KEYWORDS	U41339.1 GI:1244707
SOURCE	
ORGANISM	Arabidopsis thaliana (thale cress)
	Arabidopsis thaliana
	Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
	Spermatophyta; Magnoliophyta, eudicotyledons; core eudicotyledons;
	rosids; eurosids II; Brassicales, Brassicaceae; Arabidopsie.
REFERENCE	1 (bases 1 to 1905)
AUTHORS	Elliotte,R.C., Betzner,A.S., Huttner,E., Oakes,M.P., Tucker,W.Q.,
TITLE	Gerentes,D., Perez,P. and Smyth,D.R.
JOURNAL	AINTEGMENTA, an APTALAA-like gene of Arabidopsis with pleiotropic
PUBMED	roles in ovule development and floral organ growth
REFERENCE	Plant Cell 8 (2), 155-168 (1996)
AUTHORS	8742707
TITLE	2 (bases 1 to 1905)
JOURNAL	Smyth,D.R.
PUBMED	Direct Submission
REFERENCE	Submitted (27-NOV-1995) David Smyth, Genetics and Dev. Biology,
AUTHORS	Monash University, Wellington Road, Clayton, VIC 3168, Australia
TITLE	Location/Qualifiers
FEATURES	1..1905
SOURCE	

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  1. .1905
  38. .1705
  /gene="AINTEGUMENTA"
  /note="similar to APETALA2 protein encoded by GenBank
  Accession Number U12546"
  /codon_start=1
  /product="ANT"
  /protein_id="AAB17364.1"
  /db_xref="GI:1244708"
  /translation="MSKPCDDNDNNHNTNTNLGLFSLSSNMHMGGRGGEATYSST
  SNAATSSSVLPOLVVGDNSTNSFCVCGSNPGGIIYSHMSVPLRLSGLCLMEALNR
  SSSHNHEEDSPRYEDFGTHNNHTSHKEAMLSLSLFTNTTHEPTTTFCEPSF
  PQRNHEEDSTRNGDPSLTHGSSFNFGVYGEEQSLSLMSGSGSSCITGSHHHQQ
  NQNMQHSQCHQOISEALVETSVGFETTTAAAKRGRDVAVVQGGQIVHRSKIDT
  FGQRTSGVGTWRRTGRYEALHMDNSFKEEGSHRGRDVLVGGYEMEKARAYLD
  AALKYMGPSHTNPSAENVYKEIEDMKNNRQSVYALRLKSGSFGSAIYGVGTH
  HCGRQWARTGRVAGNAGDLYLGTGQOEALAEAYDAALKEFGNTAVNTGDIERYVD
  RINSSNTLSGELARRNNNSIYVRNTEDDQYALAAVYVGGSGNSKREVSPTERLSPALFA
  LPVQNMCRFGSNMGKNSPMTSPNPAELKTVALTLFPMVFAAMAUS"
  878. .1108
  /gene="AINTEGUMENTA"
  /note="encodes first AP2 domain"
  1184. .1391
  /gene="AINTEGUMENTA"
  /note="encodes second AP2 domain"

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Query Match 0.9%; Score 37; DB 15; Length 1905;
Best Local Similarity 100.0%; Pred. No. 7.9e-05;
Matches 37; Conservative 0; Mismatches 0; Gaps 0;

Qy		4192 ATGAGAAAGAGAGACGAATCCAAAAAAGAACC 4228
Db	1	ATAGAAAGAGAGAGCGAACCAAAAAAAGAACC 37

RESULT 32	
CASAP6G/c	
LOCUS	
CASAP6G	
2317 bp	DNA
	linear
	PLN 18-APR-2005

```

DEFINITION C. albicans (Ca74) SAP7 gene for aspartyl protease.
ACCESSION Z30193
VERSION Z30193.1
KEYWORDS aspartyl protease; SAP7 gene.
SOURCE Candida albicans
ORGANISM Candida albicans
REFERENCE 1 (bases 1 to 2317)
AUTHORS Monod,M., Togni,G., Hube,B. and Sanglard,D.
TITLE Multiplicity of genes encoding secreted aspartic proteinases in Candida species
JOURNAL Mol. Microbiol. 13 (2), 357-368 (1994)
PUBMED 7984113
REFERENCE 2 (bases 1 to 2317)
AUTHORS Monod,M., Togni,G., Hube,B. and Sanglard,D.
TITLE Multiplicity of genes encoding secreted aspartic proteases in Candida species
JOURNAL Candida species
REFERENCE 3 (bases 1 to 2317)
AUTHORS Sanglard,D.
TITLE Direct Submission
JOURNAL Submitted (21-FEB-1994) Dominique SANGLARD, Inst.de Microbiologie F509/Biochimie, Centre, Hôpitaller Universitaire Vaudois (CHUV), 155, Ch. de Boveresses, Epalinges, 1066, Switzerland
FEATURES
     source
         1..2317
             /organism="Candida albicans"
             /mol_type="genomic DNA"
             /strain="Ca74"
             /db_xref="taxon:5476"
             283..2049
                 /gene="SAP7"
                 283..2049
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                     /codon_start=1
                     /transl_table=12
                     /product="aspartyl protease"
                     /protein_id="CA082925.1"
                     /db_xref="GI:578123"
                     /db_xref="GCA:P43096"
                     /db_xref="interPro:IPR001461"
                     /db_xref="interPro:IPR001969"
                     /db_xref="interPro:IPR009007"
                     /db_xref="UniProt/Swiss-Prot:P43096"
                     /translation="MQRVLELLSLSTLAVIGGFALPYKHLQAGSGAHPFNRRLP
                     IPDVNGVAKSVEDDVNOIIGPIFGNGIPSGGSIQGTSGNGSHVKTEVLSPPSAAKQ
                     GSNPSTDNKDPDPSKGTGRFLDLMNSISTDPNNLIGANKPRFSSDNKGKDALPTFS
                     AVSGVEOPTSKSVETIAPGASASASSSSSSASQSEBSOPSSSANKKTGAFFLS
                     LDNQTLVTATLTKVGSQAQEVQVNIITGSSDLPWFISGNSGCKVNGSIIIDCKGVDP
                     KSNKSWHDKNTDYSISYDDDKASGTCGNITFPADGFSIENAFVIDNTTSGIVG
                     FGVEYPELEAVNSKYTLNLPFAMKEONLIKAYSLYIDSRVAVGYILFGIDIAFPTF
                     GDLKAPDIVOCDNKVYVYSLPITVSAISLNNYTAAGLPGASHPKGAYVYNGTDFR
                     NGVDLKDITLTLDITGTTTSTLSKDQVESYGLIGNVTTNDAGAKAYEPCVGNPNVY
                     LEHFKNKEQYIKVPTSEFVLSVGTVASGAEICVFGILPGTHSILGDNFMSSVYAVFDL
                     EDHYSIAQAYVNNHVAWPTE"
                     916..2046
                         /gene="SAP7"
                         /product="aspartyl protease (putative)"
     origin
         Query Match 0.8%; Score 33; DB 15; Length 2317;
         Best Local Similarity 100.0%; Pred. No. 0.0042;
         Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

DEFINITION	SEQUENCE 26 FROM PATENT US 5859336.
ACCESSION	AR029517
VERSION	AR029517.1 GI:5941490
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 4162)
AUTHORS	Koziet,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V., Crossland,L.D., Wright,M.S., Merlin,E.J., Launis,K.L., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M. and Suttie,J.L.
TITLE	Synthetic DNA sequence having enhanced activity in maize
JOURNAL	Patent: US 5859336-A 26 12-JUN-1999;
FEATURES	Location/Qualifiers
SOURCE	1..4162
ORIGIN	/organism="unknown"
	/mol_type="unassigned DNA"
Query Match	0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity	100.0%; Pred. No. 0.0096;
Matches 32; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CY	19 TGGCTAATACGACTCACTATAGGAGCTCGA 50
Db	4162 TGGCTAATACGACTCACTATAGGAGCTCGA 4131
RESULT 34	
LOCUS	AR098470 4162 bp DNA linear PAT 14-FEB-2001
DEFINITION	Sequence 26 from patent US 6075185.
ACCESSION	AR098470
VERSION	AR098470.1 GI:12807727
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 4162)
AUTHORS	Koziet,M.G., Desai,N.M., Lewis,K.S., Warren,G.W., Evola,S.V., Wright,M.S., Launis,K.L., Rothsfein,S.J., Bowman,C.G., Dawson,J.L., Dunder,E.M., Pace,G.M. and Suttie,J.L.
TITLE	Synthetic DNA sequence having enhanced insecticidal activity in maize
JOURNAL	Patent: US 6075185-A 26 13-JUN-2000;
FEATURES	Location/Qualifiers
SOURCE	1..4162
	/organism="unknown"
	/mol_type="unassigned DNA"
ORIGIN	
Query Match	0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity	100.0%; Pred. No. 0.0096;
Matches 32; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
CY	19 TGGCTAATACGACTCACTATAGGAGCTCGA 50
Db	4162 TGGCTAATACGACTCACTATAGGAGCTCGA 4131
RESULT 35	
LOCUS	AR494979 4162 bp DNA linear PAT 15-MAY-2004
DEFINITION	Sequence 26 from patent US 6720488.
ACCESSION	AR494979
VERSION	AR494979.1 GI:47270333
KEYWORDS	
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 4162)
AUTHORS	Koziet,M., Desai,N., Pace,G.M., Suttie,J., Carozzi,N., Boyce,C., Dawson,J.L., Dunder,E., Wright,M., Launis,K., Rothsfein,S.J.,

TITLE Lewis, K., Warren, G., and Ewola, S.
JOURNAL Transgenic maize seed and method for controlling insect pests
Patent: US 6720486-A 26 13-APR-2004;
Syngenta Investment Corporation; Wilmington, DE

FEATURES
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1. .4162
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN

Query Match 0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGCCCTAATCGACTCACTATAGGAGCTCGA 50
|||||
Db 4162 TGCCCTAATCGACTCACTATAGGAGCTCGA 4131

RESULT 36
AX441395/c 4162 bp DNA linear PAT 03-JUL-2002

LOCUS AX441395
DEFINITION Sequence 26 from Patent EP1209237.
ACCESSION AX441395
VERSION AX441395.1 GI:21690378
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
AUTHORS Kozielec, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,
Ewola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launus, K.L.
and Rothstein, S.J.
TITLE Synthetic dna sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: EP 1209237-A 26 29-MAY-2002;
Syngenta Participations AG (CH)

FEATURES
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1418. .1427
/note="start of mRNA"

misc_feature
1481. .2366
/note="start of mRNA"

exon 2367. .2451
intron 2452. .2602
exon 2603. .2690
intron 2691. .2804
exon 2805. .2906
intron 2907. .3075
exon 3076. .3177
intron 3178. .3304
exon 3305. .3398
intron 3399. .3498
exon 3499. .3713
intron 3714. .3811

ORIGIN

Query Match 0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGCCCTAATCGACTCACTATAGGAGCTCGA 50
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Db 4162 TGCCCTAATCGACTCACTATAGGAGCTCGA 4131

RESULT 37
AX453891/c 4162 bp DNA linear PAT 06-JUL-2002

LOCUS AX453891

DEFINITION Sequence 26 from Patent EP1213356.
ACCESSION AX453891
VERSION AX453891.1 GI:21713549
KEYWORDS
SOURCE Zea mays
ORGANISM Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoidae; Andropogoneae; Zea.

REFERENCE
AUTHORS Kozielec, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,
Ewola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launus, K.L.
and Rothstein, S.J.
TITLE Synthetic dna sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: EP 1213356-A 26 12-JUN-2002;
Syngenta Participations AG (CH)

FEATURES
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/note="start of mRNA"

misc_feature
1481. .2366
/note="start of mRNA"

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exon 2603. .2690
intron 2691. .2804
exon 2805. .2906
intron 2907. .3075
exon 3076. .3177
intron 3178. .3304
exon 3305. .3398
intron 3399. .3498
exon 3499. .3713
intron 3714. .3811

ORIGIN

Query Match 0.8%; Score 32; DB 6; Length 4162;
Best Local Similarity 100.0%; Pred. No. 0.0096;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 TGCCCTAATCGACTCACTATAGGAGCTCGA 50
|||||
Db 4162 TGCCCTAATCGACTCACTATAGGAGCTCGA 4131

RESULT 38
I41430/c 4165 bp DNA linear PAT 13-MAY-1997

LOCUS I41430
DEFINITION Sequence 26 from patent US 5625136.
ACCESSION I41430
VERSION I41430.1 GI:2082020
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.

REFERENCE
AUTHORS Kozielec, M.G., Desai, N.M., Lewis, K.S., Kramer, V.C., Warren, G.W.,
Ewola, S.V., Crossland, L.D., Wright, M.S., Merlin, E.J., Launus, K.L.,
Rothstein, S.J., Bowman, C.G., Dawson, J.L., Dunder, E.M., Pace, G.M.
and Sutcliffe, J.L.
TITLE Synthetic DNA sequence having enhanced insecticidal activity in
maize
JOURNAL Patent: US 5625136-A 26 29-APR-1997;
Syngenta Participations AG (CH)

FEATURES
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1. .4165
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN

Query Match 0.7%; Score 31; DB 6; Length 4165;

ORIGIN

sim5.S.
 Direct Submission
 Submitted (10-JUN-2001) Sanger Centre, Hinxton, Cambridgeshire
 CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
 requests: clonerequest@sanger.ac.uk
 On Feb 21, 2001 this sequence version replaced gi:12964544.
 ----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humquery@sanger.ac.uk
 ----- Project Information
 Center project name: ba380B6
 ----- Summary Statistics
 Assembly program: XMAP4, version 4.5
 Sequencing vector: plasmid, L08752; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Consensus quality: 176636 bases at least Q40
 Consensus quality: 177204 bases at least Q30
 Consensus quality: 177479 bases at least Q20
 Insert size: 176538, sum-of-contigs
 Insert size: 173713, 9.6% error; agarose-fp
 Quality coverage: 6.77x in Q20 bases; sum-of-contigs quality
 coverage: 6.93x in Q20 bases; agarose-fp

NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of 'N', but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will then be preserved.

*		
*		
*	3693	contig of 3693 bp in length
*	3694	3793: gap of 100 bp
*	3794	70507: contig of 66714 bp in length
*	70508	70607: gap of 100 bp
*	70608	1394990: contig of 68883 bp in length
*	139491	1395990: gap of 100 bp
*	139591	177938: contig of 38346 bp in length
	Location/Qualifiers	

1

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/note="assembly_fragment:01110
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ORIGIN

Query Match      0.7%: Score 29; DB 14; Length 177938;
Best Local Similarity 100.0%; Pred. No. 0.061;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3471 AAAAAAAAAAAGCTTTCATTTATTA 3499
Db      20564 AAAAAAAAAAAGTTTCATTTATTA 20592

RESULT 41
AC134627
LOCUS      Rattus norvegicus clone CH230-368N4, WORKING DRAFT SEQUENCE, 5
DEFINITION
AC134627
AC134627.2 GI:25138679
HTG: HTGS_PHASE1: HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Rattus norvegicus (Norway rat)
ORGANISM    Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
            Sciurognathi; Muridae; Murinae; Murinae; Rattus.
            1 (bases 1 to 204712)
REFERENCE   1
            Muzny, D., Marie, Metzker, M., Lee, Abramson, S., Adams, C., Alder, J.,
            Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,
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            Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,
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            Chacko, J., Chavez, D., Chen, G., Chen, Y., Chen, Z., Chu, J.,
            Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,
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            Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K.,
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            Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,
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            Gunaratne, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,
            Harvey, J., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,
            Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hognes, M.,
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            Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jollivet, A.,
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            Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,
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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F.,
Rivers, C., Rodkey, T., Rojas, A., Rose, R., Ruiz, S., J.,
Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H.,
Shetty, J., Shvartsbeyn, A., Siseon, I., Sitter, C.D., Smas, D.,
Sneed, A., Sodergren, E., Song, X., Z., Sorelle, R., Soas, J.,
Stemle, M., Strong, R., Sutton, A., Svatek, A., Tabor, P., Taylor, C.,
Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Usmani, K.,
Valae, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,
Wang, O., Wang, S., Warren, J., Warren, R., Wei, X., White, F.,
Williams, G., Willson, R., Wiczek, R., Wooden, H., Worley, K.,
Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V.,
Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhou, S., Zhao, S., Dunn, D., von
Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,
Weinstock, G., and Gibbs, R.A.
Direct Submission

Unpublished
2 (bases 1 to 204712)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (28-SEP-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 204712)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (20-NOV-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 20, 2002 this sequence version replaced gi:23343609.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.

----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: KC20
Center clone name: CH230-368N4
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 186320 bases at least Q40
Consensus quality: 188335 bases at least Q30
Consensus quality: 189791 bases at least Q20
Estimated insert size: 187550; sum-of-contigs estimation
Quality coverage: 7x in Q20 bases; sum-of-contigs estimation

NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
1
* 6702: contig of 6702 bp in length
* 6703
* 6803
* 6803: contig of 6936 bp in length
* 76788: gap of unknown length
* 76789
* 76889: contig of 51011 bp in length
* 127900
* 127900: gap of unknown length

```

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* 128000 153581: contig of 25582 bp in length
* 153582 153681: gap of unknown length
* 153682 204712: contig of 51031 bp in length.
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Best Local Similarity 100.0%; Pred. No. 0.059;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      704 ACATACACATATTTTGTGTTTGTGTTT 732
Db      164536 ACATACACATATTTTGTGTTTGTGTTT 164564
RESULT 42
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DEFINITION
AC123561 215429 bp DNA linear HTG 11-OCT-2002
Rattus norvegicus clone CH230-165B21, *** SEQUENCING IN PROGRESS
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AC123561 GI:23666273
HTG; HTG_PHASE2; HTG_DRAFT; HTG_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
1 (bases 1 to 215429)
Nuzyn,D,Marie, Metzker,M,Lee, Abramzon,S, Adams,C, Alder,J,
Allen,C, Allen,H, Alebrooks,S, Amlin,A, Anguiano,D,
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Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Center,A,
Chaco,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
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Karpachy,S, Kelly,S, Kelly,S, Khan,Z, Kling,L, Kovar,C,

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TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Kowig,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
Lorenshewa,L, Louisedge,H, Lozada,R,J, Lu,X, Ma,J,
Maheshwari,M, Mahindartine,M, Mahmud,M, Malloy,K, Mangum,A,
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McInerney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,
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Yu,F, Zhang,J, Zhou,J, Zhou,X, Zhao,S, Dunn,D, von
Niederhausern,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O,
Weinstock,G, and Gibbs,R,A.
Direct Submission
Unpublished
2 (bases 1 to 215429)
Worley,K,C.
Direct Submission
Submitted (31-MAY-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 215429)
Rat Genome Sequencing Consortium.
Direct Submission
Submitted (11-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Oct 10, 2002 this sequence version replaced gi:21281285.
The sequence in this assembly is a combination of BAC based reads
and whole genome shotgun sequencing reads assembled using Atlas
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
in the feature table below represents a scaffold in the Atlas
assembly (a 'contig-scaffold'). Within each contig-scaffold,
individual sequence contigs are ordered and oriented, and separated
by sized gaps filled with Ns to the estimated size. The sequence
may extend beyond the ends of the clone and there may be sequence
contigs within a contig-scaffold that consist entirely of whole
genome shotgun sequence reads. Both end sequences and whole genome
shotgun sequence only contigs will be indicated in the feature
table.
----- Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help@bcm.tmc.edu
----- Project Information
Center project name: GXSW
Center clone name: CH230-165B21
----- Summary Statistics
Assembly program: Phrap; version 0.990329
Consensus quality: 178659 bases at least Q40
Consensus quality: 181922 bases at least Q30
Consensus quality: 184135 bases at least Q20
Estimated insert size: 186300; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html).
* NOTE: This is a 'working draft' sequence. It currently

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* consists of 1 contigs. Gaps between the contigs
 * are represented as runs of N. The order of the pieces
 * is believed to be correct as given, however the pieces
 * of the gaps between them are based on estimates that have
 * provided by the submitter.
 * This sequence will be replaced
 * by the finished sequence as soon as it is available and
 * the accession number will be preserved.
 1 215429: contig of 215429 bp in length.
 Location/Qualifiers

source
 /organism="Rattus norvegicus"
 /mol_type="genomic DNA"
 /db_xref="taxon:10116"
 /clone="CH230-165B21"
 720..1470
 /note="clone boundary
 clone_end:17
 site:ECORI
 end_sequence=BH272105"

ORIGIN

Query Match 0.7%; Score 29; DB 14; Length 215429;
 Best Local Similarity 100.0%; Pred. No. 0.058;
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 704 ACATACACATATTTTGTGTTGTTT 732
 Db 212351 ACATACACATATTTTGTGTTGTTT 212379

RESULT 43
 AC095481/c 276881 bp DNA linear HTG 09-MAY-2003
 LOCUS Rattus norvegicus clone CH230-7K20, *** SEQUENCING IN PROGRESS ***,
 5 unordered pieces.

ACCESSION AC095481 GI:30467658
 VERSION HTG: HTGS_PHASE1, HTGS_DRAFT, HTGS_ENRICHED.
 KEYWORDS Rattus norvegicus (Norway rat)
 SOURCE Rattus norvegicus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muridae; Muridae; Murinae; Rattus.

REFERENCE
 AUTHORS Muzny,D,Marie, Metzker,M,Lee, Abramson,S, Adams,C, Alder,J,
 Allen,C, Allen,H, Alsbrooks,S, Amin,A, Anguiano,D,
 Anyalebech,V, Aoyagi,A, Ayodeji,M, Baca,B, Baden,H,
 Baldwin,D, Bandaranaike,D, Barber,M, Barnstead,M, Benahmed,F,
 Bismuto,K, Blair,J, Blankenburg,K, Blych,P, Brown,M,
 Bryant,N, Buhay,C, Burch,P, Burrell,K, Calderon,E,
 Cardenas,V, Carter,K, Cavazos,I, Ceasar,H, Center,A,
 Chacko,J, Chavez,D, Chen,G, Chen,R, Chen,Y, Chen,Z, Chu,J,
 Cleveland,C, Cockrell,R, Cox,C, Coyle,M, Cree,A, D'Souza,L,
 Davila,M,L, Davis,C, Davy-Carroll,L, De Anda,C, Dederich,D,
 Delgado,O, Denison,S, Deramo,C, Ding,Y, Dinh,H, Divya,K,
 Draper,H, Dugan-Rocha,S, Dunn,A, Durbin,K, Duval,B, Bayee,K,
 Egan,A, Escotto,M, Eugene,C, Evans,C,A, Falls,T, Fan,G,
 Fernandez,S, Finley,M, Flagg,N, Forbes,L, Foster,M, Foster,P,
 Frazer,C,M, Gabisi,A, Ganta,R, Garcia,A, Garner,T, Gervais,
 Gebregiorgis,E, Geer,K, Gill,R, Grady,M, Guerra,M, Guevara,W,
 Gunaratne,P, Haaland,W, Hamill,C, Hamilton,C, Hamilton,K,
 Harvey,Y, Hawlak,P, Hawes,A, Henderson,N, Hernandez,J,
 Hernandez,R, Hines,S, Hladun,S,L, Hodgson,A, Hogues,M,
 Hollins,B, Howells,S, Huylk,S, Hume,J, Idlebird,D, Jackson,A,
 Jackson,B, Jacob,L, Jiang,H, Johnson,B, Johnson,R, Jolivet,A,
 Karpathy,S, Kelly,S, Kelly,S, Khan,Z, King,L, Kovar,C,
 Kowls,C, Kraft,C,L, Lebow,H, Levan,J, Lewis,L, Li,Z, Liu,J,
 Liu,J, Liu,W, Liu,Y, London,P, Longacre,S, Lopez,J,
 Lorensuwa,L, Louieged,H, Lozano,R,J, Lu,X, Ma,J,
 Maheshwari,M, Mahindartne,M, Mahmoud,K, Mallory,K, Mangum,A,
 Mangum,B, Mapua,P, Martin,K, Martin,R, Martinez,E,
 Mawhney,S, McLeod,M,P, McNeill,T,Z, Meenen,E,

TITLE
 JOURNAL
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL

REFERENCE
 AUTHORS
 TITLE
 JOURNAL

COMMENT

Milosavljevic,A, Miner,G, Minja,E, Montemayor,J, Moore,S,
 Morgan,M, Morris,K, Morris,S, Muntass,M, Murphy,M, Nair,L,
 Nankervis,C, Neal,D, Newton,N, Nguyen,N, Norris,S,
 Nwokediemen,O, Okunodu,G, Olampunsgoon,A, Pal,S, Parks,K,
 Pasternak,S, Paul,H, Perez,A, Perez,L, Frankoch,C,
 Plopper,F, Polinder,A, Popovic,D, Prims,E, Pu,L,
 Puazo,M, Quiroz,J, Rachlin,E, Reeves,K, Regier,M,A, Reigh,R,
 Reilly,B, Reilly,M, Ren,Y, Reuter,M, Richards,S, Riggs,F,
 Rives,C, Rodkey,T, Rojas,A, Rose,M, Rose,R, Ruiz,S,J,
 Sanders,M, Saverly,G, Scherer,S, Scott,G, Shatman,S, Shen,H,
 Shetty,J, Shvartbeyn,A, Sisson,I, Sitter,C,D, Smajda,D,
 Sneed,A, Sodergren,E, Song,X,-Z, Sorelle,R, Sosa,J,
 Steidle,M, Strong,R, Sutton,A, Svatek,A, Tabors,P, Taylor,C,
 Taylor,T, Thomas,N, Thomas,S, Tingey,A, Trejos,Z, Umani,K,
 Valas,R, Vera,V, Villaseana,D, Waldron,L, Walker,B, Wang,J,
 Wang,Q, Wang,S, Warren,J, Warren,R, Wei,X, White,P,
 Williams,G, Willson,R, Wleczyk,R, Wooden,H, Worley,K,
 Wright,D, Wright,R, Wu,J, Yakub,S, Yen,J, Yoon,L, Yoon,V,
 Yu,F, Zhang,J, Zhou,X, Zhou,S, Zhao,S, Dunn,D, von
 Niederhausen,A, Weiss,R, Smith,D,R, Holt,R,A, Smith,H,O,
 Weinstein,G, and Gibbs,R.A.
 Direct Submission
 Unpublished
 2 (bases 1 to 276881)
 Worley,K.C.
 Direct Submission
 Submitted (17-SEP-2001) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 3 (bases 1 to 276881)
 Rat Genome Sequencing Consortium.
 Submitted (09-MAY-2003) Human Genome Sequencing Center, Department
 of Molecular and Human Genetics, Baylor College of Medicine, One
 Baylor Plaza, Houston, TX 77030, USA
 On May 9, 2003 this sequence version replaced gi:24941064.
 The sequence in this assembly is a combination of BAC based reads
 and whole genome shotgun sequencing reads assembled using Atlas
 (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described
 in the feature table below represents a scaffold in the Atlas
 assembly (a 'contig-scaffold'). Within each contig-scaffold,
 individual sequence contigs are ordered and oriented, and separated
 by sized gaps filled with Ns to the estimated size. The sequence
 may extend beyond the ends of the clone and there may be sequence
 contigs within a contig-scaffold that consist entirely of whole
 genome shotgun sequence reads. Both end sequences and whole genome
 shotgun sequence only contigs will be indicated in the feature
 table.

----- Genome Center
 Center: Baylor College of Medicine
 Center code: BCM
 Web site: http://www.hgsc.bcm.tmc.edu/
 Contact: hgsc-help@bcm.tmc.edu
 ----- Project Information
 Center project name: GCKM
 Center clone name: CH230-7K20
 ----- Summary Statistics
 Assembly program: Atlas;
 Consensus quality: 222954 bases at least Q40
 Consensus quality: 228004 bases at least Q30
 Consensus quality: 230763 bases at least Q20
 Estimated insert size: 23155; sum-of-contigs estimation
 Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

 * NOTE: Estimated insert size may differ from sequence length
 * (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 5 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.
* 1 241308: contig of 241308 bp in length
* 241309 241408: gap of unknown length
* 241409 270462: contig of 29054 bp in length
* 270463 270562: gap of unknown length
* 270563 271681: contig of 1119 bp in length
* 271682 271781: gap of unknown length
* 271782 272810: contig of 1029 bp in length
* 272811 272910: gap of unknown length
* 272911 276881: contig of 3971 bp in length.
FEATURES
source
1. .276881
/organism="Rattus norvegicus"
/mol_type="genomic DNA"
/db_xref="taxon:10116"
/clone="CH230-7K20"
misc_feature
1. .1235
/note="wgs contig"
63196. .65045
/note="wgs contig"
167109. .168091
/note="wgs contig"
misc_feature
241309. .241408
/estimated_length=unknown
gap
270463. .270562
/estimated_length=unknown
gap
271682. .271781
/estimated_length=unknown
gap
272811. .272910
/estimated_length=unknown
ORIGIN
Query Match 0.7%; Score 29; DB 14; Length 276881;
Best Local Similarity 100.0%; Pred. No. 0.053;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 704 ACATACCATTAATTTTGTGTTTGTGTTT 732
Db 156792 ACATACCATTAATTTTGTGTTTGTGTTT 156764
RESULT 44
SYNLMASH1
LOCUS Cloning vector lambda-SHLX1 DNA, partial sequence.
DEFINITION M37056
ACCESSION M37056.1 GI:208752
VERSION
KEYWORDS lambda-SHLX.
SOURCE unidentified cloning vector
ORGANISM unidentified cloning vector
REFERENCE
1 (bases 1 to 105)
Palazzo, M.J., Hamilton, B.A., Ding, D.L., Martin, C.H., Mead, D.A.,
Mierendorf, R.C., Raghavan, K.V., Meyerowitz, E.M., and Lipshitz, H.D.
Phage lambda cDNA cloning vectors for subtractive hybridization,
fusion-protein synthesis and Cre-loxP automatic plasmid subcloning
Gene 88 (1), 25-36 (1990)
JOURNAL PUBMED 2140336
COMMENT Original source text: Cloning vector DNA.
FEATURES
source
1. .105
/organism="unidentified cloning vector"
/mol_type="genomic DNA"
/db_xref="taxon:45196"
/clone="PSHLX1"
ORIGIN
Query Match 0.7%; Score 28; DB 11; Length 105;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCGA 50
|||||

Db 15 CTATACGACTCACTATAGGAGCTCGA 42
RESULT 45
A91914
LOCUS A91914 3484 bp DNA linear PAT 22-JAN-2000
DEFINITION Sequence 1 from Patent WO9822599.
ACCESSION A91914
VERSION A91914.1 GI:6740781
KEYWORDS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE
Asteraceae; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 3484)
OHL, S.A. and Klapp, J.
NEMATODE-INDUCIBLE REGULATORY DNA SEQUENCES
Patent: WO 9822599-A 1 28-MAY-1998;
LEE FREDERIQUE MARIANNE V D (NL); OHL STEPHAN ANDREAS (NL)
JOURNAL
TITLE
FEATURES
source
1. .3484
/organism="Arabidopsis thaliana"
/mol_type="unassigned DNA"
/db_xref="taxon:3702"
/ecotype="C24"
CDS
<3481. .>3484
/note="unnamed protein product"
/codon_start=2
/protein_id="CA669451.1"
/db_xref="GI:6740782"
/translation="M"
ORIGIN
Query Match 0.7%; Score 28; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCGA 50
Db 698 CTATACGACTCACTATAGGAGCTCGA 725

RESULT 46
AR309120
LOCUS AR309120 3484 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 1 from patent US 6555529.
ACCESSION AR309120
VERSION AR309120.1 GI:31700962
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 3484)
Funaba, Y., Koike, J., Tanahashi, M., Okazaki, S. and Ito, M.
Remedies for intramedullary diseases
Patent: US 6555529-A 1 29-APR-2003;
Toray Industries, Inc.; Tokyo;
JPX;
JOURNAL
TITLE
FEATURES
source
1. .3484
/organism="unknown"
/mol_type="genomic DNA"
ORIGIN
Query Match 0.7%; Score 28; DB 6; Length 3484;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTATACGACTCACTATAGGAGCTCGA 50
Db 698 CTATACGACTCACTATAGGAGCTCGA 725

[illegible]

Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	23	CTATACGACTCACTATAGGAGCTCGA	50						
Db	698	CTATACGACTCACTATAGGAGCTCGA	725						
RESULT 49									
LOCUS	AL355005								
DEFINITION	Mouse DNA sequence from clone RP21-429M4 on chromosome X, complete sequence.								
ACCESSION	AL355005								
KEYWORDS	AL355005.3	GI:9797242							
ORGANISM	mus musculus (house mouse)								
REFERENCE	Mus musculus								
AUTHORS	Emkaryotis; Metazoa; Chordata; Craniata; Vertebrata; Euclelostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Mus.								
TITLE	1 (bases 1 to 140069)								
JOURNAL	Direct Submission								
COMMENT	Submitted (29-JUN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk Clone request: clonerequest@sanger.ac.uk On Aug 12, 2000 this sequence version replaced gi:7940000. During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em; EMBL; Sw; SWISSPROT; Tr; TrEMBL; Wp; WormPep; Information on the WormPep database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP21-429M4 is from the RPCI-21 Mouse PAC library constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm VECTOR: pPAC								
FEATURES									
Source									
	Location/Qualifiers								
	1..140069								
	/organism="Mus musculus"								
	/mol_type="genomic DNA"								
	/db_xref="taxon:10090"								
	/chromosome="X"								
	/clone="RP21-429M4"								
	/clone_1kb="RPCI-21"								
ORIGIN									
Query Match	0.7%;	Score 28;	DB 9;	Length 140069;					
Best Local Similarity	100.0%;	Prod. NO. 0.18;							
Matches	28;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
QY	84	GTGCTGCTGCTGCTTTAAGTCAATTA	111						
Db	74821	GTGCTGCTGCTGCTTTAAGTCAATTA	74848						

```

RESULT 50
BX530096
LOCUS BX530096
DEFINITION BX530096 183958 bp DNA linear HTG 03-JUL-2003
MUS musculus chromosome X clone RP23-476H16, WORKING DRAFT
SEQUENCE.
ACCESSION BX530096
VERSION BX530096.2 GI:32451242
KEYWORDS HTG, HTGS_PHASE2, HTGS_ACTIVEFIN, HTGS_DRAFT, HTGS_FULLTOP.
SOURCE MUS musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Murioidea; Muridae; Murinae; Mus.
1 (bases 1 to 183958)
REFERENCE
AUTHORS Chapman,J.
TITLE Direct Submision
JOURNAL Submitted (02-JUL-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk
humquerry@sanger.ac.uk
On Jul 3, 2003 this sequence version replaced gi:31335656.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BM476H16
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Chemistry: Dye-terminator; 100% of reads
Consensus quality: 183848 bases at least Q40
Consensus quality: 183908 bases at least Q30
Consensus quality: 183938 bases at least Q20
Insert size: 183958; sum-of-contigs
Insert size: 185334; 2.3% error; agarose-fp
Quality coverage: 9.32x in Q20 bases; sum-of-contigs Quality
coverage: 9.48x in Q20 bases; agarose-fp
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 1 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
* 1 183958: contig of 183958 bp in length.
Location/Qualifiers
1. 183958
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-476H16"
/clone_11b="RPCL-23"
1. 183958
/notes="assembly_fragment:01273"
ORIGIN
Query Match 0.7%; Score 28; DB 14; Length 183958;
Best Local Similarity 100.0%; Pred. No. 0.17;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
84 GGTGTGTGTGTGTTTAAGTCAATTA 111
DB 80990 GTGTGTGTGTGTGTTTAAGTCAATTA 81017

```

```

RESULT 51
AL732410/c 220894 bp DNA linear ROD 17-JAN-2003
LOCUS Mouse sequence from clone RP23-91L2 on chromosome X, complete
DEFINITION
AL732410
ACCESSION
AL732410
VERSION
AL732410.6 GI:27802745
KEYWORDS
HTG.
SOURCE
Mus musculus (house mouse)
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murineae; Mus.
1 (bases 1 to 220894)
Kay, M.
REFERENCE
Direct Submission
Submitted (17-JAN-2003) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
hunquerry@sanger.ac.uk
Clone request: clonerequest@sanger.ac.uk
On Jan 18, 2003 this sequence version replaced g1:2136719.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
-----
Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: hunquerry@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone or more than one M13 subclone; and the
assembly was confirmed by restriction digest, except on the rare
occasion of the clone being a YAC.
RP23-91L2 is from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see http://www.choi.org/bacpac/home.htm
VECTOR: pBAC3.6
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to confirm this sequence. Sequence data
from the whole genome shotgun alone has only been used where it has
a phred quality of at least 30.
Location/Qualifiers
1..220894
/organism="Mus musculus"
/mol_type="genomic DNA"
/db_xref="taxon:10090"
/chromosome="X"
/clone="RP23-91L2"
/clone_1bp="RPCI-23"
ORIGIN
Query Match 0.7%; Score 28; DB 9; Length 220894;
Best Local Similarity 100.0%; Pzid. No. 0.16;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
04 GTGTGTGTGTGTGTGTAAATTCATTA 111
DB 217776 GTGTGTGTGTGTGTGTAAATTCATTA 217749

```

RESULT 52
CS088900/c
LOCUS CS088900 374 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 34 from Patent EP1449849.
ACCESSION CS088900
VERSION CS088900.1 GI:66714222
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Light,D.R., Andrews,W.H., Clarke,J.H., Wydro,R.M. and Young,P.A.
TITLE Protease-resistant thrombomodulin analog
JOURNAL Patent: EP 1449849-A 34 25-AUG-2004;
Paton GmbH (DE)
FEATURES
source
Location/Qualifiers
1.374
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Clal-SmaI fragment from pTHR515 containing the 3aa deletion of the Nterminus of DNFL into the Clal-SmaI partial of pTHR512."

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAGCTCG 49
Db 147 CTAATACGACTCACTATAGGAGCTCG 121

RESULT 53
CS088904/c
LOCUS CS088904 374 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 38 from Patent EP1449849.
ACCESSION CS088904
VERSION CS088904.1 GI:66714226
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Light,D.R., Andrews,W.H., Clarke,J.H., Wydro,R.M. and Young,P.A.
TITLE Protease-resistant thrombomodulin analog
JOURNAL Patent: EP 1449849-A 38 25-AUG-2004;
Paton GmbH (DE)
FEATURES
source
Location/Qualifiers
1.374
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="NotI-XbaI fragment from pTHR498 containing the DNFL gene into the NotI-XbaI sites of pGEM92F-. This plasmid is designated 'A' in the strategy for construction of a Patent TM production plasmid."

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAGCTCG 49
Db 147 CTAATACGACTCACTATAGGAGCTCG 121

RESULT 54
CS088909/c
LOCUS CS088909 374 bp DNA linear PAT 25-MAY-2005
DEFINITION Sequence 43 from Patent EP1449849.

ACCESSION CS088909
VERSION CS088909.1 GI:66714231
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Light,D.R., Andrews,W.H., Clarke,J.H., Wydro,R.M. and Young,P.A.
TITLE Protease-resistant thrombomodulin analog
JOURNAL Patent: EP 1449849-A 43 25-AUG-2004;
Paton GmbH (DE)
FEATURES
source
Location/Qualifiers
1.374
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="MluI-NotI fragment from pTHR514 containing a 7aa deletion at the end of the link region of DNFL, the S474A, the R456G and the H457Q mutations into the MluI-NotI sites of pTHR518."

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 374;
Best Local Similarity 100.0%; Pred. No. 3.1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAATACGACTCACTATAGGAGCTCG 49
Db 147 CTAATACGACTCACTATAGGAGCTCG 121

RESULT 55
CVGEM92FM/c
LOCUS CVGEM92FM 2912 bp DNA circular SYN 06-FEB-2001
DEFINITION Cloning vector pGEM-92F(-).
ACCESSION X65312
VERSION X65312.2 GI:12711304
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1
AUTHORS Technical Services.
TITLE Direct Submission
JOURNAL Submitted (28-MAY-1993) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, WI 53711-5399, USA revised by [3]
REMARK 3 (bases 1 to 2912)
AUTHORS Technical Services.
TITLE Direct Submission
JOURNAL Submitted (05-FEB-2001) Technical Services, Promega Corporation, 2800 Woods Hollow Road, Madison, WI 53711-5399, USA
COMMENT On Feb 7, 2001 this sequence version replaced g1:58182. See X65300-X65335 for related vector sequences
This vector can be obtained from Promega Corporation, Madison, WI. Call one of the following numbers for order or technical information:
Order or Technical 800-356-9526
In Wisconsin 800-356-9526
Outside U.S. 608-274-4330.
FEATURES
source
Location/Qualifiers
1.2912
/organism="Cloning vector pGEM-92F(-)"
/mol_type="other DNA"
/db_xref="taxon:90118"

	misc_feature	1	/note="SP6 transcription initiation site"
	promoter	53..72	/note="T7 promoter"
	misc_feature	55	
	misc_feature	93..321	/note="T7 transcription initiation site"
	misc_feature	102..118	/note="lac operon sequence"
	gene	complement(104..106)	/note="PUC/M13 reverse primer binding site"
	misc_feature	complement(104..106)	/gene="lacZ"
	misc_feature	126..142	/gene="lacZ"
	gene	complement(1263..2123)	/note="lac operator"
	CDS	complement(1263..2123)	/gene="bla"
		/codon_start=1	
		/transl_table=11	
		/product="beta-lactamase"	
		/protein_id="CA46404.1"	
		/db_xref="GI:58183"	
		/translation="MSIQHFRVALIPEPAFCLPVAPETLVKVDALDQLGARVGY IELNDISKILDESFPVERPPMSTFKYLGGAVLSRIDAOEGRIHHYSONDLVEE YSPVTRKHLLTDGMFVRRLCSAITMSDNTANILLTTIGPKELTAFLAHMGDHVPPL DRMPRELNAEIPIPIRDEPTDTVMVAATTIRKLITSELTLSRSQILIIMEDADKAGTL LRSLDPGWMTIADKSAGERSRGITALGPDGPSRVIVITTGSAIDERNROIA ERISGLIKHM"	
ORIGIN	misc_feature	2255..2710	/note="phase fi region"
	misc_feature	2712..2868	
	misc_feature	/note="lac operon sequence"	
	misc_feature	2831..2847	
	misc_feature	/note="PUC/M13 reverse primer binding site"	
	misc_feature	2876..2887	
	promoter	/note="multiple cloning sites"	
		2896..2912	
		/note="SP6 promoter"	
Query Match		0.6%; Score 27; DB 11; Length 2912;	
Best Local Similarity		100.0%; Pred. No. 1.7;	
Matches	27; Conservative	0; Mismatches	0; Indels
		0; Gaps	0;
Dy	23 CTAATACGACTCCTATTAGGAGCTCG	49	
Dd	73 CTAATACGACTCCTATTAGGAGCTCG	47	
RESULT 56			
CVE311872	CVE311872	5824 bp	DNA circular SYN 09-JUL-2002
LOCUS	Cloning vector PHANNIBL.		
DEFINITION	AJ311872		
VERSION	AJ311872.1 GI:15982214		
KEYWORDS	AMP gene; ampicillin resistance protein; pdk gene; promoter.		
SOURCE	Cloning vector PHANNIBL		
ORGANISM	Cloning vector PHANNIBL		
REFERENCE	Other sequences; artificial sequences; vectors.		
AUTHORS	1 Wesley,V.S., Helliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q., Gooding,P.B., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P., Glave,A.P., Green,A.G. and Waterhouse,P.M. Construct design for efficient, effective and high-throughput gene silencing in plants Plant J. 27 (6), 581-590 (2001)		
JOURNAL	PUBMED	11576441	
REFERENCE	2 (bases 1 to 5824)		
AUTHORS	Waterhouse,P.M.		

FEATURES	source	1..5824
TITLE	Direct Submission	
JOURNAL	Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry, C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA	
source	location/Qualifiers	
source	1..5824	
source	/organism="Cloning vector PHANNIBAL"	
source	/mol_type="other DNA"	
source	/db_xref="taxon:167047"	
source	/lab_host="Escherichia coli"	
source	/focus	
source	/note="PHANNIBAL is a derivative of cloning vector PART7 which was a derivative of pGEM-9Zt(-)"	
source	1..2864	
source	/organism="Escherichia coli K12"	
source	/mol_type="other DNA"	
source	/strain="K12"	
source	/db_xref="taxon:83333"	
source	2865..4210	
source	/organism="Cauliflower mosaic virus"	
source	/mol_type="other DNA"	
source	/db_xref="taxon:10641"	
source	4254..4995	
source	/organism="Flaveria trinervia"	
source	/mol_type="other DNA"	
source	/db_xref="taxon:4227"	
source	5049..5814	
source	/organism="Agrobacterium tumefaciens"	
source	/mol_type="other DNA"	
source	/db_xref="taxon:358"	
source	775..1635	
source	/gene="amp"	
source	775..1635	
source	/gene="amp"	
source	/codon_start=1	
source	/transl_table=11	
source	/product="ampicillin resistance protein"	
source	/protein_id="CAC86250.1"	
source	/db_xref="GI:15982215"	
source	/translation="MSIQPRVALIPFAAFLPEPAHPETLVKVDADPOLGARVGY	
source	IELDLSGKILSPREPRPPMSTFVLICAVLSRIDAGOEQGRIRHYSDNLVBE	
source	YSPTEKHLIDGMYRELCSAITSNTLANLLITIGPKETATLHNMGDVYTL	
source	DRSPTELEATPDERDITPMVAATLTLLTELLTLASROQLIDMWEADKVGSL	
source	LRSLPAGWFIADKSGAGERSGRIIALPDGKPSRIVIYTTGSQATDERNRQIAL	
source	ELGSLIKHM"	
source	2865..4210	
source	/function="35S promoter"	
source	4254..4995	
source	/gene="pdk"	
source	4254..4995	
source	/gene="pdk"	
source	/note="from pyruvate orthophosphate dikinase (pdk)"	
source	/number=2	
source	5049..5814	
source	/note="octopline esynthase (ocs) terminator"	
ORIGIN		
Query Match	0.64; Score 27; DB 11; Length 5824;	
Best Local Similarity	100.0%; Pred. No. 1.3;	
Matches	27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OR		
23	CTAATACGACTCATTATGAGAGCTCG 49	
DB	2826 CTAATACGACTCATTATGAGAGCTCG 2852	
RESULT 57		
CVE311873	6063 bp	DNA
LOCUS	DEFINITION	cloning vector PHANNIBAL.
VERSION	Accession	AFJ11873.1 GI:15982216
KEYWORDS	can gene; kanamycin resistance protein; pdk gene; promoter.	
SOURCE	Cloning vector PHANNIBAL	

ORGANISM Cloning vector pKANNBAL
other sequences; artificial sequences; vectors.
REFERENCE 1 Wesley,V.S., Halliwell,C., Smith,N.A., Wang,M.B., Rouse,D., Liu,Q.,
AUTHORS Gooding,P., Singh,S.R., Abbott,D., Stoutjesdijk,A., Robinson,S.P.,
Gleave,A.P., Green,A.G. and Waterhouse,P.M.
TITLE Construct design for efficient, effective and high-throughput gene
silencing in plants
JOURNAL Plant J. 27 (6), 581-590 (2001)
PUBMED 11576441
REFERENCE 2 (bases 1 to 6063)
AUTHORS Waterhouse,P.M.
TITLE Direct Submission
JOURNAL Submitted (04-MAY-2001) Waterhouse P.M., Plant Industry,
C.S.I.R.O., P.O. Box 1600, Canberra, ACT 2601, AUSTRALIA
FEATURES
source
1. .6063
Location/Qualifiers
/organism="Cloning vector pKANNBAL"
/mol_type="other DNA"
/db_xref="taxon:167048"
/lab_host="Escherichia coli"
/focus
/note="pKANNBAL is a derivative of cloning vector pART7
which was a derivative of pGEM-9ZF(-)"
1. .3103
/organism="Escherichia coli K12"
/mol_type="other DNA"
/strain="K12"
/db_xref="taxon:83333"
3104. .4449
/organism="Cauliflower mosaic virus"
/mol_type="other DNA"
/db_xref="taxon:10641"
4493. .5234
/organism="Flaveria trinervia"
/mol_type="other DNA"
/db_xref="taxon:4227"
5288. .6053
/organism="Agrobacterium tumefaciens"
/mol_type="other DNA"
/db_xref="taxon:358"
1075. .1869
/gene="kan"
1075. .1869
/gene="kan"
/gene="kan"
/codon_start=1
/transl_table=11
/product="kanamycin resistance protein"
/protein_id="CAC86251.1"
/db_xref="GI:15982217"
/translation="MAKMRISPLKLIIEKRYCKOTEGNSPAKYVKLVGENNYLIK
MTDSRYKGTIVDERKMMLEGLPVKVIHFERHDSWMLNSEADGVLCSEBY
EDQSPDKETIELVAECTRLPHSIDSCPTNSLDLSRLADYLLNNDLADVCEBWE
EDPFPDPRLELYDLKTEKPEBELVPSHGIDGDSNIFVKDGYSGFDLGRSGRADKM
YDIAPCVRSIRREIIGEEQVYELFPDILGIXPDWEKIKYVILDELFP"
3104. .4449
/function="35S promoter"
4493. .5234
/gene="pdk"
4493. .5234
/gene="pdk"
/note="from pyruvate orthophosphate dikinase (pdk)"
/number=2
5288. .6053
/note="octopline esynthase (oce) terminator"
ORIGIN
Query Match 0.6%; Score 27, DB 11, Length 6063;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
23 CTATACGACTCACTATAGGAGCTCG 49
|||||

Db 3065 CTATACGACTCACTATAGGAGCTCG 3091
RESULT 58
BD263403/c 7038 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
ACCESSION BD263403
VERSION BD263403.1 GI:33073171
KEYWORDS JP 2002537790-A/181.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 7038)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 181 12-NOV-2002;
INVITROGEN CORP
COMMENT
OS Artificial Sequence
PN JP 2002537790-A/181
PD 12-NOV-2002
PF 02-MAR-2000 JP 2000602252
PR 02-MAR-1999 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC
C12N15/09,C07K14/00,C12N1/15,C12N1/19,C12N1/21,C12N5/10,C12N15/PC
00,C12N5/00
CC pMAB85
FH Key
FT source
Location/Qualifiers
1. .7038
/organism="Artificial Sequence".
FEATURES
source
1. .7038
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"
ORIGIN
Query Match 0.6%; Score 27, DB 6, Length 7038;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
24 TAATACGACTCACTATAGGAGCTCGA 50
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Db 6005 TAATACGACTCACTATAGGAGCTCGA 5979
RESULT 59
BD263400/c 8815 bp DNA linear PAT 17-JUL-2003
LOCUS
DEFINITION
ACCESSION BD263400
VERSION BD263400.1 GI:33073168
KEYWORDS JP 2002537790-A/178.
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 8815)
AUTHORS Hartley,J.L., Brasch,M.A., Temple,G.F. and Cheo,D.
TITLE Compositions and methods for use in recombinational cloning of
nucleic acids
JOURNAL Patent: JP 2002537790-A 178 12-NOV-2002;
INVITROGEN CORP
COMMENT
OS Artificial Sequence
PN JP 2002537790-A/178
PD 12-NOV-2002 JP 2000602252
PF 02-MAR-2000 US 60/122389,23-MAR-1999 US 60/126049 PR
28-MAY-1999 US 60/136744
PI JAMES L HARTLEY,MICHAEL A BRASCH,GARY F TEMPLE,DAVID CHEO PC

C12N15/09, C07K14/00, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N15/ PC
00, C12N5/00
CC pDEST33
FH Key Location/Qualifiers
FT source 1. 8815
FT /organism='Artificial Sequence',
1. 8815
Location/Qualifiers
/organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

ORIGIN
Query Match 0.6%; Score 27; DB 6; Length 8815;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TAAATACGACTCATTATAGGAGCTCGA 50
|||||
Db 7782 TAAATACGACTCATTATAGGAGCTCGA 7756
|||||

RESULT 60
LOCUS AY189825 14271 bp DNA circular SYN 09-APR-2003
DEFINITION His-3 Integration vector pKYM026, complete sequence.
ACCESSION AY189825
VERSION AY189825.1 GI:28435535
KEYWORDS his-3 integration vector pKYM026
SOURCE his-3 integration vector pKYM026
ORGANISM his-3 integration vector pKYM026
REFERENCE 1 (bases 1 to 14271)
AUTHORS Lee, D.W., Haag, J.R. and Aramayo, R.
TITLE Construction of strains for rapid homokaryon purification after
integration of constructs at the histidine-3 (his-3) locus of
Neurospora crassa
JOURNAL Curr. Genet. 43 (1), 17-23 (2003)
PUBMED 12684841
REFERENCE 2 (bases 1 to 14271)
AUTHORS Lee, D.W., Haag, J.R. and Aramayo, R.
TITLE Direct Submission
JOURNAL Submitted (03-DEC-2002) Biology, Texas A&M University, BSBW 415,
College Station, TX 77843-3258, USA
Location/Qualifiers
1. 14271
/organism="his-3 integration vector pKYM026"
/mol_type="genomic DNA"
/db_xref="taxon:220723"
/focus
2584. 5465
/organism="Cloning vector pGEM-9ZE (-)"
/mol_type="genomic DNA"
/db_xref="taxon:90118"
complement(1.. 2583)
/note="benzomyl resistant marker"
5466. 14271
/note="his-3 HindIII fragment"
10661..10713
/note="multi-cloning sites"

ORIGIN
Query Match 0.6%; Score 27; DB 11; Length 14271;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTAATACGACTCATTATAGGAGCTCG 49
|||||
Db 2609 CTAATACGACTCATTATAGGAGCTCG 2583
|||||

RESULT 61
AC157620/c

LOCUS AC157620 155363 bp DNA linear HTG 15-MAR-2005
DEFINITION Papio anubis clone Rp41-436B14, WORKING DRAFT SEQUENCE, 9 ordered
pieces.
ACCESSION AC157620
VERSION AC157620.2 GI:61179916
KEYWORDS HTG; HTGS PHASE2; HTGS DRAFT.
SOURCE Papio anubis (olive baboon)
ORGANISM Papio anubis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Cercopithecoidea; Cercopithecinae; Papio.
1 (bases 1 to 155363)
REFERENCE 1
AUTHORS Antonellis, A., Ayele, K., Benjamin, B., Blakesley, R.W., Boake, A.,
Bouffard, G.G., Brinkley, C., Brooks, S., Chu, G., Coleman, H.,
Engle, J., Geisiole, M., Guan, X., Gupta, J., Haghighi, P., Han, J.,
Hansen, N., Ho, S.-L., Hu, P., Hunter, G., Hurle, B., Idol, J.R.,
Kwong, P., Latic, P., Larson, S., Lee-Jin, S.-O., Legaspi, R.,
Madden, M., Maduro, Q.L., Maduro, V.B., Margulies, E.H., Mastello, C.,
Meekeri, B., McDowell, J., Mojidi, H.A., Mullikin, J.C.,
Oestreicher, J.S., Park, M., Portnoy, M.E., Prasad, A., Puri, O.,
Reddy-Dugue, N., Roese, B., Schandler, K., Schuler, M.G., Sison, C.,
Stantrop, S., Stephen, E., Teye, A., Thomas, J.W., Thomas, P.J.,
Tsipouri, V., Ung, L., Vogt, J.L., Wetherby, K.D., Young, A. and
Green, E.D.
NISC Comparative Sequencing Initiative
Unpublished
2 (bases 1 to 155363)
REFERENCE 2
AUTHORS Green, E.D.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
3 (bases 1 to 155363)
REFERENCE 3
AUTHORS Green, E.D.
TITLE Direct Submission
JOURNAL Submitted (15-MAR-2005) NIH Intramural Sequencing Center, 5625
Fishers Lane, Rockville, MD 20852, USA
On Mar 15, 2005 this sequence version replaced gi:60223183.
COMMENT
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc.zoo@bgr.nih.gov
----- Project Information
Center project name: Kic
Center clone name: 436B14

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is generally based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 153372 bases at least Q40
Consensus quality: 154068 bases at least Q30
Consensus quality: 154387 bases at least Q20
Insert size: 163000; agarose-fp
Insert size: 154563; sum-of-contigs
Quality coverage: 7.59x in Q20 bases; agarose-fp
Quality coverage: 8.00x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

*	1	33922: contig of 33922 bp in length
*	33923	34022: gap of unknown length
*	34023	42723: contig of 8701 bp in length
*	42724	42823: gap of unknown length
*	42824	67972: contig of 25149 bp in length
*	67973	68072: gap of unknown length
*	68073	115800: contig of 47728 bp in length
*	115801	115900: gap of unknown length
*	115801	121755: contig of 5855 bp in length
*	121756	121855: gap of unknown length
*	121856	123794: contig of 1939 bp in length
*	123795	123894: gap of unknown length
*	123895	143354: contig of 19460 bp in length
*	143355	143454: gap of unknown length
*	143455	152511: contig of 9057 bp in length
*	152512	152611: gap of unknown length
*	152612	155393: contig of 2752 bp in length.

source	Location/Qualifiers
misc_feature	1..155363 /organism="Papio anubis" /mol_type="genomic DNA" /db_xref="taxon:9555" /clone="RP41-436B14" /clone_11b="RP41" /note="BAC resource: http://bacpac.chori.org/ "
misc_feature	1..48923 /note="clone overlaps with Genbank Accession Number AC150628 clone RP41-38K18 (center project name hbu)"
misc_feature	1..33922 /note="assembly_fragment clone_end:17 vector_side:left"
gap	33923..34022 /estimated_length=unknown
misc_feature	34023..42723 /note="assembly_fragment"
gap	42724..42823 /estimated_length=unknown
misc_feature	42824..67972 /note="assembly_fragment"
gap	67973..68072 /estimated_length=unknown
misc_feature	68073..115800 /note="assembly_fragment"
misc_feature	103272..155363 /note="clone overlaps with Genbank Accession Number AC149446 clone RP41-168H19 (center project name hbc)"
gap	115801..115900 /estimated_length=unknown
misc_feature	115901..121755 /note="assembly_fragment"
gap	121756..121855 /estimated_length=unknown
misc_feature	121856..123794 /note="assembly_fragment"
gap	123795..123894 /estimated_length=unknown
misc_feature	123895..143354 /note="assembly_fragment"
gap	143355..143454 /estimated_length=unknown
misc_feature	143455..152511 /note="assembly_fragment"
gap	152512..152611 /estimated_length=unknown
misc_feature	152612..155363 /note="assembly_fragment"

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clone_end:SP6
vector_side:right"
ORIGIN
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Query Match	0.6%	Score 27	DB 14	length 155363
Best Local Similarity	100.0%	Pred. No. 0.48		
Matches 27	Conservative 0	Mismatches 0	Indels 0	Gaps 0

Qy	3910	AAAAATAAAAATAAAAATAAAGTAAAG	3936
Db	74820	AAAAATAAAAATAAAAATAAAGTAAAG	74794

RESULT 62
AC139294

SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus

REFERENCE	AUTHORS
1 (bases 1 to 183363)	Kruchowski, S., Haglund, K., Meyer, R. and Haakenson, W

COMMENT On Nov 1, 2004 this sequence version replaced gi:47605114.

NOTICE:

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality > 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For

additional information about the map position of this sequence, see <http://genome.wustl.edu>

SOURCE INFORMATION:
The RPCI-24 BAC library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

Location/Qualifiers

1. 183363

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="14"

/map="14"

/clone="RP24-239E14"

/clone_lib="RPCI-24"

90991..91258

/note="Sequence derived from one plasmid subclone."

96920..96921

/transposon="Bacterial transposon insertion in clone
excluded here."

ORIGIN

Query Match 0.6%; Score 27; DB 9; Length 183363;

Best Local Similarity 100.0%; Pred. No. 0.46;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3913 AATTAATAATTAATAATTAAGTAAAGAAA 3939

Db 53286 AATTAATAATTAATAATTAAGTAAAGAAA 53312

```

RESULT 63
AC151836      AC151836      230502 bp      DNA      linear      ROD 20-JUL-2005
LOCUS         Mus musculus BAC clone RP23-359Fs from chromosome 14, complete
DEFINITION   sequence.
ACCESSION    AC151836
VERSION      AC151836.3  GI:71037561
KEYWORDS     HTG.
SOURCE       Mus musculus (house mouse)
ORGANISM     Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 230502)
Velzer, J., Lewis, S., Kozlowski, A., Bielicki, L. and Haglund, K.
The sequence of Mus musculus BAC clone RP23-359Fs
2 (bases 1 to 230502)
Unpublished (2001)
Wilson, R.K.
Direct Submission
Submitted (06-OCT-2004) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
3 (bases 1 to 230502)
Wilson, R.K.
Direct Submission
Submitted (13-MAR-2005) Genome Sequencing Center, 4444 Forest Park
Parkway, St. Louis, MO 63108, USA
4 (bases 1 to 230502)
Wilson, R.K.
Direct Submission
Submitted (20-JUL-2005) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Jul 20, 2005 this sequence version replaced gi:61098484.
-----
Center: Washington University Genome Sequencing Center
Center code: WUGSC

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Web site: <http://genome.wustl.edu>
Contact: submissions@wustl.edu
----- Summary Statistics
Center project name: M_BA0359F05

NOTICE:

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e. phred quality
>30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one plasmid subclone, fosmid clone or direct clone walk sequence.
Sequence from the Mouse Genome Sequencing Consortium whole genome
shotgun may have been used to obtain the consensus sequence. The
assembly was confirmed by restriction digest.
This finishing standard has slightly changed from the previous
human standard. Specifically, standards for regions of low sequence
complexity (such as dinucleotide repeats and small unit tandem
repeats) have been relaxed. These regions are very prevalent in the
mouse genome, and the return on extended finishing efforts is
minimal.

If a sequence meets the criteria of the above statement, it needs
no comments or tags. If the criteria are not met, such as ambiguous
bases, then the region is duly annotated.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Wes Warren,
Department of Genetics, Washington University, St. Louis MO. For
additional information about the map position of this sequence, see
<http://genome.wustl.edu>

SOURCE INFORMATION:

The BAC library has been constructed by Kazutoyo Oeegawa and
Minako Tateo in the laboratory of Pieter de Jong
(<http://www.chori.org>) from female C57BL/6J mouse kidney and/or
brain genomic DNA. The clone and detailed information can be
obtained from Research Genetics, Inc. (<http://www.resgen.com>) or
Pieter de Jong and coworkers at <http://www.chori.org>

This sequence is the entire insert of the clone.

Location/Qualifiers

1. 230502

/organism="Mus musculus"

/mol_type="genomic DNA"

/db_xref="taxon:10090"

/chromosome="14"

/clone="RP23-359Fs"

/clone_lib="RPCI-23"

48876..49550

/note="Unresolved tandem repeat."

102204..102242

/note="Sequence derived from PCR product of project DNA"

102747..102809

/note="Unresolved tandem repeat."

ORIGIN

Query Match 0.6%; Score 27; DB 9; Length 230502;

Best Local Similarity 100.0%; Pred. No. 0.42;

Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3913 AATTAATAATTAATAATTAAGTAAAGAAA 3939

Db 170689 AATTAATAATTAATAATTAAGTAAAGAAA 170715

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RESULT 64
BD272600      BD272600      38 bp      DNA      linear      PAT 17-JUL-2003
LOCUS         Amplification of CYP24 and uses thereof.
DEFINITION   BD272600
ACCESSION    BD272600
VERSION      BD272600.1  GI:33082368

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KEYWORDS JP 2002540798-A/6.
SOURCE synthetic construct
ORGANISM other sequences; artificial sequences.
REFERENCE 1 (bases 1 to 38)
AUTHORS Albertson,D.G., Pinkel,D., Collins,C., Gray,J.W. and Yestra,B.
TITLE Amplification of CYP24 and uses thereof
JOURNAL Patent: JP 2002540798-A 6 03-DEC-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT OS Artificial Sequence
PN JP 2002540798-A/6
PD 03-DEC-2002
PR 06-MAR-2000 JP 200609598
PI 02-APR-1999 US 09/285292
PI DONNA G ALBERTSON,DANIEL PINKEL, COLIN COLLINS,JOE W GRAY,BAUKE
PT YSTRPA
PC
C12N15/09,A61K31/59,A61K31/7105,A61K31/711,A61K38/00,A61K45/00, PC
A61K48/00,
PC A61P35/00,A61P35/04,C12Q1/02,C12Q1/26,C12Q1/68,G01N33/15, PC
G01N33/50,
PC G01N33/53,G01N33/566,G01N33/573,G01N33/574,C12N15/00,A61K37/02
CC Description of Artificial Sequence:ZNF217 reverse PCR primer
FH Key Location/Qualifiers
FT source 1..38
FT /organism='Artificial Sequence'.
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1..38
/organism="synthetic construct"
/mol_type="genomic DNA"
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Best Local Similarity 100.0%; Pred.No.18;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 24 TAATACGACTCACTATAGGAGCTCG 49
DB 1 TAATACGACTCACTATAGGAGCTCG 26
RESULT 65
AX020362 40 bp DNA linear PAT 07-SEP-2000
LOCUS AX020362
DEFINITION Sequence 2 from Patent WO9936517.
ACCESSION AX020362
VERSION AX020362.1 GI:10044095
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Jemne,A.
TITLE Method for selecting ribozymes which are capable of covalently
JOURNAL modifying the ribonucleic acids on 2'-oh-groups in trans
JENNE ANDREAS (DE)
FEATURES
source
1..40
location/Qualifiers
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Oligonucleotid"
ORIGIN
Query Match 0.6%; Score 26; DB 6; Length 40;
Best Local Similarity 100.0%; Pred.No.17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTAATACGACTCACTATAGGAGCTC 48
DB 1 CTAATACGACTCACTATAGGAGCTC 48

DB 2 CTAATACGACTCACTATAGGAGCTC 27
RESULT 66
CS122533 43 bp DNA linear PAT 16-JUL-2005
LOCUS CS122533
DEFINITION Sequence 216 from Patent WO2005056802.
ACCESSION CS122533
VERSION CS122533.1 GI:70911323
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS Glover,D.
TITLE Materials and methods relating to cell cycle control
JOURNAL Patent: WO 2005056802-A 216 23-JUN-2005;
Cancer Research Technology Limited (GB)
FEATURES
source
1..43
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="Primer"
ORIGIN
Query Match 0.6%; Score 26; DB 6; Length 43;
Best Local Similarity 100.0%; Pred.No.17;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 CTAATACGACTCACTATAGGAGCTC 48
DB 5 CTAATACGACTCACTATAGGAGCTC 30
RESULT 67
AY720436 4151 bp DNA circular SYN 18-SEP-2004
LOCUS AY720436
DEFINITION Plant expression vector pPESiTa, complete sequence.
ACCESSION AY720436
VERSION AY720436.1 GI:51989440
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1
AUTHORS
TITLE
JOURNAL
Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
FEATURES
source
1..4151
/organism="Plant expression vector pPESiTa"
/mol_type="Other DNA"
/db_xref="taxon:292601"
1..18
/note="Tch1111, NotI, XhoI, KpnI, MCS promoter"
19..758
/note="duplicated 35S CamV (cabb B-VI isolate); 35S;
overexpression in plants"
759..793
/note="HindIII, NcoI, SmaI, XbaI, BglII, MCS upstream"
794..805
/note="N-term strep-tag II"
806..994
/note="PIV2 optimized; prevents detection of epitope tag
in bacteria"
995..1009
/note="C-term strep-tag II"
1010..1035
/note="SalI, BamHI, PstI, EcoRI; MCS downstream"
1036..1288
/note="polyadenylation signal from nopaline synthase gene

of the Agrobacterium Ti plasmid; NOS terminator"
1289. .1358
/note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
misc_feature
complement(1359. .1587)
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/gene="bla"
/note="resistance to ampicillin"
/codon_start=1
/product="beta-lactamase"
/protein_id="AAU21235.1"
/db_xref="GI:51969441"
/translation="MSIQHFRVALIPFPAACLPVFAHPETLVVKQADQLGARVGY
IEDLNSGKILDSRPERPFPMSDFYLLCGAVLSRIDAGQDQLGRRIHYSQNDLVE
YSPVTEKHLDGMTVRELCSAATMSDNTANLLLTIGSKRELTAFLHMGDVTPL
DRWEPELNEAIIPNDERDTPVAAATTLRLKLTGELLTLASRQQLIDMEADKVAGPL
LRSLAPGAWFIADSGAGERSRGIINALGPDGKPSRIIVITYTTSQATYDERNRQIA
EIGASLTIKHW"

Query Match 0.6%; Score 26; DB 11; Length 4151;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTAGGAGCTCG 49
Db 1338 TAATACGACTCATTAGGAGCTCG 1313

RESULT 68
AY720435/c 4152 bp DNA circular SYN 18-SEP-2004
LOCUS Plant expression vector pPES1Tb, complete sequence.
DEFINITION
ACCESSION AY720435
VERSION AY720435.1 GI:51969438
KEYWORDS
SOURCE Plant expression vector pPES1Tb
ORGANISM Plant expression vector pPES1Tb
REFERENCE
AUTHORS other sequences; artificial sequences; vectors.
TITL 1 (bases 1 to 4152)
JOURNAL Direct Submission
PUBMED Berendzen,K.W., Breuer,F., Oberbachall,A., Schell,J. and Koncz,C.
10886775 Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
JOURNML Location/Qualifiers
FEATURES
source
1. .4152
/organism="Plant expression vector pPES1Tb"
/mol_type="other DNA"
/db_xref="taxon:292600"
misc_feature
1. .18
/note="Tth111I, NotI, XhoI, KpnI; MCS promoter"
promoter
19. .758
/note="duplicated 35S CamV (Cabb B-J1 isolate); 35S;
overexpression in plants"
misc_feature
759. .793
/note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
misc_feature
794. .805
/note="N-term strep-tag II"
intron
806. .994
/note="PIV2 optimized; prevents detection of epitope tag
in bacteria"
misc_feature
995. .1009
/note="C-term strep-tag II"
misc_feature
1011. .1036
/note="Sall, BamHI, PstI, EcoRI; MCS downstream"
terminator
1037. .1289
/note="polyadenylation signal from nopaline synthase gene
of the Agrobacterium Ti plasmid; NOS terminator"
misc_feature
1290. .1359
/note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
complement(1360. .1588)

/note="LacI"
gene
complement(2530. .3390)
/gene="bla"
CDS
complement(2530. .3390)
/gene="bla"
/note="resistance to ampicillin"
/codon_start=1
/product="beta-lactamase"
/protein_id="AAU21234.1"
/db_xref="GI:51969439"
/translation="MSIQHFRVALIPFPAACLPVFAHPETLVVKQADQLGARVGY
IEDLNSGKILDSRPERPFPMSDFYLLCGAVLSRIDAGQDQLGRRIHYSQNDLVE
YSPVTEKHLDGMTVRELCSAATMSDNTANLLLTIGSKRELTAFLHMGDVTPL
DRWEPELNEAIIPNDERDTPVAAATTLRLKLTGELLTLASRQQLIDMEADKVAGPL
LRSLAPGAWFIADSGAGERSRGIINALGPDGKPSRIIVITYTTSQATYDERNRQIA
EIGASLTIKHW"

Query Match 0.6%; Score 26; DB 11; Length 4152;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCATTAGGAGCTCG 49
Db 1339 TAATACGACTCATTAGGAGCTCG 1314

RESULT 69
AY720438/c 4152 bp DNA circular SYN 18-SEP-2004
LOCUS Plant expression vector pMENCHU, complete sequence.
DEFINITION
ACCESSION AY720438
VERSION AY720438.1 GI:51969444
KEYWORDS
SOURCE Plant expression vector pMENCHU
ORGANISM Plant expression vector pMENCHU
REFERENCE
AUTHORS other sequences; artificial sequences; vectors.
TITL 1 (bases 1 to 4152)
JOURNAL Ferrando,A., Farrae,R., Jasik,J., Schell,J. and Koncz,C.
10886775 Intron-tagged epitope: a tool for facile detection and purification
of proteins expressed in Agrobacterium-transformed plant cells
Plant J. 22 (6), 553-560 (2000)
PUBMED
2 (bases 1 to 4152)
REFERENCE Berendzen,K.W. and Koncz,C.
10886775 Direct Submission
JOURNML Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
JOURNML Location/Qualifiers
FEATURES
source
1. .4152
/organism="Plant expression vector pMENCHU"
/mol_type="other DNA"
/db_xref="taxon:292603"
misc_feature
1. .18
/note="Tth111I, NotI, XhoI, KpnI; MCS promoter"
promoter
19. .758
/note="duplicated 35S CamV (Cabb B-J1 isolate); 35S;
overexpression in plants"
misc_feature
759. .793
/note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
misc_feature
794. .805
/note="N-term HA epitope"
intron
806. .994
/note="PIV2 optimized; prevents detection of epitope tag
in bacteria"
misc_feature
995. .1009
/note="C-term HA epitope"
misc_feature
1010. .1036
/note="Sall, BamHI, PstI, EcoRI; MCS downstream"
terminator
1037. .1289
/note="polyadenylation signal from nopaline synthase gene
of the Agrobacterium Ti plasmid; NOS terminator"
misc_feature
1290. .1359

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misc_feature      /note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
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gene              /note="LacI"
                  complement(2530..3390)
                  /gene="ampR"
                  complement(2530..3390)
CDS              /gene="ampR"
                  /note="resistance to ampicillin"
                  /codon_start=1
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                  /protein_id="AAU21237.1"
                  /db_xref="GI:51989445"
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                  IEDLNSGKILSPFPRPEPPKPMSTFKVILCGAVLSRIDGQGLRRIHYSQNDLVE
                  YSPVTEKHLLDGTAVRELCSAALTMSDNTAANLLTTIGSPKSLTAPLHMGGVYTRL
                  DRWEPELNEALIPNDERDTTPVMAATLRLTGLLETLASRQQLIDMMEADYVAGPL
                  LRSALPAGWFIADKSGAGERSGRIIALALGPDGKPSRIIVITYTTSQATWDERNRQIA
                  EIGASLIKHM"

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Query Match      0.6%; Score 26; DB 11; Length 4152;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy              24 TAATAGACTCCTATAGGAGCTCG 49
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Db              1339 TAATAGACTCCTATAGGAGCTCG 1314

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RESULT 70
LOCUS            AY720433            4153 bp      DNA      circular SYN 18-SEP-2004
DEFINITION      Plant expression vector pPILY, complete sequence.
ACCESSION        AY720433
VERSION          AY720433.1 GI:51989434
KEYWORDS
SOURCE           .
ORGANISM         Plant expression vector pPILY
                 plant expression vector pPILY
                 other sequences; artificial sequences; vectors.
REFERENCE        1 (bases 1 to 4153)
AUTHORS          Ferrando,A., Fairrae,R., Jasik,J., Scheil,J. and Koncz,C.
TITLE            Intron-tagged epitope: a tool for facile detection and purification
                 of proteins expressed in Agrobacterium-transformed plant cells
JOURNAL          Plant J. 22 (6), 553-560 (2000)
PUBMED           10865775
REFERENCE        2 (bases 1 to 4153)
AUTHORS          Berendzen,K.W. and Koncz,C.
TITLE            Direct Submision
JOURNAL          Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
                 Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany

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FEATURES
source           1..4153
                 /organism="Plant expression vector pPILY"
                 /mol_type="other DNA"
                 /db_xref="taxon:292598"
misc_feature      1..18
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promoter         19..758
                 /note="duplicated 35S CamV (Cabb B-VI isolate); 35S;
                 overexpression in plants"
misc_feature      759..793
                 /note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
misc_feature      794..805
                 /note="N-term HA epitope"
intron           806..994
                 /note="PIV2 optimized; prevents detection of epitope tag
                 in bacteria"
misc_feature      995..1009
                 /note="C-term HA epitope"
misc_feature      1010..1037
                 /note="Sali, BamHI, PstI, EcoRI; MCS downstream"
terminator       1038..1290
                 /note="polyadenylation signal from nopaline synthase gene

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misc_feature      1291..1360
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                  complement(1361..1589)
misc_feature      complement(1361..1589)
gene              /note="LacI"
                  complement(2531..3391)
                  /gene="ampR"
                  complement(2531..3391)
CDS              /gene="ampR"
                  /note="resistance to ampicillin"
                  /codon_start=1
                  /product="beta-lactamase"
                  /protein_id="AAU21232.1"
                  /db_xref="GI:51989435"
                  /translation="MSIOHPRVALIPFPAAFCLPVFAHPETLVKVKDAEDQLGARVY
                  IEDLNSGKILSPFPRPEPPKPMSTFKVILCGAVLSRIDAGQGLRRIHYSQNDLVE
                  YSPVTEKHLLDGTAVRELCSAALTMSDNTAANLLTTIGSPKSLTAPLHMGGVYTRL
                  DRWEPELNEALIPNDERDTTPVMAATLRLTGLLETLASRQQLIDMMEADYVAGPL
                  LRSALPAGWFIADKSGAGERSGRIIALALGPDGKPSRIIVITYTTSQATWDERNRQIA
                  EIGASLIKHM"

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Query Match      0.6%; Score 26; DB 11; Length 4153;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy              24 TAATAGACTCCTATAGGAGCTCG 49
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Db              1340 TAATAGACTCCTATAGGAGCTCG 1315

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RESULT 71
LOCUS            AY720434            4153 bp      DNA      circular SYN 18-SEP-2004
DEFINITION      Plant expression vector pPESITc, complete sequence.
ACCESSION        AY720434
VERSION          AY720434.1 GI:51989436
KEYWORDS
SOURCE           .
ORGANISM         Plant expression vector pPESITc
                 plant expression vector pPESITc
                 other sequences; artificial sequences; vectors.
REFERENCE        1 (bases 1 to 4153)
AUTHORS          Berendzen,K.W., Breuer,F., Oberbachl,A., Scheil,J. and Koncz,C.
TITLE            Direct Submision
JOURNAL          Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
                 Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany

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FEATURES
source           1..4153
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misc_feature      1..18
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promoter         19..758
                 /note="duplicated 35S CamV (Cabb B-VI isolate); 35S;
                 overexpression in plants"
misc_feature      759..793
                 /note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
misc_feature      794..805
                 /note="N-term strep-tag II"
intron           806..994
                 /note="PIV2 optimized; prevents detection of epitope tag
                 in bacteria"
misc_feature      995..1009
                 /note="C-term strep-tag II"
misc_feature      1012..1037
                 /note="Sali, BamHI, PstI, EcoRI; MCS downstream"
terminator       1038..1290
                 /note="polyadenylation signal from nopaline synthase gene
                 of the Agrobacterium Ti plasmid; NOS terminator"
misc_feature      1291..1360
                 /note="KpnI, SacI, NotI, SacI, T7, SfiI; MCS terminator"
misc_feature      complement(1361..1589)

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gene      /note="lact"
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CDS       /gene="bla"
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           YSPVTEKHLLTDGMTVRELCSAATMSDNTANLLITIGPKELTAPLHNGDVYTRL
           DRWPEPELNEAIPNDERDTPMPVAMATLRKLTLGELLTASRQQLIDWMEADKVGAPL
           LRSLAPGWEPIDAKSGAGERSGRTIAALGPDGKPRIVIVITGSOATWDERRQRLA
           EIGASLIKHM"

ORIGIN
Query Match      0.6%; Score 26; DB 11; Length 4153;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      24  TAATACGACTCAGTATAGGAGCTCG 49
Db      1340 TAATACGACTCAGTATAGGAGCTCG 1315

RESULT 72
AY720437      4154 bp      DNA      circular SYN 18-SEP-2004
LOCUS      Plant expression vector pMESH1, complete sequence.
DEFINITION
ACCESSION      AY720437
VERSION      AY720437.1 GI:51989442
KEYWORDS
SOURCE      Plant expression vector pMESH1
ORGANISM      Plant expression vector pMESH1
REFERENCE      1 (bases 1 to 4154)
AUTHORS      Ferrando,A., Koncz-Kalman,Z., Farras,R., Tiburcio,A., Schell,J. and
              Koncz,C.
TITLE      Detection of in vivo protein interactions between Snf1-related
              kinase subunits with intron-tagged epitope-labelling in plants
              cells
JOURNAL      Nucleic Acids Res. 29 (17), 3685-3693 (2001)
PUBMED      11522840
REFERENCE      2 (bases 1 to 4154)
AUTHORS      Berendzen,K.W. and Koncz,C.
TITLE      Direct Submision
JOURNAL      Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
              Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
              Location/Qualifiers
FEATURES
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1. .4154
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   /db_xref="taxon:292602"
   1. .18
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   19. .758
   /note="duplicated 35S CamV (Cabb B-U1 isolate); 35S;
   overexpression in plants"
   759. .793
   /note="HindIII, NcoI, SmaI, XbaI, BglII; MCS upstream"
   794. .808
   /note="N-term c-myc epitope"
   809. .997
   /note="PIV2 optimized; prevents detection of epitope tag
   in bacteria"
   998. .1012
   /note="C-term c-myc epitope"
   1013. .1038
   /note="Sall, BamHI, PstI, EcoRI; MCS downstream"
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   /note="polyadenylation signal from nopaline synthase gene

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misc_feature      1292. .1361
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misc_feature      complement (1362. .1590)
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                  /complement (2532. .3392)
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                  /note="ampR"
                  /note="resistance to ampicillin"
                  /codon_start=1
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                  /db_xref="GI:51989443"
                  /translation="MSIQHPRVALIPFPAAFCUVPVAPHPETLVVKQDAEQLGARVGY
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Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      24  TAATACGACTCAGTATAGGAGCTCG 49
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LOCUS      Plant expression vector pLOLA, complete sequence.
DEFINITION
ACCESSION      AY720439
VERSION      AY720439.1 GI:51989446
KEYWORDS
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ORGANISM      Plant expression vector pLOLA
REFERENCE      1 (bases 1 to 4156)
AUTHORS      Ferrando,A., Koncz-Kalman,Z., Farras,R., Tiburcio,A., Schell,J. and
              Koncz,C.
TITLE      Detection of in vivo protein interactions between Snf1-related
              kinase subunits with intron-tagged epitope-labelling in plants
              cells
JOURNAL      Nucleic Acids Res. 29 (17), 3685-3693 (2001)
PUBMED      11522840
REFERENCE      2 (bases 1 to 4156)
AUTHORS      Berendzen,K.W. and Koncz,C.
TITLE      Direct Submision
JOURNAL      Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
              Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
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ORIGIN

Query Match 0.6%; Score 26; DB 11; Length 4156;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCAGTATAGGAGCTCG 49
Db 1343 TAATACGACTCAGTATAGGAGCTCG 1318

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DEFINITION Plant expression vector pGIG1, complete sequence.
ACCESSION AY720440
VERSION AY720440.1 GI:51989448
KEYWORDS
SOURCE .
ORGANISM Plant expression vector pGIG1
REFERENCE
1 (bases 1 to 4157)
other sequences; artificial sequences; vectors.
Farrado,A., Koncz-Kalman,Z., Farkas,R., Tiburcio,A., Scheil,J. and
Koncz,C.
TITLE
Detection of in vivo protein interactions between Snf1-related
kinase subunits with intron-tagged epitope-labelling in plants
cellls
Nucleic Acids Res. 29 (17), 3685-3693 (2001)

JOURNAL
PUBMED 11522840
AUTHORS 2 (bases 1 to 4157)
Berendzen,K.W. and Koncz,C.
TITLE Direct Submission
JOURNAL Submitted (12-AUG-2004) Development, Max-Planck Institute for Plant
Breeding Research, Carl-von-Linne-Weg 10, Cologne D-50829, Germany
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overexpression in plants"
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Query Match 0.6%; Score 26; DB 11; Length 4157;
Best Local Similarity 100.0%; Pred. No. 4.1;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TAATACGACTCAGTATAGGAGCTCG 49
Db 1344 TAATACGACTCAGTATAGGAGCTCG 1319

RESULT 75
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LOCUS BD235520
DEFINITION Desaturase gene for modifying lipid profile in corn.
ACCESSION BD235520
VERSION BD235520.1 GI:33045290
KEYWORDS
SOURCE JP 2002517984-A/55.
ORGANISM Zea mays
Zea mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 6337)
Shen,J.B.J.
TITLE Desaturase gene for modifying lipid profile in corn
JOURNAL Patent: JP 2002517984-A 55 25-JUN-2002;
ET DU PONT DE NEMOURS AND CO
OS Zea mays (maize)
PN JP 2002517984-A/55
PD 25-JUN-2002
PF 09-JUN-1999 JP 2000553569
PR 11-JUN-1998 US 60/088987
PI JENNIE BIH JIEN SHEN
PC C12N15/09,A01H5/00,A23D7/00,A23D9/00,C12N5/10,C12N15/00,C12N5/00
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Location/Qualifiers
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 DB 6312 CTATACGACTCACTATATAGGAGCTC 6337

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 Job time : 13896 secs

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Title: US-10-623-477-3

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SUMMARIES

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6	71.4	1.7	1141	US-09-806-708B-22	Sequence 22, Appl1
7	68.6	1.6	18773	US-09-949-016-14164	Sequence 22, Appl1
8	67.4	1.6	1055	US-09-806-708B-23	Sequence 23, Appl1
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10	67.4	1.6	191569	US-09-949-016-15940	Sequence 15940, A
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13	62.8	1.5	119153	US-09-949-016-12378	Sequence 12378, A
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C 35	58.4	1.4	18682	3	US-09-949-002-786	Sequence 786, App
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ALIGNMENTS

RESULT 1
US-09-227-421-3
Sequence 3, Application US/09227421
Patent No. 6559357

GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Mizukami, Yukiko
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Methods for Altering Organ Mass, Controlling Fertility
TITLE OF INVENTION: and Enhancing Asexual Reproduction in Plants
FILE REFERENCE: 023070-0907009C
CURRENT APPLICATION NUMBER: US/09/227,421
CURRENT FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: 1999-01-08
PRIOR FILING DATE: 1999-01-08
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 3
LENGTH: 4228
TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(4228)
OTHER INFORMATION: ANT promoter
US-09-227-421-3

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Dp	1441	ACTTCATGCAAAATTAACCTAAATTTGGTATTTTTGTCAAGTCTGTGCTTTTAAG	1500
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Dp	1501	TCGATATATTTGGTAATCTATATGTGGATATACATCCACCTAATCAATATGAT	1560
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Dp	1561	CTCCTCTGCTTATCAATAAATATCACACATTAAGTATCAAGCTAATAATATACCA	1620
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Dp	1861	ATTAACTTTGATCGAAATTCGAAATCTTTTTTAAACAATAGAAATTTTCAGCATTT	1920
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Qy	2161	TTGAAGCAAAATATCCACAGGAGATGATGGGTTAGTCCACATTCATATCTTTTGT	2220
Dp	2161	TTGAAGCAAAATATCCACAGGAGATGATGGGTTAGTCCACATTCATATCTTTTGT	2220
Qy	2221	CTTTGTTATTTATGAATAAAATAATTTATCAGAAAAAAACGTTTCTGTCTATAGTGA	2280
Dp	2221	CTTTGTTATTTATGAATAAAATAATTTATCAGAAAAAAACGTTTCTGTCTATAGTGA	2280
Qy	2281	TAAGTATTAAGTATTAACAAAATTTAATCTAGTATATGATTTTACATCTTCAAACTT	2340
Dp	2281	TAAGTATTAAGTATTAACAAAATTTAATCTAGTATATGATTTTACATCTTCAAACTT	2340
Qy	2341	ACCATCTTCAACATTAATATTTGATTCATTTTATTTTTTAACTAAACTACTTCCACTA	2400
Dp	2341	ACCATCTTCAACATTAATATTTGATTCATTTTATTTTTTAACTAAACTACTTCCACTA	2400
Qy	2401	AAAAATGCAAAAGAGATATATATTTTAAAGTCAAAAGTATTAAGATGAGTGGGTGAT	2460
Dp	2401	AAAAATGCAAAAGAGATATATATTTTAAAGTCAAAAGTATTAAGATGAGTGGGTGAT	2460

Query Match 100.0%; Score 4228; DB 3; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCTTAGGCTCACTGGCTTAATAGACCTACATATGGAGGCTCGAGATTCCTTTA 60
DB 1 GTGACCTTAGGCTCACTGGCTTAATAGACCTACATATGGAGGCTCGAGATTCCTTTA 60
QY GTTAAAAAACTTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB GTTAAAAAACTTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ACATGTATATCAAT 180
DB 121 ACATGTATATCAAT 180
QY 181 TAAAT 240
DB 181 TAAAT 240
QY 241 GTTGCACTTGAT 300
DB 241 GTTGCACTTGAT 300
QY 301 AAAAGTGAACCAAAAGAGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 AAAAGTGAACCAAAAGAGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 ATGATATATGGAAGATTAATCTTTACTTAATATATATATATATATATATATATATATAT 420
DB 361 ATGATATATGGAAGATTAATCTTTACTTAATATATATATATATATATATATATATATAT 420
QY 421 ATATGTGTAGTGTCTTCAAGTGTCTCACTGTCAAGAAATATCTGTGTATCTTACTTGA 480
DB 421 ATATGTGTAGTGTCTTCAAGTGTCTCACTGTCAAGAAATATCTGTGTATCTTACTTGA 480
QY 481 CTGAAGTGTAT 540
DB 481 CTGAAGTGTAT 540
QY 541 CGATCAAAATCAAAAT 600
DB 541 CGATCAAAATCAAAAT 600
QY 601 TACACAGCTAAGAAATTTGTACAGAGAGTGAAGAAATATATATATATATATATATATAT 660
DB 601 TACACAGCTAAGAAATTTGTACAGAGAGTGAAGAAATATATATATATATATATATATAT 660
QY 661 TATGATTTCACTTACGATTTGATTTACATTTACCAAGTATATATATATATATATATAT 720
DB 661 TATGATTTCACTTACGATTTGATTTACATTTACCAAGTATATATATATATATATATAT 720
QY 721 TGT 780
DB 721 TGT 780
QY 781 AACTGT 840
DB 781 AACTGT 840
QY 841 TACAAT 900
DB 841 TACAAT 900
QY 901 TATGTAT 960
DB 901 TATGTAT 960
QY 961 CCTTGACGGGTAT 1020
DB 961 CCTTGACGGGTAT 1020
QY 1021 TCTGTCTTAAAGATATCTACAGCTGTGCTGCTGTGTATATAGAAAGAAATTTGAATATGA 1080

DB 1021 TCTGTCTTAAAGATATCTACAGCTGTGCTGCTGTGTATATAGAAAGAAATTTGAATATGA 1080
QY 1081 GAGATCCCATCTTAGCTTTCAAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
DB 1081 GAGATCCCATCTTAGCTTTCAAGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1140
QY 1141 TTTTCTTATATGT 1200
DB 1141 TTTTCTTATATGT 1200
QY 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATCTATTTGTGAAAAAGCATTAATATGAC 1260
DB 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAGAAATCTATTTGTGAAAAAGCATTAATATGAC 1260
QY 1261 ACTTAAATTTGAT 1320
DB 1261 ACTTAAATTTGAT 1320
QY 1321 AATCAAAAG 1380
DB 1321 AATCAAAAG 1380
QY 1381 CCCATATATCTTTTATCTTCAACAAATTCATCAACAGAGAAATCTGTCTGTGATC 1440
DB 1381 CCCATATATCTTTTATCTTCAACAAATTCATCAACAGAGAAATCTGTCTGTGATC 1440
QY 1441 ACTTTCATGCAAAATTAATCTAAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
DB 1441 ACTTTCATGCAAAATTAATCTAAATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1500
QY 1501 TCGATTAATTTGTGTAAT 1560
DB 1501 TCGATTAATTTGTGTAAT 1560
QY 1561 CTCCTTCTGCTTATCAATTAATTAACACATATAGCTAATCAAGATTAATTAATTAACCA 1620
DB 1561 CTCCTTCTGCTTATCAATTAATTAACACATATAGCTAATCAAGATTAATTAATTAACCA 1620
QY 1621 CATCTCTTATCAATTTTAT 1680
DB 1621 CATCTCTTATCAATTTTAT 1680
QY 1681 GGTATTAAGCAATTAATGTGCTTATAGTCAGAGAAATTTTGTGTGTGTGTGTGTGTGTGT 1740
DB 1681 GGTATTAAGCAATTAATGTGCTTATAGTCAGAGAAATTTTGTGTGTGTGTGTGTGTGTGT 1740
QY 1741 GGAAGAAAAATCCAGCTTAAT 1800
DB 1741 GGAAGAAAAATCCAGCTTAAT 1800
QY 1801 TTTAAATTAAGATTTTGTCTTTTAAAGTTACACCGCTTAATTCATCTATATATATATAT 1860
DB 1801 TTTAAATTAAGATTTTGTCTTTTAAAGTTACACCGCTTAATTCATCTATATATATATAT 1860
QY 1861 ATTTAATTTGATCGAAATTCGAAATATCTTTTAAACATATATATATATATATATATATAT 1920
DB 1861 ATTTAATTTGATCGAAATTCGAAATATCTTTTAAACATATATATATATATATATATATAT 1920
QY 1921 TTTAAATTAAGGAT 1980
DB 1921 TTTAAATTAAGGAT 1980
QY 1981 TTTAACCAATGAT 2040
DB 1981 TTTAACCAATGAT 2040
QY 2041 TTTAACCGTCATCCGATTTGTAATATATATATATATATATATATATATATATATATATAT 2100
DB 2041 TTTAACCGTCATCCGATTTGTAATATATATATATATATATATATATATATATATATATAT 2100
QY 2101 AATCTGTATTAATTTCTCTGTGTGTATATCTTGACGCAATTTGACCAAGACTATATATAT 2160

Db 2101 AATCTGTTAAATTCCTCTGCTGATCATCTTGACGACCTTTGACCAACGACTATACATA 2160
Qy 2161 TTGAAAGCAAAATTCACCGAGGATGATAGGGTTAGATCCCACTTCATATCTTTTGT 2220
Db 2161 TTGAAAGCAAAATTCACCGAGGATGATAGGGTTAGATCCCACTTCATATCTTTTGT 2220
Qy 2221 CTTTGTATTATATGAAAAACAATATTATGAGGAAAAAAGTTCTCTCTAGTGGTA 2280
Db 2221 CTTTGTATTATATGAAAAACAATATTATGAGGAAAAAAGTTCTCTCTAGTGGTA 2280
Qy 2281 TAACTATAGATTAATTAACAAATTTTAATCTAGTTAATGATTTACTATCTTCAAACTT 2340
Db 2281 TAACTATAGATTAATTAACAAATTTTAATCTAGTTAATGATTTACTATCTTCAAACTT 2340
Qy 2341 AACATCCTTCAACATTAATATGATCAATTTTTTATTTTTTACTAACTACTCCACTA 2400
Db 2341 AACATCCTTCAACATTAATATGATCAATTTTTTATTTTTTACTAACTACTCCACTA 2400
Qy 2401 AAAAAATGCAAAAAGAGATATATATTTAGTCAAAAGTAAATTAAGAATGATGGTGAT 2460
Db 2401 AAAAAATGCAAAAAGAGATATATATTTAGTCAAAAGTAAATTAAGAATGATGGTGAT 2460
Qy 2461 TCTTCAGCAAAAACGGCCGCTAGAGAGTGTCTTATCTCATTTACAGCTGGGTGGCAG 2520
Db 2461 TCTTCAGCAAAAACGGCCGCTAGAGAGTGTCTTATCTCAATTAACGCTGGGTGGCAG 2520
Qy 2521 ACATCATAGGGCCTACGTATATTTGAGCTTTACTGTACGTAAAGCTTTTACATATCTAGT 2580
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Qy 2581 TAGTTCCTCATCTGTACAAACAAACAAATTCATTCGTACATATATACAAATCTACTA 2640
Db 2581 TAGTTCCTCATCTGTACAAACAAACAAATTCATTCGTACATATATACAAATCTACTA 2640
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Db 2641 GTACTAGATTAGCTGATACATACGCTTTTGGCAAACTTCTAACTAATCTATACAA 2700
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Db 2701 CAAACTGGAATGTTGTTTGTGTAATTTATCTTAAACCAAGTTTGAATTTGCAATGGG 2760
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Qy 2821 ATTTAAACCAAAATTTTATTTGTGTGTAAGTCAAAACATGTACATATATAGGA 2880
Db 2821 ATTTAAACCAAAATTTTATTTGTGTGTAAGTCAAAACATGTACATATATAGGA 2880
Qy 2881 CAGCATGTTTATACAAATATATGTTGATGTAATGGAATCAATATATGAATTA 2940
Db 2881 CAGCATGTTTATACAAATATATGTTGATGTAATGGAATCAATATATGAATTA 2940
Qy 2941 GCGACTCACTGTTTAAATGTTTGAAGATTAATGAATTAATAAATGAATCAAGATA 3000
Db 2941 GCGACTCACTGTTTAAATGTTTGAAGATTAATGAATTAATAAATGAATCAAGATA 3000
Qy 3001 CAGAGCTATATATGCGGTCAATTTAGACCGGTACCAAAAGTTTCGTCGTAATTTTCTAC 3060
Db 3001 CAGAGCTATATATGCGGTCAATTTAGACCGGTACCAAAAGTTTCGTCGTAATTTTCTAC 3060
Qy 3061 GGTGCGTCAATGAATTTTGAATTTTCTTCAACCTTTTATGAATCTGTATAGTTTT 3120
Db 3061 GGTGCGTCAATGAATTTTGAATTTTCTTCAACCTTTTATGAATCTGTATAGTTTT 3120
Qy 3121 TGTGCGATTATATTTGTATTCGTAATTTTTTGTTCATATATGATAGTAATTCGA 3180
Db 3121 TGTGCGATTATATTTGTATTCGTAATTTTTTGTTCATATATGATAGTAATTCGA 3180
Qy 3181 CGATTAAGAAAGACTTTTATTTATTTAAATTTGAATTTAAACCTTTGTTTGGAAATGACT 3240
Db 3181 CGATTAAGAAAGACTTTTATTTATTTAAATTTGAATTTAAACCTTTGTTTGGAAATGACT 3240

Qy 3241 CATACAGAGTTAAAGTTTATGATGTATCCAAATTTACAAAATGTTTCGAGATGCGTTC 3300
Db 3241 CATACAGAGTTAAAGTTTATGATGTATCCAAATTTACAAAATGTTTCGAGATGCGTTC 3300
Qy 3301 GAGTGTCTTACCACTCGTACCAACTGTATGGGTTATATATAGGTTTTTTCTTCTT 3360
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Qy 3361 TTTCCAAATGCTTTATATATGAAACCACTCTAAATTTCTTTTAAATTAAGTTAAGAT 3420
Db 3361 TTTCCAAATGCTTTATATATGAAACCACTCTAAATTTCTTTTAAATTAAGTTAAGAT 3420
Qy 3421 CTTGAAATTTTCTGTGATTTTAAACCAAGTTTCAATCTCTCTAGCACAAAAAAAA 3480
Db 3421 CTTGAAATTTTCTGTGATTTTAAACCAAGTTTCAATCTCTCTAGCACAAAAAAAA 3480
Qy 3481 AAAAGTTTCAATTAATTAAGAACTTAAATTTTGAAGTTCAAGTTTAAATGATAGCT 3540
Db 3481 AAAAGTTTCAATTAATTAAGAACTTAAATTTTGAAGTTCAAGTTTAAATGATAGCT 3540
Qy 3541 GAAAGTTATGATGATTTGCAAGTTTGCACAAGAAATGTCATAGTATATCAAAAA 3600
Db 3541 GAAAGTTATGATGATTTGCAAGTTTGCACAAGAAATGTCATAGTATATCAAAAA 3600
Qy 3601 CATGATCAAAATTAATATTTCTGTAGCAAGAAACGATGAAATTAACAGAACAT 3660
Db 3601 CATGATCAAAATTAATATTTCTGTAGCAAGAAACGATGAAATTAACAGAACAT 3660
Qy 3661 CGTTAACACTTAAATTTTGAATTAATTTTGTAGATTAATTTTCTGTAGAGAGAGG 3720
Db 3661 CGTTAACACTTAAATTTTGAATTAATTTTGTAGATTAATTTTCTGTAGAGAGAGG 3720
Qy 3721 TATCATATCTTACAAAAAAAACCTCATTCAGATTAATATATGTTCTCAATCGTTACA 3780
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Qy 3781 AGTATGTTTTTGTCTGATCATGTTGATGTAATCTGTCTTGAACATATATGTTCTAAG 3840
Db 3781 AGTATGTTTTTGTCTGATCATGTTGATGTAATCTGTCTTGAACATATATGTTCTAAG 3840
Qy 3841 TTTTAAATGTTTCAAGAATTTCACAAATTAATTAATATAGTGGAAATTTGTAGGG 3900
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Db 4021 CTTCAAAAAACCTCTCTATATCTCTTAAAGCCCCCTTCTTGTCTCTACCGCA 4080
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Db 4081 CAAAGAAAAACAAGTTTGAAGAAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4140
Qy 4141 TTTAGCTTACTTTCAGAGATTTATTAAGAAAGAGTAAGATCAATTAAGAAAGA 4200
Db 4141 TTTAGCTTACTTTCAGAGATTTATTAAGAAAGAGTAAGATCAATTAAGAAAGA 4200
Qy 4201 AGAGAGCAAAACCAAAAAAGAACCC 4228
Db 4201 AGAGAGCAAAACCAAAAAAGAACCC 4228

RESULT 3
US-09-227-421-1
; Sequence 1, Application US/09227421

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; Patent No. 6559357
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Method for Altering Organ Mass, Controlling Fertility
; FILE REFERENCE: 023070-090700PC
; CURRENT APPLICATION NUMBER: US/09/227,421
; PRIOR FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: US 09/227,421
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2148
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (269)..(1936)
; OTHER INFORMATION: AINTEGUMENTA (ANT)
; NAME/KEY: misc feature
; LOCATION: (1109)..(1339)
; OTHER INFORMATION: encodes first AP2 domain
; NAME/KEY: misc feature
; LOCATION: (1340)..(1414)
; OTHER INFORMATION: encodes linker region
; NAME/KEY: misc feature
; LOCATION: (1415)..(1621)
; OTHER INFORMATION: encodes second AP2 domain
; US-09-227-421-1
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Query Match 6.3%; Score 268; DB 3; Length 2148;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 3961 AGATCCCAAGGATTCACAGCAAAATTTGTGCTTCTCTCTTATTAATATC 4020
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QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTTGTCTTACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTTGTCTTACCGCA 120
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DB 121 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTTCTGTGTAACCAATGATGGGT 180
QY 4141 TTAGCTTACTACTCGAGAGATTATTAAGAAAGAGATTAATTAAGAAAG 4200
DB 181 TTAGCTTACTACTCGAGAGATTATTAAGAAAGAGATTAATTAAGAAAG 240
QY 4201 AGAAGACAGAAACCAAAAAAGAAACC 4228
DB 241 AGAAGACAGAAACCAAAAAAGAAACC 268

RESULT 4
US-09-479-855-1
; Sequence 1, Application US/09479855
; Patent No. 6639128
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Mizukami, Yukiko
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Method for Altering Organ Mass, Controlling Fertility
; FILE REFERENCE: 023070-090720US
; CURRENT APPLICATION NUMBER: US/09/479,855
; CURRENT FILING DATE: 2000-01-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent In Ver. 2.1
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; SEQ ID NO 1
; LENGTH: 2148
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; OTHER INFORMATION: AINTEGUMENTA (ANT) cDNA
; NAME/KEY: CDS
; LOCATION: (269)..(1936)
; OTHER INFORMATION: AINTEGUMENTA (ANT)
; US-09-479-855-1
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Query Match 6.3%; Score 268; DB 3; Length 2148;
Best Local Similarity 100.0%; Pred. No. 7e-42;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 AGATCCCAAGGATTCACAGCAAAATTTGTGCTTCTCTCTTATTAATATC 60
QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTTGTCTTACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTTGTCTTACCGCA 120
QY 4081 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTTCTGTGTAACCAATGATGGGT 4140
DB 121 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTTCTGTGTAACCAATGATGGGT 180
QY 4141 TTAGCTTACTACTCGAGAGATTATTAAGAAAGAGATTAATTAAGAAAG 4200
DB 181 TTAGCTTACTACTCGAGAGATTATTAAGAAAGAGATTAATTAAGAAAG 240
QY 4201 AGAAGACAGAAACCAAAAAAGAAACC 4228
DB 241 AGAAGACAGAAACCAAAAAAGAAACC 268
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RESULT 5
US-09-806-708B-22
; Sequence 22, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In version 3.0
; SEQ ID NO 22
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(1141)
; OTHER INFORMATION: consensus sequence of A.c., L.a., and B.n. PAB1 promoters
; US-09-806-708B-22
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Query Match 1.7%; Score 72.4; DB 3; Length 1141;
Best Local Similarity 10.7%; Pred. No. 0.00011;
Matches 107; Conservative 373; Mismatches 511; Indels 6; Gaps 1;
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QY 1459 ACTAATTTTGGTATTTTGTCAAGTTCTGCTTTAAGTCGATTAATTTGTAATAC 1518
DB 53 MSKSRKWTWABYCKRBYRNKNSRWKMGYKKKBVCANNYSBRYHABRWKMTAYBM 112
QY 1519 TATATGTGATATACATCAAGCTAATCAATTAATGATCTCTTGTCTTAACAT 1578
DB 113 TWTNKWKGKGMHRWYRWABMDYVDHVTAMNNAMWTTCMDDKDKTRWKKNNNA 172
QY 1579 AATTAACACCATTAAGCTAATCAAGCTAATTAATTAACACCATCTCTATCAATTTT 1638
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Db 173 TCGDDDDTKHMMNNNGBYTMMVRYKTDKSDSKRNNYGBMBKMMSYDVTYTWWD 232
Qy 1639 TATATGGTATAATAAACAACGACTAGCTACAGAGTGTGATTAAGCATTAATG 1698
Db 233 MCRKRVAVRTGRBMVYVAMBTAHRRYNNQWTBAMA YRBTMMNNNNNAKAMCKRA 292
Qy 1699 CCTTCTAGTGAAGAAATTTTGTATGATACATCGTGGGAAAAAATCAAGCTTA 1758
Db 293 KYGMMNABVNSTCTTKSKTKYRTSCMANNCAGDANDHKMKMSAMGVYMMNNNN 352
Qy 1759 ATATGCTATTAAAGATATGATTAATGCTTAATCACTAATAAATAAGCTTTT 1818
Db 353 NMNTYKARBARBDWVHSAKMHAAHYSKKTBYRKKTMMNNNNCTMKKMA 412
Qy 1819 GCTTTTAAAGTTACCAACGCTTAATCATCATAGAGAATATTAACCTTGATGAAT 1878
Db 413 MYWMDMDGTYNNNNNGRTYGYTKKKMMTYKMKANNCKRAMDHKTTHNTTW 472
Qy 1879 TCCAAATATCTTTTAAACATAGAATAATTTACAGATTTTAAATTAAGGTACAT 1938
Db 473 WKXKTYNNCYKMSMTGKSHRBAAYTYWMMWRBYAHANNNDY-----WYRAC 526
Qy 1939 TATGGGTCAATATATATGTTCCAGTAAAGTTGAGGTTAAACAATGAATGTT 1998
Db 527 WYTYBVCSKMMNYAAYTYSWNTSRTRYRKTKNNSWRNRSDRSGRANTYABHYG 586
Qy 1999 TTTGATTTAAAAACATATAATTTCTAGTAATTAACATTTTAAACGTCATCCAGA 2058
Db 587 YKNTNRMBWSHTBHBAGAAHYMMBMYBAKCHCKAMWKAKGVAGAGSNNNNNN 646
Qy 2059 TTGTATTAAGTGAACAATCTGAAAACATTTTCTTGAATCTTGTTAATTC 2118
Db 647 NNNNNNNATCAADDYPAASRWYAMANAKEYYGBAANNA YTTANMMWGCNNATDTR 706
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Db 707 TMMKNNNNNAGTKNNNNNNNAKASAAKYAABAAPAKKMMWAKMARGHADA 766
Qy 2179 CCAAGGATAGAGGTAGATCCACATCAATCTTTTGTCTTGTATTAATGA 2238
Db 767 BTDDKRNAGAYTKYTTNNNNNTYRGVLTAAABGMMNNNNNNNNNNNGMSDMVTV 826
Qy 2239 ACAATAATTTATCAGAAAAACGTTCTCTAGTGTATTAAGTATAATAC 2298
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Qy 2299 AAAATTAATAGTATGATTAATGATTAATCTCAACTTACATCCTTCAACATTA 2358
Db 887 YMSDTCDAMKMDATKNNATTYRGTAAMRTNNNNNNMTMKYBBAAMNNNNNGKMC 946
Qy 2359 TATGATCAATTTTATTTTATTTTACTTAACACTACTCAATAAATAAGCAAGAGA 2418
Db 947 TATTTWCKATKTKTGCMNCTTTCRKYKNNCTYTTMTTTRTWTVAATRKNNATGSM 1006
Qy 2419 GATATATATTTAAGTCAAGTAAATTAAGATGAG 2455
Db 1007 TRCNATGKNNNNYTWGKTRTAYRATRMKAMWV 1043

RESULT 6
US-09-806-708B-22/c
Sequence 22, Application US/09806708B
Patent No. 6784342
GENERAL INFORMATION:
APPLICANT: The University of British Columbia
TITLE OR INVENTION: Regulation of Embryonic Transcription in Plants
FILE REFERENCE: 4810-58741
CURRENT APPLICATION NUMBER: US/09/806, 708B
CURRENT FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: US 60/147,133
PRIOR FILING DATE: 1999-08-04
NUMBER OF SEQ ID NOS: 23

SOFTWARE: PatentIn version 3.0
SEQ ID NO 22
LENGTH: 1141
TYPE: DNA
ORGANISM: Artificial sequence
FEATURES:
NAME/KEY: promoter
LOCATION: (1)..(1141)
OTHER INFORMATION: consensus sequence of A.t., L.a., and B.n. PAEI promoters
US-09-806-708B-22

Query Match 1.7%; Score 71.4; DB 3; Length 1141;
Best Local Similarity 12.8%; Pred. No. 0.00016;
Matches 127; Conservative 359; Mismatches 497; Indels 12; Gaps 3;

Qy 1463 AATTGGTATTTTGTCAAGTCTTGTGTTAAGCATTAATTTGATATATATA 1522
Db 1138 WRYTCHGNTTTTKTYKANNNNNNNNNGMGKDMRMDATKWSATGTAMTTHAKRGA 1079
Qy 1523 TGTGTGATATACATCCAAAGCTAATCAATTAATGATCTCTTGTGCTATCAATAAT 1582
Db 1078 WYWTGTGNRMCRTYAMRTYRSNANWSCATKBMWMTMKYATYRTAAMWMCAMR 1019
Qy 1583 TACACGATTAAGTATCAAGCTAATATAATTAACAACATCTCTATCAATTTTATA 1642
Db 1018 NNNMWCATNGYASCATNNNAWYATTTAAAYAAKARBMGNMRTGAAAGKMGCM 959
Qy 1643 TGTATATAATAACAACGACTATAGCTACAGAGTGTATTAAGCATTAATGCTT 1702
Db 958 MATGMBWADTAGMCCNNNNNNNTTVDVRAAMKAKNNNNNAWYTA CYNBAATNNK 899
Qy 1703 CTAGTCAGAAATTTT--GTATGATTAACCTCTGTGGAAAAAATCCAGCTAAT 1760
Db 898 WMKYTHGASHKRPTRHTTRCTCRKYNNNNNNATYVYHHAARBMNAWTRNNNN 839
Qy 1761 ATGCTATTAAGGATTAATGATTAATGCTTAATCAATTAATAAAGTTTTTGC 1820
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Db 718 CTNNNNNNMKAAYAHAATNNWGMNNTDARTNNITVMBRRWNTNKTWYSTRHHY 659
Qy 1938 TTAATGGCTCAATTAATATGTTTCCAGTAAAGTTGAAGTTAACACAGATGTT 1997
Db 658 TGAATNNNNNNNNNNNNNSCCCTRMWMTMRWTKGDSMTVRKV-----KRDITC 606
Qy 1998 TTTTATTTAAAAACAATAAATTTCTAGTAATTAACATTTTAAACGTCATCCAG 2057
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Qy 2058 ATTGATTAAGTGAACAATCTGAAAACATTTTCTTGAATCTTGTTAATCTT 2117
Db 545 ARWTRNNMMWSGBVRMAGTMMWRHMNNNNNTDTRYWMMKRAABITTYVDSMC 486
Qy 2118 CTGCTGCAATCTTGACGAGCATTTGACAACGACTATACATTAATGAAGAAATATCC 2177
Db 485 MMRGNMNRKMMWMAANDGADHDHTYMGNTMRRMRAKMMNNMCRBAYCANN 426
Qy 2178 ACCAGGATAGAGGTAGATCCACATTCATTAATCTTTGTGTTATTAATGA 2237
Db 425 RACVYHGHKMMRWTKMMKDA CANNNBKAMYRVAMMYTSDPTNTDMMWTS 366
Qy 2238 AACAAATATTTTACAGAAAAACGTTCTCTAGTGTATTAAGTATAATTA 2297
Db 365 YTVDTYMMRAMNNNNNNNNWBCKTYSMMWMDHNHTCTYGNNTWGSAYBMA 306
Qy 2298 CAAATTTAATAGTATGATTAATGATTAATCTTCAATCAATCAATCAATTA 2357
Db 2357

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Db      305 ASNBVTYNNMCWMTYNGKMTNNNNNNKAYRYRTKVAMCNRYYDDTAVTEKRYKYC 246
QY      2358 ATATGATGCAATTTTATTTTCTTAAGTACTTCCATTAAGAAATGCAAAAGAG 2417
Db      245 YAYBMYBYMGMGHHBMMRRABHRSNNMMWVKCRNRYWVSMHYHARBYKMAAVGCCNN 186
QY      2418 AGATATATATTTTAAGTCAAAAGTAAATTAAGATGGA 2452
Db      185 NMDRMAHHHMCATNNNNMMWYAYMHMHMKKGA 151

RESULT 7
US-09-949-016-14164/c
; Sequence 14164, Application US/094949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FaSeqSeq for Windows Version 4.0
; SEQ ID NO 14164
; LENGTH: 18773
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14164

Query Match      1.64; Score 68.6; DB 3; Length 18773;
Best Local Similarity 43.64; Pred. No. 0.00088;
Matches 554; Conservative 0; Mismatches 704; Indels 13; Gaps 5;

QY      2628 ACAATATCTAGTACTAGATTACGCTACGTAATACATCGCTTTTCGAAATTTCTAAA 2687
Db      18351 AATATATCTATATTAATAATATATATATATATATATATATATATATATATATATATG 18292
QY      2688 CTATATCTATCAACAACCTGAATGTTTGTGTAATTAATCTTAACAACAAGTTTGA 2747
Db      18291 AATATATATATATATATATATATATATATATATATATATATATATATATATATAT 18232
QY      2748 ATTGTCATTTGGAGCTACACTAGTCCCTTTTCCCAAAATATCTCCTTACATC 2807
Db      18231 AATATATATATATATATATATATATATATATATATATATATATATATATATATAT 18172
QY      2808 GACCGGTTAAAGTATTAACCAACAATTTAATTTGTTGCGAAGGTAACAACATGTC 2867
Db      18171 TA-----TATATATATATATATATATATATATATATATATATATATATATAT 18117
QY      2868 ACATATATATGAGACAGATCGTTATATACAATAATGTCATGATTTGGAATCAATA 2927
Db      18116 AATATATATATATATATATATATATATATATATATATATATATATATATATATAT 18057
QY      2928 TAAATATGATATGCGCATCTGTTGTTAATAGTTTGAAGATTAATGAATATTAATAATG 2987
Db      18056 AATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17997
QY      2988 AATTCAGAGATACAGAGCTATATATGTCGGGTCAITTTAGAGCGGTGACCAAAAGTTTCG 3047
Db      17996 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 17942
QY      3048 TCGTATATTTCTAGCGTCGCTCAATGAAGAAATTTGACCTTTTTCACCCCTTTATGACT 3107
Db      17941 AATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17882
QY      3108 TCTGATATGTTTTTGTGCGATATATATTTGTATGATATATTTTGTGTTCTAATATG 3167
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Db      17881 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17822
QY      3168 ATATGTAATATCAAGTATGAAGAAAGACTCTTTTATATATATTTGATTTAAACCTTTGTT 3227
Db      17821 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17762
QY      3228 TTTGAAATGACTCATACACAAGGTAAAGTTGATGTATCCAAATTTTCAAAATGTTT 3287
Db      17761 TAT-ATATATATATATATATATATATATATATATATATATATATATATATATAT 17703
QY      3288 CGAGAGTGGCTTGCAGTGTCTTACACACATCGTACCACTCGTAGGGTTATATATAGG 3347
Db      17702 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17644
QY      3348 TTTTTCCTCTTTTCCATGCTTTTATATATATTTGAACCACTCTAATTTCTTTTAAA 3407
Db      17643 TATTTTATATATATATATATATATATATATATATATATATATATATATATATAT 17584
QY      3408 TTATGTTAAGAAATCTGAATTTTCTGTGATTTTAAACCAAGTTTCAATCTTCTTAG 3467
Db      17583 TTATATATCTATATTTTATATATATATATATATATATATATATATATATATATAT 17524
QY      3468 CACAAAAAAGGTTTCAATTTTAAAGAAATCTAAATTTTTCAGTTCAAGAG 3527
Db      17523 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17464
QY      3528 TTTAATGATAGCTGAAAGATTTGAATGATTTGCAAGTTTGCACAGAAAGTGTAGTAG 3587
Db      17463 ATTGATATATATATATATATATATATATATATATATATATATATATATATATAT 17404
QY      3588 TACATATCAAAAAATCATGATCAAAATTAATATTTTGTGCTTACAGAGAAACGATTGAAA 3647
Db      17403 AATATATATATATATATATATATATATATATATATATATATATATATATATATAT 17344
QY      3648 TAAACAGAAATCTGTTAACCACTTAAAAATCTTGAATATATTTTGTAGTAAATTTTC 3707
Db      17343 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 17284
QY      3708 TGTATAGAGAGGTATCATATCTTACAAAAAATCTCATTTGAGATTAATAATGTTGT 3767
Db      17283 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 17225
QY      3768 CCAATGTTACCAAGATGTTTGTGCTGATCATGATTTGATTTGAATCTGCTTACGCC 3827
Db      17224 ACATATTTATATAGAAATATATATATATATATATATATATATATATATATATAT 17165
QY      3828 ATATAGTTCTAAGTTTAAATGTTTCAAGACTTTTACAAAAATTAATATATATAGGT 3887
Db      17164 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 17105
QY      3888 GGAATTTGTAG 3898
Db      17104 AGAAATCTGCG 17094

RESULT 8
US-09-806-708B-23
; Sequence 23, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-56741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 23
; LENGTH: 1055
; TYPE: DNA
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ORGANISM: Artificial sequence
FEATURE:
NAME/KEY: promoter
LOCATION: (1)..(1055)
OTHER INFORMATION: consensus sequence of A.T. and L.A. PAB1 promoters
US-09-806-708B-23
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Query Match 1.6%; Score 67.4; DB 3; Length 1055;
Best Local Similarity 24.1%; Pred. No. 0.0093;
Matches 230; Conservative 183; Mismatches 534; Indels 7; Gaps 2;
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QY 1598 AATCAAGTAAATTAACACACATCTCTATCAATTTTATATGATTAATAAAC 1657
D 5 AKMAAAMVAKVAGTANNNGRTTGTGKTWYCAANTGKCYARBKATTAATTAATK 64
QY 1658 AACCGATATAGGCTACAGAGTTGATTAAGCATTAATGCTTAGTCGAAGAATT 1717
D 65 WGTGTAATRTMRMAAMKTRKMCSTAMNNNAWTCTARKKRTGTMTTNNNAATGTRW 124
QY 1718 TTTTGTATGATTAACCTGCTGGAAAAAATCCAGCTTAATATGCTCATTAAGGAT 1777
D 125 WTYGMMNNNGCSMTWABRYKTRRWCYTAMWYGASWAGNASTRRRTTYTMRMKCKRK 184
QY 1778 AATGATTTAAAGCTTAATCAATTAATAAAGTTTTGCTTTAAAGTTACACACC 1837
D 185 SABARATRGARRYARATYTAARRGTGKAAVATAMTNNNNNAKACCKRATTWGRPAK 244
QY 1838 GCTTAATTCATCATTAAGAGAAATTAATTAAGTTGATCGAAATTCGAAATATCTTTTAAAC 1897
D 245 SNGCTTAGGTTTBRATCGAAATCGAGMATKKTWTSAMGTMNNNNNNNTTTTKAA 304
QY 1898 ACATTAAGAAATTTTCAACATTTTAAATAAAGGTAATTAATGAGTTCATTAATAT 1957
D 305 MYAARMMWMSATTTWMAAATWSRKTWYGRKTAAMNNNGTCTWMTWMTWMMKTK 364
QY 1958 GTTCCACGTAAGTTGAGGTTTAAACACATGATGTTTTTGAATTTAAAAACAT 2017
D 365 GTTTNNNGRRTYGTGTTKRAATTTTAKANNCTTAARKMTCTMNTTAAKATTTWATCY 424
QY 2018 AATTTTCTAGTATTAACATTTTAAACGTCATCGATGTAATTAAGTGAATATC 2077
D 425 WKSMTNGSTRYAAARATYTAARWTRRYAANNNTKTWRACTWYTKRCTTAATTAAT 484
QY 2078 TGAACACATTTTCTTGAATCTGTTAAATCTCTGCTGCACTTATGAGG 2137
D 485 YTKSANCTSRTRMKTNCRAGSKTASMBRAYARAYWYGKMTAWAYCMTWYVRAG 544
QY 2138 CATTTGACCAACGATTAATTAAGCAAAATCCACGAGGATATAGGCTTAG 2197
D 545 AATTAATYMTSATCTCTAATTAAGTCAGAGSTAKGNNNNNNCCAAATCARMKCTPAS 604
QY 2198 ATCCCATCTC-----AATATCTTTTGTCTTGTATTTAAGAAAAAATAATATTA 2252
D 605 AACMAAATTCCTYAAANATTTAANATGCMAATKTAATMTNNNNNAAGTNNNNNN 664
QY 2253 GGAAGAAAAAGTTCTCTAGTGTATAGTATTAAGTATTAACAAAATTAATCT 2312
D 665 AKMASATATYAAAMATATKATANTTAAAGAVARAAATYTRANNNGACTTTTNNNT 724
QY 2313 AGTTAATGATTAATCTTCAACTTACATCTTCAACATTAATTAATGATCAATTT 2372
D 725 GGRRTYTAARAGVANNNNNNNNNNNGACMAWRTTATANCGTNNNNNNNNNAATTT 784
QY 2373 TATTTTCTAATTAATCTCACTTAATAAATAAGAAAGAGATATATATTAAG 2432
D 785 NTATTTTWTTRKANNNNNNNNNAAYYGAAMKANTTTCMTCAAMMAATGAATTTNAG 844
QY 2433 TCAAGATTAATTA--GATGATGGGATGATTTCTTACGAAACGCGCGCTAGAGGTC 2490
D 845 TATATNNNNNATATATTTTAAATNGACATATTTTCTATTTTGGCMTCTTCAKYGAC 904
QY 2491 TTATCTACATTAAGCTGGGTTGTGGACACATCATAGGCGCTAGATATTT 2544
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DB 905 TACTAATTTATTCAGATNGTATGATGATGATGATGATGATGATGATGATGAT 958
RESULT 9
US-09-949-016-12776/c
Sequence 12776, Application US/0949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CU001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12776
LENGTH: 187169
TYPE: DNA
ORGANISM: Human
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(187169)
OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12776
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Query Match 1.6%; Score 67.4; DB 3; Length 187169;
Best Local Similarity 45.1%; Pred. No. 0.0022;
Matches 421; Conservative 0; Mismatches 496; Indels 16; Gaps 4;
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QY 1410 TCATTCACAGGAAATCTGCTCGTATCATCTTATGCAAAATTAATTAATTTTG 1469
D 1375 TCTTAGAACTAAATATATATATATTTTAAATATATATATATATATATATATAT 1316
QY 1470 GATTTTGTCAAGTCTGCTGTTTAAAGTATATTTGTAATACATATATGCTG 1529
D 1315 ATATATTTATTTATATATATATATATATATATATATATATATATATATATAT 1256
QY 1530 ATATACATCAAGCTAATCAATTAATGATCTCTGCTTATCAATTAATACCA 1589
D 1255 ATATATTTATATATATATATATATATATATATATATATATATATATATATAT 1196
QY 1590 CATTAAGTAACTAATTAATTAATCAACAACTCTCTATCAATTTTATATGTA 1649
D 1195 TTATATATATATATATATATATATATATATATATATATATATATATATATAT 1136
QY 1650 AATPAAACA-----ACGACTATAGCTACAGATGCTGATTAAGGATTAATG 1703
D 1135 TATATATATATATATATATATATATATATATATATATATATATATATATAT 1076
QY 1704 TAGTCGAAGAAATTTTGTATGATTAACACTCGTGGAAAAAATCCAGCTAATATG 1763
D 1075 TATTTTATATATATATATATATATATATATATATATATATATATATATATAT 1016
QY 1764 CTATTTAAAGATTAATGATTAATTAATGCTTATATCAATTAATAAAGTTTGT 1823
D 1015 TATTTTATATATATATATATATATATATATATATATATATATATATATATAT 956
QY 1824 TAAAGGTACACCGCTAATTCATCATTAAGGAAATTAATTAATCTTATGGAAT 1883
D 955 TATATATATATATATATATATATATATATATATATATATATATATATATAT 896
QY 1884 A-----ATATCTTTTAAACATATAAATAATTTTACGATTTTAAATTAAGGTA 1939
D 895 ATTTTATATATTTTATATATATTTTATATATATTTTATATATATATATATAT 836
QY 1940 ATGGGCTTAATTAATATATGTTTCCAGTAAAGTTTGGAGGTTTAAACATGAAT 1999
```


LENGTH: 32392
TYPE: DNA
ORGANISM: Ambacia moorei entomopoxvirus
US-09-662-254B-27

Query Match 1.6%; Score 66.2; DB 3; Length 32392;

Best Local Similarity 45.3%; Pred. No. 0.0028;
Matches 447; Conservative 0; Mismatches 523; Indels 17; Gaps 5;

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QY 1465 TTTTGTATTTTGTGCAAGTCTGCTGTTTAAAGTCGATTTTGGTAACTATATG 1524
DB 8551 TTTCGAATATTTTCAACATTTATTTTATTTTAAATAAATTCATTTAA 8492
QY 1525 TGTGATATACATCCAGCTAATCAATATGATCTCTGCTTATCAATTA 1584
DB 8491 TGTGAATAATATATTAATCAACATCTATATATGTTTATTCATATATAATTT 8432
QY 1585 CACCACTTACGTAATCAAGCTAATTAATTAACCACTCTTATCAATTTTATATG 1644
DB 8431 ATCTGTAGTATATATTTTGTATTAATTTTTCATTCATTTTATTTTATAT 8372
QY 1645 GTATTAATTAACCAACGACTATAGGCTACAGATGCTATTAAGCATTTGCTTCT 1704
DB 8371 TATTTATATATATACATCTGTATTAATAATCAATATATACAAATTAATCAATAT 8312
QY 1705 AGTCGAAGATTTTGTATATATACACTGCTGGAAAAAATCCAGCTTAATATGC 1764
DB 8311 ATCTAAATTTTAAATTTTAAATTAATTCGATGTA-----GTATCAT 8260
QY 1765 TCATTTAAGATTAATGATTTAATGCTTTAATCATTAATAAAGTTTGTGCTTT 1824
DB 8259 TTATATATTTATATATTAATTAATTAATTAATTTTTCATTAATAATTAATTA 8200
QY 1825 AAAGGTACCAACGCTTATCATCATATAGAGAAATTAATTTGATTCGAATTCGAAA 1884
DB 8199 AATTTTATTTTGAATATTTATCAAGATTAATATATCATCTATATATTAATC---AA 8143
QY 1885 ATACTTTTATACATATAGAAAATTTTACAGATTTTAAATTAAGGATCATTTATGG 1944
DB 8142 TATATTTTAAATTAATCTTAAATTAATTAATCTTATATATTTTATTTTAAATTA 8083
QY 1945 GTTCAATTAATATGTTTCCAGTAAGTTTGAGGTTTAACCATATGAATGTTTGTAT 2004
DB 8082 TATATATTTAATTTATATAGATATATAT---GGTTTATATCAATTAATTTGTGTT 8027
QY 2005 TTAATAAACAATTAATTTTCTAGTAATTAATCAATTTTAAACGTCATCAGATGTA 2064
DB 8026 TTTTATATATATTTTATTTTATTTTAAACATTTTAAAGAAATTAATTAATTAATTA 7967
QY 2065 TTAAGTCAAAATCTGAACAAATTTTCTTGAATCTGTAATCTCTGCT 2124
DB 7966 TTATTTATCTAAATTTAATTCGATTAATTTAATTTATTTCTATTAATTTATATTTACT 7907
QY 2125 GCAT-ACCTGACGACATTTGACCAACGATTAATATATGAAGCAAAATTCACACGAG 2183
DB 7906 ATATCAATATTTATTTAAGTGAATATCTCAATAGATTAATAATTAAGTATTTTCATA 7847
QY 2184 GATATAGGTTAGATCCCAATTCATATCTTTTGTCTGTTATTTAGAAAAACAA 2243
DB 7846 TTATCTATATGCAATTTTCAATTTTATATATATTAACCTTTTAACTTTAATATATTA 7787
QY 2244 TATTTATCAGAAAAAAG-TTTCTTCTGATGATTAAGTAAAGATTAATTAACAAA 2302
DB 7786 TTTCATCAAAAACGATTTTATTTTATTTATTTATTTATTTATTTCAATATTTTATA 7727
QY 2303 TTTAATCTAGTAAATGATTTTATCTTAATCTTAACATTCCTTCAATATATAT 2362
DB 7726 TTTTAAACAATTTTAAATTTTAAATCAATTAATTTATTAAGTACAAATTTTAAATTT 7667
QY 2363 GATCAATTTTATTTTATTTTATCTAAACTCTCACTAAAAAATGCAAAAGAGATA 2422
DB 7666 TGTAAATTCGATGAATTTAATTAATCAATATATATTTTATTTGTAATTAATATATA 7607
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QY 2423 TATATTTAGCAAGTAAATTAAGAT 2449
DB 7606 GATATATTTATTAATTTAGTTAAATAT 7580

RESULT 12

US-09-949-016-13703/C

Sequence 13703, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: C0001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13703

LENGTH: 67755

TYPE: DNA

ORGANISM: Human

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)..(67755)

OTHER INFORMATION: n = A,T,C or G

US-09-949-016-13703

Query Match 1.5%; Score 64; DB 3; Length 67755;

Best Local Similarity 45.1%; Pred. No. 0.0082;

Matches 321; Conservative 0; Mismatches 385; Indels 6; Gaps 2;

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QY 1749 ATCCAGCTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTAATCATTAATA 1808
DB 41201 ATCTAAAAAACAACACATACATATTAATTAATATATATATATATATATATTT 41142
QY 1809 AAAGTTTGTCTTTAAAGTTTCAACGCTTATATCATTAATGAGAAATTAATCTT 1868
DB 41141 ATATATTAATATATATATATATATATATATATATATATATATATATATATAT 41082
QY 1869 TGATCAAAATTCAAAATATCTTTTAAACATTAAGAAAATTTTACATTTTAAATTA 1928
DB 41081 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 41022
QY 1929 AGGTACATTTATGCTCAATTAATATGTTTCCAGTAAGTTTGAGGTTTAAACAC 1988
DB 41021 ATATATCATATATATATATATATATATATATATATATATATATATATATATAT 40962
QY 1989 ATGAATGTTTTCATTTTAAACACATTAATTTCTAGTAATTAACATTTTAAACG 2048
DB 40961 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 40902
QY 2049 TCCATCCAGATGTAATATAGTAAATCTGAACAAATTTTCTTGAATCTTGT 2108
DB 40901 TATCATATATATATATATATATATATATATATATATATATATATATATATATAT 40844
QY 2109 TTAATTTCTCTGCTGATCTTGCAGGATTTGACCAACGATTAATTAATGAAAGC 2168
DB 40843 ATAAATATATTTTAAATATATATATATATATATATATATATATATATATATATAT 40784
QY 2169 AAAATATCCACAGGATATAGGTTAGATCCCAATTCATATCTTTTGTCTTGTGTA 2228
DB 40783 ATATATATATATATATATATATATATATATATATATATATATATATATATAT 40724
QY 2229 TTTATGAAAAAACAATTTTATATCAGAAAAAAGTTTCTCTGATGTAATAGATA 2288
DB 40723 TTAATATATATATATATATATATATATATATATATATATATATATATATATATAT 40664
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QY 3223 TTGTTTGGAAATGACATACAGAGTTAAGTTGATGCAATTACAAA 3282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 403 TTTTATATATTTATATTTATTTTATTTTATTTTATTTTATTTTAT 344
QY 3283 TGTTCAGAGTGGCTTCAGATGCTACACACATCGACCACTCGATGGTTATTA 3342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 343 TTTTATATATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 284
QY 3343 TTAGTTTTTTCTCTCTTTTCCAAATGCTTTATTAATGAACACCTAAATTTCTTTT 3402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 283 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 224
QY 3403 TTAATATAGGTAAAGATCTGAATTTCTGTTGATTTTAAACAAGTTTCAATCTT 3462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 223 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 164
QY 3463 CTT 3465
    |||
DB 163 TTT 161

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RESULT 15
US-09-949-016-12378/c
; Sequence 12378, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 12378
; LENGTH: 119153
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(119153)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12378

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Query Match 1.5%, Score 61.8; DB 3; Length 119153;
Best Local Similarity 44.4%; Pred. No. 0.023;
Matches 381; Conservative 0; Mismatches 472; Indels 6; Gaps 3;

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QY 3052 AATTTCACGCTGCGATATAAGAAATTTTGACCTTTCTCACCTTTATGAATCTTG 3111
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 87041 AATATATATATATATTAATTTATATATTTTACATTTATATATATATATATTA 86982
QY 3112 TATAGTTTTGTGCGATTATATATTTTGTATATATTTTGTCTATATATGATAC 3171
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86981 TAAATATATATTTATTAATATATTTTATTAATATATATATATATATATATAT 86922
QY 3172 GTAATTCACGATAGAGAAAGCTCTTTTATTTTA-ATTGATTTAAACTTTGTTTT 3230
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86921 TAAATATATATATATATATATATATATATATATATATATATATATATATAT 86862
QY 3231 GGAATGACCTATACACAGATTAAAGTTGATGCTATCCAATTTACAAAATGTTTGA 3290
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86861 ATATATATATATATATATATATATATATATATATATATATATATATATATATA 86802
QY 3291 GAGTGCCTTGAAGTCTTACACACATCGTACCAACTGATAGGCTTATATATAGTTT 3350
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86801 TATCTTATATATATATATATATATATATATATATATATATATATATATATATAT 86742

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QY 3351 TTTTCTTCTTTTCCAAATGCTTTATATATGAAACCACTTAAATTTCT----TTTTTAA 3406
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86741 TTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 86682
QY 3407 ATTAGTTAAGAAATCTGAATTTTCTGTGATTTTAAACCAAGTTTCAATTTCTTGA 3466
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86681 ATTTATATATATATATATATATATATATATATATATATATATATATATATATATATA 86622
QY 3467 GCACAAAAAAGTTTCAATTTTAAAGATCTAAATTTTGTAGTTTCAAGA 3526
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86621 GTATATATATATATATATATATATATATATATATATATATATATATATATATATA 86562
QY 3527 GTTATATATATATATATATATATATATATATATATATATATATATATATATAT 3585
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86561 TATTTACATATATATATATATATATATATATATATATATATATATATATATAT 86502
QY 3586 AGTACATATCAAAAAATGATGATCAAAATTAATTTGCTTACGAGAAACGATTTGA 3645
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86501 GATATATATATATATATATATATATATATATATATATATATATATATATATATAT 86442
QY 3646 AATTAACGAAACATCGTTAACCACTTAAATCTTGAATTTTGTAGTAAATTT 3705
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86441 TATATATATATATATATATATATATATATATATATATATATATATATATATATA 86382
QY 3706 TCTGTAAGAGAGGTATCATATCTTACAAAAAATCTCATTTGATTAATATGTT 3765
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86381 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 86322
QY 3766 GTCCAAATCGTTACCAATATGTTTGTCTGTCATGATTTGATATGTAATCGTCTAG 3825
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86321 ATATATATATATATATATATATATATATATATATATATATATATATATATATAT 86262
QY 3826 CCAATATAGTTCTAAGTTTAAATGTTTCAAGCTTTACAAAAATTAATTAATAG 3885
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86261 TATATATATATATATATATATATATATATATATATATATATATATATATATATA 86202
QY 3886 GTGGAATTTGTAGGCTTAA 3904
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 86201 ATATATATATATATATATATATATATATATATATATATATATATATATATATA 86183

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Search completed: February 27, 2006, 16:39:41
 Job time : 504 secs

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Db 241 GTTGCACTGATATAGATCTACTATATATTAACCTGGGTTATTTTAAATCCGTACCCATTAAC 300
Qy 301 AAAAGTGCACCAAAACGAGATCCAGTGTGTTGTTTACTTGTGTGTTTACCAAGATTAAT 360
Db 301 AAAAGTGCACCAAAACGAGATCCAGTGTGTTGTTTACTTGTGTGTTTACCAAGATTAAT 360
Qy 361 ATGATTAATGGAAGATTAATCTTTTACTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
Db 361 ATGATTAATGGAAGATTAATCTTTTACTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 420
Qy 421 ATATGTTGAGTGTCTTCAAGTGTCTCACTGTTCAAGAAATTAATCTGTTTATCTTAATTGAA 480
Db 421 ATATGTTGAGTGTCTTCAAGTGTCTCACTGTTCAAGAAATTAATCTGTTTATCTTAATTGAA 480
Qy 481 CTGAAATGATATATCTTAACACGTAATATTTTAAACGACGTTACATTAACATGAT 540
Db 481 CTGAAATGATATATCTTAACACGTAATATTTTAAACGACGTTACATTAACATGAT 540
Qy 541 CGATCAAAATACAAATTAATTAATGAGACTAGAAATCCAGATGAGATGACTCTAGACAGATA 600
Db 541 CGATCAAAATACAAATTAATTAATGAGACTAGAAATCCAGATGAGATGACTCTAGACAGATA 600
Qy 601 TACACAGCTAAGAAATTTTGAACAAGAGTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 660
Db 601 TACACAGCTAAGAAATTTTGAACAAGAGTCAAAAATTAATTAATTAATTAATTAATTAATTAAT 660
Qy 661 TATGATATTCAGTTAGGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 720
Db 661 TATGATATTCAGTTAGGATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 720
Qy 721 TGTATTTGTTTACCAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Db 721 TGTATTTGTTTACCAGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 780
Qy 781 AACTGTTTATGTTTAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
Db 781 AACTGTTTATGTTTAACTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 840
Qy 841 TACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Db 841 TACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 900
Qy 901 TATGTTAAGTCTCAAAATTTTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Db 901 TATGTTAAGTCTCAAAATTTTCTCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 960
Qy 961 CTTTGAAGGGTATTAAGTCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Db 961 CTTTGAAGGGTATTAAGTCTCACTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1020
Qy 1021 TCTGTCCTTAAGATCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Db 1021 TCTGTCCTTAAGATCTTAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1080
Qy 1081 GAGATCCCATCTAGCGTTTCAAGTGTGCTTCCGTCGCAACTTTGGCGGTTGTTGAT 1140
Db 1081 GAGATCCCATCTAGCGTTTCAAGTGTGCTTCCGTCGCAACTTTGGCGGTTGTTGAT 1140
Qy 1141 TTTTTCCTTAATGCTGTTTGAATAATTTCTCAAGATGAGATGATGATGATGATGATGATGATGAT 1200
Db 1141 TTTTTCCTTAATGCTGTTTGAATAATTTCTCAAGATGAGATGATGATGATGATGATGATGATGAT 1200
Qy 1201 AATATTCGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG 1260
Db 1201 AATATTCGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAG 1260
Qy 1261 ACTTAAATGGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1320
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Qy 1321 AATCAAG 1380
Db 1321 AATCAAG 1380
Qy 1381 CCCATATCTTTTACTTCCAAAGAAATCAATTCACAGAGAAATCTGTCTGATC 1440
Db 1381 CCCATATCTTTTACTTCCAAAGAAATCAATTCACAGAGAAATCTGTCTGATC 1440
Qy 1441 ACTTTCATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
Db 1441 ACTTTCATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
Qy 1501 TCGATTAATTTGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Db 1501 TCGATTAATTTGGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
Qy 1561 CTCCTTCGCTTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
Db 1561 CTCCTTCGCTTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
Qy 1621 CATTCCTTAATCAATTTTATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
Db 1621 CATTCCTTAATCAATTTTATATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1680
Qy 1681 GGTATTAAGGCAATTAATGCTTCTAGTCAAGAGAAATTTTGTATGATTAACATCTG 1740
Db 1681 GGTATTAAGGCAATTAATGCTTCTAGTCAAGAGAAATTTTGTATGATTAACATCTG 1740
Qy 1741 GGAATAAATCCAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
Db 1741 GGAATAAATCCAGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1800
Qy 1801 TTAATAAAGGTTTCTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTT 1860
Db 1801 TTAATAAAGGTTTCTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTT 1860
Qy 1861 ATTAACCTTGAATCGAAATTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
Db 1861 ATTAACCTTGAATCGAAATTCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
Qy 1921 TTAATAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGG 1980
Db 1921 TTAATAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGGTTTAAAGG 1980
Qy 1981 TTAACCAATGAATGTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
Db 1981 TTAACCAATGAATGTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2040
Qy 2041 TTTAACCGTCCATCCAGATTTGATTAATGAAGCAAAATCTGAAAACATTTTCTG 2100
Db 2041 TTTAACCGTCCATCCAGATTTGATTAATGAAGCAAAATCTGAAAACATTTTCTG 2100
Qy 2101 AATCTGTTTAAATCTCTCTGCTGATCTTGCAGGCAATTTGACCAAGCATTAATCA 2160
Db 2101 AATCTGTTTAAATCTCTCTGCTGATCTTGCAGGCAATTTGACCAAGCATTAATCA 2160
Qy 2161 TTGAAGCAAAATATCCACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Db 2161 TTGAAGCAAAATATCCACAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Qy 2221 CTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2280
Db 2221 CTTTGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2280
Qy 2281 TAAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2340
Db 2281 TAAATTAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2340
Qy 2341 ACCATCTTCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2400
Db 2341 ACCATCTTCAACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2400
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Db 2401 AAAAAATGCAAAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2460

QY 2461 TCTTACGAAAACGGCCGAGAGGTCTTATCTACATTACAGCTGGTGTGACAG 2520
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 QY 2521 ACATCATAGGGCCCTACGTATATTGAGCTTTACTGTACGTAAAGCTTTAACAATCTAGT 2580
 DB 2521 ACATCATAGGGCCCTACGTATATTGAGCTTTACTGTACGTAAAGCTTTAACAATCTAGT 2580
 QY 2581 TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTAATATATACAAATCTACTA 2640
 DB 2581 TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTAATATATACAAATCTACTA 2640
 QY 2641 GTACTAATATACGTACGTATACATCGCTTTTGGCAATTTCTAAATCTAATCTATCAA 2700
 DB 2641 GTACTAATATACGTACGTATACATCGCTTTTGGCAATTTCTAAATCTAATCTAATCAA 2700
 QY 2701 CAAACTTGAATGTTGTTGTAATTTATCTTAAACCAAGTTTGAATTGTGCAATTGGG 2760
 DB 2701 CAAACTTGAATGTTGTTGTAATTTATCTTAAACCAAGTTTGAATTGTGCAATTGGG 2760
 QY 2761 AGCTACACTCTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAAGT 2820
 DB 2761 AGCTACACTCTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAAGT 2820
 QY 2821 ATTTAAACCAACAAATTTTAAATTTGTTGCTGAAGGTACAAATGTCAATATATAGA 2880
 DB 2821 ATTTAAACCAACAAATTTTAAATTTGTTGCTGAAGGTACAAATGTCAATATATAGA 2880
 QY 2881 CAGCATGTTATATCAATATATGTTGATGTTATTTGAAATCAATATATATAGAAATTA 2940
 DB 2881 CAGCATGTTATATCAATATATGTTGATGTTATTTGAAATCAATATATATAGAAATTA 2940
 QY 2941 GCGACTCACTGTTTAAATGTTTGAAGATATATATATATATATATATATATATATAT 3000
 DB 2941 GCGACTCACTGTTTAAATGTTTGAAGATATATATATATATATATATATATATATAT 3000
 QY 3001 CAGAAGCTATATATGTCGGGTCAATTAGACCGGTGACCAAAAGTTTGTCTGTAATTTTAC 3060
 DB 3001 CAGAAGCTATATATGTCGGGTCAATTAGACCGGTGACCAAAAGTTTGTCTGTAATTTTAC 3060
 QY 3061 GGTGCGATTAAGAAATTTTGAATCTTCACTTTTATGAACTCTGTAATGTTT 3120
 DB 3061 GGTGCGATTAAGAAATTTTGAATCTTCACTTTTATGAACTCTGTAATGTTT 3120
 QY 3121 TGTGGAATTAATATATGTAATCTGTAATTTTGTCTAATATATATATATATATATAT 3180
 DB 3121 TGTGGAATTAATATATGTAATCTGTAATTTTGTCTAATATATATATATATATATAT 3180
 QY 3181 CGATTAAGAAACCTCTTTTATTTAATTTGATTTAAACCTTTTGTGTTGAAATGACT 3240
 DB 3181 CGATTAAGAAACCTCTTTTATTTAATTTGATTTAAACCTTTTGTGTTGAAATGACT 3240
 QY 3241 CATACCAAGTTTAAAGTTTGAATGTAATCAATTTAAGAAATGTTTGGAGGCGTTC 3300
 DB 3241 CATACCAAGTTTAAAGTTTGAATGTAATCAATTTAAGAAATGTTTGGAGGCGTTC 3300
 QY 3301 GAGTGTCTCAACACATGTAACCACTGTAATGAGGTTTATATATATATATATATATAT 3360
 DB 3301 GAGTGTCTCAACACATGTAACCACTGTAATGAGGTTTATATATATATATATATATAT 3360
 QY 3361 TTTCCAAATGCTTTTAAATTAATGAACCACTTAATTTCTTTTAAATTAAGTTAAGAT 3420
 DB 3361 TTTCCAAATGCTTTTAAATTAATGAACCACTTAATTTCTTTTAAATTAAGTTAAGAT 3420
 QY 3421 CTGGAATTTCTGTTGATTTTAAACCAAGTTTCAATTTCTTTAGACAAATATATATAT 3480
 DB 3421 CTGGAATTTCTGTTGATTTTAAACCAAGTTTCAATTTCTTTAGACAAATATATATAT 3480
 QY 3481 AAAAGTTTCAATTTTAAAGATCTAAATTTTGAAGTTCAAGATTTTAAATGATAGCT 3540
 DB 3481 AAAAGTTTCAATTTTAAAGATCTAAATTTTGAAGTTCAAGATTTTAAATGATAGCT 3540

QY 3541 GAAAGTTATGAATGATTGCAAGTTTGCAACAGAAATGCTGATGATATATCAAAA 3600
 DB 3541 GAAAGTTATGAATGATTGCAAGTTTGCAACAGAAATGCTGATGATATATCAAAA 3600
 QY 3601 CATGATCAAAATTAATATATGTCGTTAGCAAGAAACGATTGAATTAACAGAAAT 3660
 DB 3601 CATGATCAAAATTAATATATGTCGTTAGCAAGAAACGATTGAATTAACAGAAAT 3660
 QY 3661 CGTTAACCACTTAAATCTTGAATATTTTGTAGTAAATTTCTGTAGAGAGAGG 3720
 DB 3661 CGTTAACCACTTAAATCTTGAATATTTTGTAGTAAATTTCTGTAGAGAGAGG 3720
 QY 3721 TATCATATCTTACAAAAAATCTCATTCAGATTAATATATATATATATATATATAT 3780
 DB 3721 TATCATATCTTACAAAAAATCTCATTCAGATTAATATATATATATATATATATAT 3780
 QY 3781 AGTATGTTTGTGTCATCATGTTGTAATGTAATGTAATGTAATGTAATGTAATG 3840
 DB 3781 AGTATGTTTGTGTCATCATGTTGTAATGTAATGTAATGTAATGTAATGTAATG 3840
 QY 3841 TTTTAAATGTTTCAAAAGCTTTTCAAAATTAATTAATTAATTAATTAATTAATTA 3900
 DB 3841 TTTTAAATGTTTCAAAAGCTTTTCAAAATTAATTAATTAATTAATTAATTAATTA 3900
 QY 3901 CTAAAGCCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3960
 DB 3901 CTAAAGCCGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3960
 QY 3961 AGATCCCAAGGATTCAAACAGCAAAATTTGCTGTTGCTCTCTCTATATATATAT 4020
 DB 3961 AGATCCCAAGGATTCAAACAGCAAAATTTGCTGTTGCTCTCTCTATATATATAT 4020
 QY 4021 CTCTCAAAACCTCTCTATATCTCTCTAAAGCCCTCTCTCTCTCTCTCTCTCTCT 4080
 DB 4021 CTCTCAAAACCTCTCTATATCTCTCTAAAGCCCTCTCTCTCTCTCTCTCTCTCT 4080
 QY 4081 CAAAGAAAAACAAAGTTTGAAGAAATGCTGTTGTTGTTGTTGTTGTTGTTGTTG 4140
 DB 4081 CAAAGAAAAACAAAGTTTGAAGAAATGCTGTTGTTGTTGTTGTTGTTGTTGTTG 4140
 QY 4141 TTTAGCTTACTCTGAGAGATTTATTAAGAAAGATGATGATGATGATGATGATGAT 4200
 DB 4141 TTTAGCTTACTCTGAGAGATTTATTAAGAAAGATGATGATGATGATGATGATGAT 4200
 QY 4201 AGAAGACAGAAACCAAAAGAAAGCC 4228
 DB 4201 AGAAGACAGAAACCAAAAGAAAGCC 4228

RESULT 2
 US-10-059-911-3
 ; Sequence 3, Application US/10059911
 ; Publication No. US20030159180A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Fischer, Robert L.
 ; APPLICANT: Mizukami, Yukiko
 ; TITLE OF INVENTION: Methods for Altering Organ Mass in Plants
 ; FILE REFERENCE: 023070-090730US
 ; CURRENT APPLICATION NUMBER: US/10/059, 911
 ; NUMBER OF SEQ ID NOS: 42
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 4228
 ; TYPE: DNA
 ; ORGANISM: Arabidopsis thaliana
 ; FEATURES:
 ; OTHER INFORMATION: AINTEGUMENTA (ANT) promoter, 5'-upstream sequence
 ; US-10-059-911-3

Query Match 99.4%; Score 4203.4; DB 6; Length 4228;

Beat Local Similarity 99.9%; Pred. No. 0;
Matches 4226; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

[illegible]

Db	1021	1CTGCTCCAAAGATATATCTACAGCGCTCTCGCCTGTGAATPAGAGAAATTAATGAATGA	1080
OY	1081	GAGATCCCATCTAGCGTTTCACGTTTGCGTTCTCCGTGCAACTTTGGCGGTTGTGACT	1140
Db	1081	GAGATCCCATCTAGCGTTTCACGTTTGCGTTCTCCGTGCAACTTTGGCGGTTGTGACT	1140
OY	1141	TTTTTTCCTAATGCTGGTTGTGACTAAATTTCTGAGTGGAGAGTGATCAAGAAACT	1200
Db	1141	TTTTTTCCTAATGCTGGTTGTGACTAAATTTCTGAGTGGAGAGTGATCAAGAAACT	1200
OY	1201	AATATTCGAAAAGAGAAAAGAAAAAGCAAGAAAATATTTGCAAAAAGACATAATATGAC	1260
Db	1201	AATATTCGAAAAGAGAAAAGAAAAAGCAAGAAAATATTTGCAAAAAGACATAATATGAC	1260
OY	1261	ACTAAATTTGGATTATTTAAATAATGGTATATATGTTTGGTGAATTTATATCATTTACAA	1320
Db	1261	ACTAAATTTGGATTATTTAAATAATGGTATATATGTTTGGTGAATTTATATCATTTACAA	1320
OY	1321	AATCAAAAGAGAGAGAGGGAAGCTCTTCGCGCTTATGATTTCCCTCCCAACAATGCT	1380
Db	1321	AATCAAAAGAGAGAGAGGGAAGCTCTTCGCGCTTATGATTTCCCTCCCAACAATGCT	1380
OY	1381	CCCACTATCTTTTATTTCTTCCAACAAAATCATTCACAGAGAAATCTGTCTCGGATC	1440
Db	1381	CCCACTATCTTTTATTTCTTCCAACAAAATCATTCACAGAGAAATCTGTCTCGGATC	1440
OY	1441	ACTTTCATGCAAAATTAACCTAAATTTTGGTATATTTTGTCAAGTTTGTGCTGTTTAAG	1500
Db	1441	ACTTTCATGCAAAATTAACCTAAATTTTGGTATATTTTGTCAAGTTTGTGCTGTTTAAG	1500
OY	1501	TGCAATATTTGGTATATCTATATGTGTGGATATACATCCAGCTAATCATTAATTTGAT	1560
Db	1501	TGCAATATTTGGTATATCTATATGTGTGGATATACATCCAGCTAATCATTAATTTGAT	1560
OY	1561	CTCCCTCGCTTATCAATRAAATTTACACACATTTAGCTAATCAAGCTAATRAAATTTACACA	1620
Db	1561	CTCCCTCGCTTATCAATRAAATTTACACACATTTAGCTAATCAAGCTAATRAAATTTACACA	1620
OY	1621	CATTCTCTTATCAATTTTATATGGTATTAATTAACAACGACTATAGCTACAGAGTT	1680
Db	1621	CATTCTCTTATCAATTTTATATGGTATTAATTAACAACAACGACTATAGCTACAGAGTT	1680
OY	1681	GGATTTAAGGCATTAATTTGCTTCTAAGTCGAAGAAATTTTGTGTATGATACTCGTG	1740
Db	1681	GGATTTAAGGCATTAATTTGCTTCTAAGTCGAAGAAATTTTGTGTATGATACTCGTG	1740
OY	1741	GGAAAAAATCCAGCTAATATGCTCATTTAAAGATTAATGATTTAATGCTTTAATCA	1800
Db	1741	GGAAAAAATCCAGCTAATATGCTCATTTAAAGATTAATGATTTAATGCTTTAATCA	1800
OY	1801	TTAAATTAAGGTTTGTCTTTTAAAGGTTTACCAACGCTTAATTCATCATTTAGAGAAAT	1860
Db	1801	TTAAATTAAGGTTTGTCTTTTAAAGGTTTACCAACGCTTAATTCATCATTTAGAGAAAT	1860
OY	1861	ATTAACCTTTGATCGAAATTCAAAAATCTTTTAAACATTAAGAAATTTTCAGCAATTT	1920
Db	1861	ATTAACCTTTGATCGAAATTCAAAAATCTTTTAAACATTAAGAAATTTTCAGCAATTT	1920
OY	1921	TTAAATTAAGGTCATTTATTTGGGTCAATTAATATGTTTCCAGTAAGTTTGGAGGT	1980
Db	1921	TTAAATTAAGGTCATTTATTTGGGTCAATTAATATGTTTCCAGTAAGTTTGGAGGT	1980
OY	1981	TTAACCATGTAATGTTTTTGATTTTAAAAAAACATAAATTTTCTAGTAATTTACACTT	2040
Db	1981	TTAACCATGTAATGTTTTTGATTTTAAAAAAACATAAATTTTCTAGTAATTTACACTT	2040
OY	2041	TTTAACCGTCATCCAGATTTGTAAATAGTGAACAATCTGAACAACTTTTTTTTCTTG	2100
Db	2041	TTTAACCGTCATCCAGATTTGTAAATAGTGAACAATCTGAACAACTTTTTTTTCTTG	2100
OY	2101	AATCTGTGTTTAAATCTCTCTGCTGCAATCTTGAGAGGACTTTGACCAAGACTATACATA	2160
Db	2101	AATCTGTGTTTAAATCTCTCTGCTGCAATCTTGAGAGGACTTTGACCAAGACTATACATA	2160

QY 2161 TTGAAGCAAAATATCCAGGAGTATAGGTTAGATCCCAATTCAATATCTTTGT 2220
 Db 2161 TTGAAGCAAAATATCCAGGAGTATAGGTTAGATCCCAATTCAATATCTTTGT 2220
 QY 2221 CTTTGTATTTATGAAAAACAATATTTATCGAGAAAAAAACGTTCTTCTAGTGTGA 2280
 Db 2221 CTTTGTATTTATGAAAAACAATATTTATCGAGAAAAAAACGTTCTTCTAGTGTGA 2280
 QY 2281 TAAATATAGATATATTAACAAATTTAATCTAGTAAATGATTTACTTCTTCAAACTT 2340
 Db 2281 TAAATATAGATATATTAACAAATTTAATCTAGTAAATGATTTACTTCTTCAAACTT 2340
 QY 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTATTTTACTTAAATCTTCCACTA 2400
 Db 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTATTTTACTTAAATCTTCCACTA 2400
 QY 2401 AAAAAATGCAAAAGAAAGATATATATTTAAGTCAAAATTAATAAGATGATGGTAT 2460
 Db 2401 AAAAAATGCAAAAGAAAGATATATATTTAAGTCAAAATTAATAAGATGATGGTAT 2460
 QY 2461 TCTTCAGCAAAACGCGCCGAGAGGTGTCTTATCTTACATTAAGCTGGGTGTGAG 2520
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 QY 2521 ACATCATAGGGCCCTAATATTTAGACTTTTACTGATGATGATGATGATGATGATGAT 2580
 Db 2521 ACATCATAGGGCCCTAATATTTAGACTTTTACTGATGATGATGATGATGATGATGAT 2580
 QY 2581 TAGTCTCATCTGACAAACAAACAAATCCATTCGTAACATATATATACAAATCTACTA 2640
 Db 2581 TAGTCTCATCTGACAAACAAACAAATCCATTCGTAACATATATATACAAATCTACTA 2640
 QY 2641 GTATCATGATTACGCTAGCTATACATGCTTTTTCGCAATTTCTAAATCTAATCTATA 2700
 Db 2641 GTATCATGATTACGCTAGCTATACATGCTTTTTCGCAATTTCTAATCTAATCTATA 2700
 QY 2701 CAAACTGAAATGTTTGTGTTGTAATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
 Db 2701 CAAACTGAAATGTTTGTGTTGTAATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
 QY 2761 AGCTACACTAGTCCCTTTTCCCAAAATATATCTTACATGACCGGTTAAAGT 2820
 Db 2761 AGCTACACTAGTCCCTTTTCCCAAAATATATCTTACATGACCGGTTAAAGT 2820
 QY 2821 ATTAAACCAACAAATTTAATTTGTGCTGAAGTACAAACATGATCAATATATAGA 2880
 Db 2821 ATTAAACCAACAAATTTAATTTGTGCTGAAGTACAAACATGATCAATATATAGA 2880
 QY 2881 CAGCATGTTTATCAAAATATGTTGATGATTTGGAATCAAAATATATATAGAAATTA 2940
 Db 2881 CAGCATGTTTATCAAAATATGTTGATGATTTGGAATCAAAATATATATAGAAATTA 2940
 QY 2941 GCGACTCATGTTTAAATGTTTGAAGATTAAGAAATTAATAAAGAT 2999
 Db 2941 GCGACTCATGTTTAAATGTTTGAAGATTAAGAAATTAATAAAGAT 2999
 QY 2999 GCGACTCATGTTTAAATGTTTGAAGATTAAGAAATTAATAAAGAT 2999
 Db 2999 GCGACTCATGTTTAAATGTTTGAAGATTAAGAAATTAATAAAGAT 2999
 QY 3000 ACAGAGCTATATATGTCGGGCTATTTAGAGCCGTGACCAAAAGTTGCTGATTTCTA 3059
 Db 3000 ACAGAGCTATATATGTCGGGCTATTTAGAGCCGTGACCAAAAGTTGCTGATTTCTA 3059
 QY 3059 CCGGCTGATTAAGAAATTTTGAAGCTTTTCAACCTTTTATGAATCTTGATATGTTT 3119
 Db 3059 CCGGCTGATTAAGAAATTTTGAAGCTTTTCAACCTTTTATGAATCTTGATATGTTT 3119
 QY 3119 TTGTCGATTAATATTTGATTTGTTTCTTAAATGATGATGATGATGATGATGATGAT 3179
 Db 3119 TTGTCGATTAATATTTGATTTGTTTCTTAAATGATGATGATGATGATGATGATGAT 3179
 QY 3179 TTGTCGATTAATATTTGATTTGTTTCTTAAATGATGATGATGATGATGATGATGAT 3179
 Db 3179 TTGTCGATTAATATTTGATTTGTTTCTTAAATGATGATGATGATGATGATGATGAT 3179
 QY 3180 ACGATTAAGAAAGCTTTTATTTATTTATTTGATTTGATTTGATTTGATTTGATTTGAT 3239
 Db 3180 ACGATTAAGAAAGCTTTTATTTATTTATTTGATTTGATTTGATTTGATTTGATTTGAT 3239

QY 3240 TCATACCAAGGTTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3299
 Db 3240 TCATACCAAGGTTAAGTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3299
 QY 3300 CAGATGCTTACCAACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3359
 Db 3300 CAGATGCTTACCAACATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3359
 QY 3360 TTTTCCAAATGCTTTATATTTGAACCACTGATTTTCTTTTATTTATTTAGTTAAGAA 3419
 Db 3360 TTTTCCAAATGCTTTATATTTGAACCACTGATTTTCTTTTATTTATTTAGTTAAGAA 3419
 QY 3420 TCTGAATTTTCTGATATTTTAAACCAAGTTTCTGATTTTCTGATTTTCTGATTTTCTGAT 3479
 Db 3420 TCTGAATTTTCTGATATTTTAAACCAAGTTTCTGATTTTCTGATTTTCTGATTTTCTGAT 3479
 QY 3480 AAAAAATGCAATTTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3539
 Db 3480 AAAAAATGCAATTTAATTAAGATGATGATGATGATGATGATGATGATGATGATGATGAT 3539
 QY 3540 TGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3599
 Db 3540 TGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3599
 QY 3600 ACATGATCAAAATTAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3659
 Db 3600 ACATGATCAAAATTAATTTGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3659
 QY 3660 TCGTTAACCACTTAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3719
 Db 3660 TCGTTAACCACTTAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3719
 QY 3720 GTATCATATCTTACAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3779
 Db 3720 GTATCATATCTTACAAATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 3779
 QY 3780 AAGTATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3839
 Db 3780 AAGTATGTTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 3839
 QY 3840 GTTTTAAATGTTTCAAAAGCTTTTCAAAATTTAAATTAATTAATTAATTAATTAATTAAT 3899
 Db 3840 GTTTTAAATGTTTCAAAAGCTTTTCAAAATTTAAATTAATTAATTAATTAATTAATTAAT 3899
 QY 3900 GCTTAAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
 Db 3900 GCTTAAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
 QY 3960 CAGATCCCAACGATTTCAAAACAGCAATTTGTGCTTGTCTTCTTCTTCTTCTTCTTCTT 4019
 Db 3960 CAGATCCCAACGATTTCAAAACAGCAATTTGTGCTTGTCTTCTTCTTCTTCTTCTTCTT 4019
 QY 4020 CTTCTCAAAACCTCTCTATATCTCTTAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4079
 Db 4020 CTTCTCAAAACCTCTCTATATCTCTTAAAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCT 4079
 QY 4080 ACAAGAAAAACAAGTTTGAAGAAATGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4139
 Db 4080 ACAAGAAAAACAAGTTTGAAGAAATGTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 4139
 QY 4140 TTTTATGCTTACTTCTGAGATTTATGAAGAAAGATGATGATGATGATGATGATGATGATGAT 4199
 Db 4140 TTTTATGCTTACTTCTGAGATTTATGAAGAAAGATGATGATGATGATGATGATGATGATGAT 4199
 QY 4200 AAGAGAGCAAGAAACCAAAAGAAAGC 4228
 Db 4200 AAGAGAGCAAGAAACCAAAAGAAAGC 4228

RESULT 3
 US-10-059-911-1
 ; Sequence 1, Application US/10059911
 ; Publication No. US20030159180A1

Db 3682 AAAAAAAAAATTCMAATTTATACACATATTAACATTAACATTAATTTTCATATTAAT 3623
 Qy 431 TGTCTGAGTGCTGCTGTGCAAGATATCTCGGTATCTTACCTTGAACCTAGAGTGG 490
 Db 3622 TTTTATATTAATTAATTTTTCATTTTATATATTTTCAATTTTATTAATTTTTCACACA 3563
 Qy 491 ATATACATTAACACAGTGATATTTTAAAGACCGTACATTAACACATGTATG-----A 543
 Db 3562 ATATTTTAAACATTAATTTTATTAATTAATTAATTTTCAATTAACATTAATTA 3503
 Qy 544 TCAATATCAAAATTTATATGAGACTAGAAATCCAAAGTAGATGACTTAGACAAATATAC 603
 Db 3502 TCATATTTTATTTTCAACAAAAAAATTTTATATATATATATTAATTAACAAATTA 3443
 Qy 604 ACAGCTAAGATTTGTCAAGAGAGTGCAGAAATATGATTTCAATTAATTAATTAATTAAT 663
 Db 3442 TAATTTTCAACATTTAACAATAATTTTAAATTAATTAATTAATTTTCAATTT 3383
 Qy 664 GGATTTCAATGACGATGATATTAATCAATTAACGAGTATGATACATTAATTTTGT 723
 Db 3382 TTATTTTATATCAATTAATTTTCAATTTTATTTTCAATTAATTAATTTT 3323
 Qy 724 TTTTGTTTTACCGATA-----TAGATGAAATGTGTGTTAAATATGTTT 776
 Db 3322 TTTTTCAAAAATTAACAACAATTAATTAATTAATTTTACATCAATTAATTAATTA 3263
 Qy 777 CTAAATCTGTTTATATGTAATATATATGCTTTCGCAATG-----AAATGAAC 830
 Db 3262 ATATATATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3203
 Qy 831 AAATCTAATTAACAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 890
 Db 3202 AACAAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3143
 Qy 891 CTCAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 950
 Db 3142 ATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3083
 Qy 951 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1010
 Db 3082 AATTCAAATTTTCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3023
 Qy 1011 AAGAGTGTCTGCTGCTAAAGATATGATTAAGCATTAATTAATTAATTAATTAATTAATTA 1070
 Db 3022 TTAAATCAATCAATTTAAATTAATTAATTAATTAATTAATTAATTAATTTTATTTTAC 2963
 Qy 1071 TGAATGATGAGATGCCATCTAGCGTTTCACTGTGGCTCTCCGTCGAACCTTGGCG 1130
 Db 2962 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTTCATTTTCA 2903
 Qy 1131 GTTGTGACTTTTCTTATGTCGTGTTGACTA--ATTTTCTAGAGTGAAGTGT 1187
 Db 2902 AATTTTATTTTTCACAAATTTTTCATTAATTAATTTTCAATTTTATATATTT 2843
 Qy 1188 AATCAAGAAATCTAATTTGCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1247
 Db 2842 TATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2783
 Qy 1248 AGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1307
 Db 2782 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2723
 Qy 1308 TAATCATTAACAAATCAAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1367
 Db 2722 TTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2663
 Qy 1368 CTAAAGAAATCTGCTGCTAATCTTTTCTTACTTCAACAAATTAATTAATTAATTAATTT 1427
 Db 2662 AT-TTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2604
 Qy 1428 CTGCTGCTGATCACTTTCAATGCAAAATTAATTAATTAATTAATTTTGTCAAGTTC 1487
 Db 2603 TTTTTCATTAATTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 2544

Qy 1488 TTGCTGTTTAAAGCATTAATTTGGTAATACTATATGNGGATATACATCCAGCTA 1547
 Db 2543 TTATTTATTAATTAATTAATTTTATTTTATTTTCAATTAATTAATTAATTTTAA 2484
 Qy 1548 ATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1607
 Db 2483 CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2424
 Qy 1608 ATAAATTAACCAATCTCTTAATCAATTTTATATGATTAATTAATTAATTAATTAATTT 1667
 Db 2423 ATATTTTATTTTAAATTTTCAAAAAATTAATTAATTAATTAATTAATTTTAAATTA 2364
 Qy 1668 AGCTACAGAGTGTGATTAAGCAATTAATGCTTCAAGTGAAGAAATTTTGTAT 1727
 Db 2363 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2304
 Qy 1728 GATTAACACTCGTGGGAAAAAATCCAGCTAATATGCTATTTAAAGATTAATTAATTT 1787
 Db 2303 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2244
 Qy 1788 AATGCTTAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTCA 1847
 Db 2243 A-----TTTATTAATTAATTAATTTTATTTTATTTTATTTTATTTTCAATTTT 2190
 Qy 1848 TCATTAAGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 1907
 Db 2189 AATTTTAAATTAATTAATTAATTTTATTTTATTTTATTTTATTTTAAATTAATTA 2130
 Qy 1908 ATTTTCAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTTTCAAGT 1967
 Db 2129 ATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTT 2070
 Qy 1968 AAGTTTGAAGTTTAAACAATGAATGTTTGTGATTTAAATTAATTAATTAATTTCTA 2027
 Db 2069 ATTAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTTTAAATTAATTTTAA 2010
 Qy 2028 GTAATTAACATTTTAAACCGTCATCAATGTAATTAATTAATTAATTAATTAATTT 2087
 Db 2009 ATTTTAAATTAATTAATTAATTAATTAATTAATTAATTTTAAATTAATTTT 1950
 Qy 2088 TTTTTCATTAATTAATTAATTAATTTCTGCTGCAATTAATTAATTAATTTTGAACA 2147
 Db 1949 TTTTATTAATTAATTAATTAATTTTATTTTAAATTTTATTTTAAATTTTAAATTA 1890
 Qy 2148 ACAGCTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTCAACT 2207
 Db 1889 AAAAAATTAATTAATTAATTAATTTTATTTTATTTTATTTTATTTTAAATTA 1830
 Qy 2208 CAATATCTTTTGTCTGTTATTAATTAATTAATTAATTAATTAATTTTATTAATTA 2253
 Db 1829 AATTTTATTTTATTAATTAATTAATTAATTAATTAATTTTAAATTTTATTTTAAAT 1770
 Qy 2254 GAAAAAAGCTTCTCTAGTGTATAGTAATTAATTAATTAATTAATTTTAAATTTTAACTTA 2313
 Db 1769 TTAATTAATTTTATTAATTTTAAATTAATTAATTAATTAATTTTAAATTAATTTTAAAT 1710
 Qy 2314 GTTAATGTA--TTTATTAATTTCAAACTTAATTAATTAATTTTAAATTTTAAATTT 2370
 Db 1709 ATTAATTAATTTTAAATTTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTT 1650
 Qy 2371 TTTATTTTATTAATTAATTAATTTTCAATTAATTAATTAATTTTAAATTTTAAATTT 2430
 Db 1649 TTTTATTAATTTTAAATTTTCAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1590
 Qy 2431 AGTCAAGTAATTAATTAATTAATTAATTTTCAAGCAAAACGCGCCGTAAGGTGC 2490
 Db 1589 AATTAATTAATTAATTAATTAATTTTAAATTAATTTTAAATTTTAAATTTTAAATTTT 1531
 Qy 2491 TTATCTTAATTAATTAATTAATTTTGAAGCAATCAATTAATTAATTTTGAAGCTT 2550
 Db 1530 TTTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAT 1471

Qy	2551	TACTGACGTAAGCTTTAACAATCTAATAGTCTCTGCTACAAACAAACAAATC	2610
Db	1470	TAATTTATTAATAAAAAATTAATTTATTTTTTTTTTAA- - - - -AAAAAATAAAAA	1415
Qy	2611	CAATTCGTAACATATATTAACAAATACTACTAGTACGTACGTAATCATCGCTT	2670
Db	1414	ATTAATAAAAAATTAATCAATTTATTTTATTAATAAAAAATTAATTTTATTAATAAAAAATTA	1355
Qy	2671	TTTCGAAATTCMAACCTAATCTATACAAACAACCTGAAGTGTGTTTGTAATTAATC	2730
Db	1354	AAATTAATTAATTTTATTTTAAATTAATAATTAATTTTATTAATTAATTAATTTTAA	1295
Qy	2731	TTTAACCAAGTTTGAATTCGACTTGGAGCTACCTCTAGTCCCTTTTCCCAA	2790
Db	1294	AAAAAATTAACATTTTATTAATATAT-ATATATCATTAACATTTTTTTTTTATTCAAAAA	1236
Qy	2791	AATATCTCCTTCATCGACCGGTAAAGATTTTAAACCAACAAATTTTAATTTGTCT	2850
Db	1235	AAATTAATTTATTA- TTAATAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTA	1177
Qy	2851	GAAAGTACAAACATGTCACATATATAGACAGCATCGTTTATACAAATAATGTCATG	2910
Db	1176	TAATATTCAAAAATATATTAATTTTAAATTTTCAATATCAAAAAAATAT- -AAAAA	1119
Qy	2911	TTATGGAAATCAATATATATATATATGCAATTAGCACTCAGTCTGTTAATAGTTGGAAGA	2970
Db	1118	CAAAATATTAACATTTTAAACATTTAAAAAACAATTTAAAAAACAATTTTTTTTTAT	1059
Qy	2971	TAAATGAATTAATAAATGAATTCAGAGATACAGACTATATATGCGGTCAATTAGAGC	3030
Db	1058	TTACATATTAATTAATTTCAAAATTTAAAAATTAATAAAAAATTTTAAAAATATATATTTT	999
Qy	3031	CGTACCAAAAGTTTCGTGTAATTTCTACGTCGTCAAGAATTTTGACTTTCT	3090
Db	998	AAAAAATTAATATATATATTTTATTCATTTAATTAATAAAAAATTAATTTTAA	939
Qy	3091	TCACCTTTATGAACTTCTGATAGTTTTGTCCGATTATATATTTGATTCGATAT	3150
Db	938	AAAAATTTATTCAAAAACAACAAAATTAATTAATAATTTTAATTAATTAACAAAT	879
Qy	3151	TTTGTTCATTAATGATACGTAATTCAGATAGAAGCTCTTTTATTTAATTT	3210
Db	878	TTTTATACATAAAAAATAAAAAACAATTTTTTTTAAATAAAAATTTTAAATAT	819
Qy	3211	GATTTAAAACTTTGTTTGGAAATGACTCATACCAAGTTAAGTTGATGCTATCC	3270
Db	818	CATTATTAATTTATTTTAAATTAATTAATTAATTAATTAATTTTAAATTTTAAATTT	759
Qy	3271	AAATTAACAATAATGTTTCGAGAGTGGTCGAGTCTTACACACATGCTAACCATCTGT	3330
Db	758	TAATAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATAA	699
Qy	3331	ATGGTTATATATAGTTTTTTTCTCTTTTCCATGCTTTATTAATGACACACT	3390
Db	698	AAATTTTATTAATTAATTAATTTTTTTTTTTTTTAAATTAATTAATTAATAAT	639
Qy	3391	AAATTTCTTTTAAATAGGTTAAGATCTGAATTTCTGTGATTTTAAACCAAG	3450
Db	638	TTTAAAAAATTTTAAATTTATTAATATTTTTTTTAAATTAATTAATTAATTAAT	579
Qy	3451	TTTTCAATCTCTTGACACAAAAAAGGTTTCAATTTATTAAGATCTAA	3510
Db	578	AAATTTAATAAACAATTAATTAATTAATTAATTAATTTTAAATTAATTAATTAAT	519
Qy	3511	TTTTTGAAGTCAAGGTTAATGATAGCTGAAAAGTTATGATGATTCGAATTCGA	3570
Db	518	ATATTAATTAAT-ATTTAATAATTTATTTTTTTTTTAAATTAATTAATTTTAA	460
Qy	3571	CAGAAATGCTGATGCTGATCATTCAAAAACATGCAAAATTAATTAATTTGCTGTC	3630
Db	459	TTAATTTTTTTTTTATTAATTTTAAAAAATAAATAATTAATTAATTAATTAATTAAT	400
Qy	3631	AAAGAAACGATTAATAATAACAAACATCGTTAACCTTAAATCTTAGATATAT	3690

Db 399 AAATTTTAAATTAAATTAATTTTATTTCAATTTTTTTTTTTTTTAAATTAATTAATTTT 340

Qy 3691 TTGTAGCATTAATTTCTGTAAAGAGAGGTATCATCTTACAAAAAACTCATTTTC 3750

Db 339 ATTATATTTTATTAATTAATTTTTTTTAAAAATAATTTTAAAAAAATTTTTTTT 280

Qy 3751 AGATTAATAATGTGTGCCAATCGTTACCAAGTATGTTTT--GGTGTATCAGTTGTA 3807

Db 279 TATTAATAATTAATTTTAAAAATTTTTTAAATTTTTTAAAAATTTTAAATAATTTT 220

Qy 3808 TTGTACTCGCTCTTAGCCATATAGTCTTAAGTTTAAATGTTTCAAGAATTACAA 3867

Db 219 TTTAAAAATTATTAATATTAATTTAAATTTAATTTAAAAAAATATATAAAAATTAATTA 160

Qy 3868 AAATTAATAATAATAAGTGGAAATTGTAGGCGTAAACGAAAAATAAAAATAATAATA 3927

Db 159 AAAATTAATAATAATAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 100

Qy 3928 AAAGTAAAGAA 3938

Db 99 AAATATAAAAA 89

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RESULT 6
US-10-473-126-386
; Sequence 386, Application US/10473126
; Publication No. US20040234973A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Methods and nucleic acids for the analysis of hematopoietic cell
; TITLE OF INVENTION: proliferative disorders
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/473,126
; CURRENT FILING DATE: 2003-09-26
; NUMBER OF SEQ ID NOS: 1258
; SEQ ID NO 386
; LENGTH: 8056
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-473-126-386

Query Match          2.5%; Score 107.8; DB 8; Length 8056;
Best Local Similarity 43.4%; Pred. No. 9.6e-09;
Matches 1170; Conservative 0; Mismatches 1477; Indels 46; Gaps 13;

QY      1505 TTATTGGTAATACCTATATGTGCGATATACACATCCAGCTAATCAATAATTGATTCGCC 1564
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1868 TAAATTAATTATTTTATTTTTTATTTATTTAAAAATTTATATATAAAAAAAAAATPA 1927

QY      1565 TTCGTGTTACAATAAATTAACACCATTAGCTAATCAGCTAATTAATTAACACACAT 1624
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1928 TTAATTTAATAATAATAATAAAAAAAAAATATATATTTTAAAATATAAATATTAATTAAT 1987

QY      1625 CTCTTATCAATTTTTATATNGTATTAATAATAAACACACGACTATAGGTACAGAGTTGTA 1684
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      1988 TTATATTAAAAATTTAATTAATAATTT---TAAATATATTTAAATATAAATATTTTAAAT 2044

QY      1685 TTAAGCATTAATTGCTCTTACGTGAAGAATTTTTTGTATGATAAACACTCGTGGCAA 1744
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2045 ATTTTATATTTTAAAAAAATTTTATTAATAAATATTTTAAATATTAATAATAATAATTA 2104

QY      1745 AAAAAATCCAGCCTAATATGCTCATTTTAAGATTAATGATTAAATGCTTATATCATTTA 1804
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2105 AATTATTTAATATTAATTTTAAATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2162

QY      1805 AATTAAGATTTTGGCTTTTAAAGTTAACACCGCTTAATCATCATTAAGAGAAATATTA 1864
        ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      2163 AAAAAAATTAATATTTTATTTAATAAATTTAATAAATAAATGAAAAAAAAAATTAATAAATA 2222

QY      1865 ACTTGATGAAATTCAAAATATCTTTTTTAACACATAGAAAAATTTTCAGCATTTTTTA 1924

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[illegible]

D	b	3252	IGTATTTGCTGTTGTTATTTTGGAAAAAATAATATGTAATGTAATAAATG	3351
O	y	3000	-ACAGAGCTATATATGTCGGGTCAATTAGACCGGTGACCAAAAGTTTCGTATATTTCT	3058
D	b	3352	AATATAATTTGAAATGATGTTAAATAATAAATGAAATGAAATGATATTTGAAATTTT	3411
O	y	3059	ACGGTCGGTCAATGAAGAAATTTTGACCTTTCTCACCTTTTATGAACTTCTGATAGTT	3118
D	b	3412	TTTAAATATTTTGTGTTAAATGTCGAAATATATATTTGTTTATATATATTAATATAA	3472
O	y	3119	TTTGGCGATATATATATTTGTAATCGTATATTTTGTGTTCTAATTAATGATACGTAAT	3178
D	b	3472	AATTTTTTTTTTGTGTTAATTAATAATATGATATATGAAATGTAATTAATATAT	3531
O	y	3179	CACGATAGAAGAACCTCTTTTATTTATTTTGAATTTGAACTTTTGTGTTTGGAAATGA	3238
D	b	3532	TTTATTTATATTAATATATGTTTAAATAATATGTTGCGAAAAATATTAATAATGAAATAT	3591
O	y	3239	CTCATPACAAAGTTTAAAGTTGATGTAACCAATTTACAAAATGTTTCAGAGTGGT	3296
D	b	3592	ATAA-----AATGAAATAATTTTAAATTAATAAATAATTTATATGAAATTT	3649
O	y	3299	TCGAGTGCCTACACCACTGCTACCACTCGTATGCGTTATATATAGTTTTTTCTTC	3356
D	b	3641	AATGTAATGTAATATATGTTTAAATTTTGAATTTTTTTTTTATTAATAATATTTTTTTA	3700
O	y	3359	TTTTTCCAACTCTTTTATTTAATTTGAACCACTCTTAATTTCTTTTTTAAATAGGTATGA	3418
D	b	3701	AAATGATTAATATATTTTAATTAATAAATAAATAAATAATTTTTTTATTTTTTTAAATA	3760
O	y	3419	ATCTGAATTTTCTGTGATTTTAAACCAAGTTTCATTTCTTCTAGCACAAAAAAA	3478
D	b	3761	ATTTTATATAT-----TTGAAATAGTATTTATATTAATTAATGTTTATATTTGTTG	3814
O	y	3479	AAAAAAGTTTTCATTTATTTAAGAAATCTAATTTTTTGAGTCTCAAGGTTTATGATATG	3538
D	b	3815	AATTTTGTTTTTTGGAAATTTTGAATAATGTAATAATTTGAAATATGATTTGTATATGAATA	3874
O	y	3539	CTGAATAAGTATGATGATTTGCAAGTTTGCAACGAATGTCGATGATATCAATA	3598
D	b	3875	AAAAATTTGAATTTGAT--TTTATGTTTATTAATAATTTTGCAAAAAATATATATATAAAT	3932
O	y	3599	AACATGCATCAAAATTAATATTTCTGCTTAGCAAGAAACGATTGAATTAACAGAAACA	3658
D	b	3933	ATATATTTATTAATTTTAAATATATAATTTTATGTTATTTAATAAAAAAATGAAATAAT	3992
O	y	3659	ATCGTTAACCACTTAAATAATTTTGAAATATTTTGATGATGTAATTTCTGTAAAGAGAGA	3718
D	b	3993	GTTTAAATGAAATGATTAATGTAATATTTTGTGTGTAATTTTGTGTAT-----G	4048
O	y	3719	GGTATCATCTTACAAAAAATACTCATTCAGATTAATAATATGTTGTCGAATCGTTAC	3778
D	b	4049	ATTATTTTTTATTTGTGTTTAAATGTTTTTTTATTTTTTGTGATATGTAATTTTTTTTA	4108
O	y	3779	CAAGTATGTTTGTGCTGTCATCAGTTGTAATTTGTAATCTGCTCTTAGCAATATAGTTCTA	3838
D	b	4109	ATTTTTTTTTTTATATGTTTTTGTTTTATTTTAAATATATTTTGTGTAATATTTTTT	4168
O	y	3839	AGTTTAAATGTTTCAAAGACTTTACAAAATTAATAATATAGGTGAATTTGTAG	3898
D	b	4169	TTATTTAATTTTTTTTTTTTTTTTGTGATTTAAATATATGAAATTTATTTGGAATTTTAA	4228
O	y	3899	GGCTTAAAGCAAAATTAATAATTAATAATGAAGAAACGCTTTCTCAATPADAAC	3958
D	b	4229	TATTTTTTTTATTAATATTAATAAATAATATTAATAATATTAATAATTTTTTTTTTGTATT	4288
O	y	3959	ACAGATCCCAACGGATTTCAAAACAGCAATTTGTGCTTGTCTCTCTATATATATATA	4018
D	b	4289	TAAATATGAATAATATATATGTTAAATAATTT--TGTAATGATATTTTTTTGAAATATTTT	4347
O	y	4019	TCTCTCAAAAACCTCTCTCTATATCTCTCTAAAGCCCCCTTCTGTGTTTCTCTACCGC	4078
D	b	4348	TATTTAAATAATATATATTTTAAATATGTTTAAATAATTTGTTTGTGTAATTTTTTTTGT	4407

OY	2803	ACATGACGCGGTTAAAGTATTTAAACAAACAATTTTAAATTTGGTCGAAGGTAACAAC	2865
Db	1224	TATTTAAAAAATTTAAATTTAAATTAATTTAAATTTTAAATTTTAAATTAATTAATTAATCGAAA	11655
OY	2863	ATGTCAATATATAGAGACAGCAGTCGTTATATCAATATATGTCAGATGTATTTGGAAATC	29222
Db	1164	ATATATTTAATTTTAAATTTTTCGAATATCGAABAAAAATTTTAAAAACG-ATATATTAAC	11060
OY	2923	AAATATTAATACGAATTACGACTCATCTTGTTTAATAGTTTGGAGATTAAGAAATAA	29823
Db	1105	TTTTTAAAAAGTTAAAAAAGAAATTAACGAATTTTAAAAAGAAATTTTAAATTTTACGTAATTA	10468
OY	2983	AAATGAATTCAAAGATACAGAGTAATATATCTGGGTCATTTAAGCCGTGACCAAG	30423
Db	1045	TTTCGAAATTTAAAAATTAATTAATTAATTTTAAAAATTAATTTTAAAAAATTAATA	986
OY	3043	TTTCGTGTAATTTCTACGTCGTCATTAAGAAATTTTGGACCTTTCTTCACCTTTAT	31020
Db	985	TATATATTTTATTCGTTTAATTAATTAATTAATTAATTAATTTTAAAAAATTTATATTC	926
OY	3103	GAACTTCGTATAGTTTGTTCGATTAATATATTTGTAATTTTGTTCATA	31623
Db	925	GAAAAACGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	866
OY	3163	TAAATATACGTAAATTCACGATTAAGAAAGACTTTTATTTAATTTGAATTTAAACTT	32222
Db	865	AAAAAATTAATAAAAAACGATTTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTT	806
OY	3223	TTGTTTTGGAATATGACTATCACAGGTTAAAGTTGATGATCCAAATTTACAAA	32823
Db	805	ATTTTAATTAATTAATTAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTA	746
OY	3283	TGTTTCGAGAGTCGTTGAGTGTCTACACACATCGTACCAACTCGTATGGGTTATTA	33422
Db	745	TTTAATTAATTAATTAATTAATTTAAATTTTAAATTAATTAATTAATTAATTAATTTT	686
OY	3343	TTAGGTTTTTTCTCTTTTCCATATCTTATATTTGAACACTTAATTTCTTTT	34020
Db	685	TTATTAATTTTAAAAATTTTAAAAATTTTAAATTAATTTTAAAAAATTTT	626
OY	3403	TTAAATTAAGTTAAGATCTTGAAATTTTCTGTGATTTTAAACAAAGTTTCAATCTT	34623
Db	625	AAAAATTAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA	566
OY	3463	CTTAGACAAAAAAGTTTTTCAATTAATTAAGATCTAAATTTTGTGAGTTC	35222
Db	565	CGTTATATTAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT	506
OY	3523	AAGAGTTTAATGATAGCTGAAAGTTATGAATGATGCAAGTTGGCAACAGATGCTGA	35822
Db	505	TATTAATTTTAAATTTTAAATTAATTAATTAATTTTAAAAATTTTAAAAATTTT	446
OY	3583	TGTAGTACATATCAAAAAACATGCAATCAAAATTAATATCTGTAGACAGAAAGCAT	36422
Db	445	TTATTTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAATAT	386
OY	3643	TGAATTAACAAGAAACATCGTTAACCACTTAAAAATCTTAGAATTAATTTGATGATTA	37022
Db	385	AAATATTTTATTTGTTTTTTTTTTTTTTTAAATTAATTAATTTTAAATTTTAAATTA	326
OY	3703	TTTTCTGTAGAGAGAGGTATCATTTCAAAAAAAGCACTCATTTGATTAATTAAT	37623
Db	325	ATTAATTTTAAAAAATTAATTTTAAAAAATTAATTTTAAAAATTTTAAAAATTT	266
OY	3763	GTTGTCCAATGTTACCAAGTATTTTGTGTCATCAGTGTGATTTGTAATCTGTCTCT	38222
Db	265	TAAAAATTTTAAAAATTTTAAATTTTAAAAATTTTAAAAATTTTAAAAATTTATAT	206
OY	3823	TAGCCATATAGTTCTAAAGTTTAAATATGTTTCAAGAATTTACAAAAATTAATTAATAT	38822
Db	205	AAATATTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	146
OY	3883	AAGGTGAATTTTATGGCTTAAAGCGAAAAATTAATTAATTAATTAATTAATTAATTAATTA	39422

[illegible]

Db 946 ATAAATTTTATTTTATTTTAAAGAAATAAATATATATATATTTTAAATAA 1005
Qy 1738 GTGGGAAAAATTCAGCCCTAATATGCTCTTTAAAGATATATGATTTAAAGCTTTAA 1797
Db 1006 ATTAATTTTAAATATTTTATTTTATTTTAAATTTTGAATTTTAATTAATTAATTAATTA 1065
Qy 1798 TCATTAATAATTAAGGTTTTCCTTTTAAAGTTTACACCGCTTAATTCATTCATAGAG 1857
Db 1066 AAATTCGTTTAAATCGTTTTCCTTTTAAAGCTTTTAAACGTTATATATTCGTTTAA 1125
Qy 1858 AATATTAATCTTGATCGAAATTCGAAATATCTTTTAAACATTAAGAAATTTTCAGCA 1917
Db 1126 A-----TATTTTTCGATTCGAAATTTAAATATATATTTTCGATATATTA 1180
Qy 1918 TTTTAAATTAAGGATTAATTTGGGTTTCATTAATATGTTTCCACGTAAGTTTGA 1977
Db 1181 TTTATTTTAAATTTTAAATTAATTTTAAATTTTAAATTAATTAATTAATTTTAAATTTTAA 1240
Qy 1978 GGT-----TAACCATGATGTTTGTGATTTTAAATTAATTAATTTTCTAGTA 2031
Db 1241 GAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAATTA 1300
Qy 2032 TTACATTTTAAACCGTCCATCCAGTTGTAATTAAGTGAATCTGAATCAATTTT 2091
Db 1301 TTATTAATTAATTAATTAATTAATTTTAAATTAATTAATTAATTTTAAATTTTAAAT 1360
Qy 2092 TTTTCTGATCTGTTTAAATTTCTCTGCTGCAATCTTGACGATTTGACCAAGA 2151
Db 1361 TTTTATTAATAATTTTATTTTATTTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAA 1420
Qy 2152 CTATACATATTT-----GAAGCAAAATATCCACAGGATGATGAGGTTAGATCCCATTC 2208
Db 1421 ATTTTATTTTAAATTAATTAATTAATTAATTTTAAATTAATTAATTAATTAATTAATTA 1480
Qy 2209 AATATCTTTTGTCTTGTATTTATTAAGAAACAAATATTTTATGAGAAATTAATCGTTCT 2268
Db 1481 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1540
Qy 2269 TCTCTAGGATTAAGTATTAAGTATTAACAAATTTTAACTAGTATTAATTAATTAAT 2328
Db 1541 AATTAATAATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1600
Qy 2329 ATCTCAATCTTCAATCTTCAACATTAATTAATTAATTTTATTTTAACTTAA 2388
Db 1601 TTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAAT 1660
Qy 2389 CTACTTCCACTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2448
Db 1661 TAATTAAGATTAATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1720
Qy 2449 TGAATGGATATCTTCAAGCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2508
Db 1721 TATTTTAAATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1780
Qy 2509 GGGTTGGCAGATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2565
Db 1781 AAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1840
Qy 2566 TTTTAACTATCTAGTATGTTCTCACTGTAACAAATTAATTAATTAATTAATTAATTAAT 2625
Db 1841 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1900
Qy 2626 ATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2685
Db 1901 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1953
Qy 2686 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2745
Db 1954 TATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2013
Qy 2746 GAATGTGATTTGGAGCTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2805

Db 2014 AATTAATTAATTAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2073
Qy 2806 TGAACGGTTTAAAGATTTTAAACCAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2865
Db 2074 AATATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2132
Qy 2866 TCATTAATTAAGACAGATCGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2921
Db 2133 TTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2192
Qy 2922 -----CAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2974
Db 2193 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2252
Qy 2975 GAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3034
Db 2253 AATATTTTAAATTAATTAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTAATTAAT 2312
Qy 3035 ACCAAAGTTTCGTGTAATTTCTACGTCGTCATTAAGAAATTTTGAATTTTCTTAC 3094
Db 2313 TATTAATTTTCGATTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2372
Qy 3095 CTTTAAATTAATTAATTAATTTTGTGATTAATTAATTAATTAATTTTAAATTTTAAATTTTAA 3154
Db 2373 TAAATTAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2432
Qy 3155 GTTCTAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTT 3214
Db 2433 TTTTAAATTAATTTTATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2490
Qy 3215 TAAATCTTTTGTGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3274
Db 2491 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2550
Qy 3275 TACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3334
Db 2551 AATTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2610
Qy 3335 GTTTTAAATTAATTAATTTTCTCTTCTTCAATGCTTAAATTAATTAATTAATTAATTAATTA 3394
Db 2611 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2670
Qy 3395 TTTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3454
Db 2671 TAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2730
Qy 3455 CAATTTCTTACCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3509
Db 2731 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2790
Qy 3510 ATTTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3569
Db 2791 ACGAATTTGTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2850
Qy 3570 ACAGAAATGTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3629
Db 2851 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2910
Qy 3630 CAAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3689
Db 2911 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2970
Qy 3690 TTTTGAATTAATTTTCTGTAAGAGAGATTAATTAATTAATTAATTAATTAATTAATTAATTA 3749
Db 2971 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3030
Qy 3750 CAGATTAATTAATTTT-ATTCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3808
Db 3031 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3090
Qy 3809 TGTAACTCGTCTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3868
Db 3091 TTTTACGCTTAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 3150

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QY 3869 AATAAAATATATAGGTGAATTTGAGGCTTAAAGCAAAAT 3915
Db 3151 AATGGTTTATATATATTTTAAATATATATTTTATATATAAAT 3197

RESULT 9
US-10-312-841-2
; Sequence 2, Application US/10312841
; Publication NO. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/MO
; CURRENT APPLICATION NUMBER: US/10/312, 841
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

Query Match 1.9%; Score 80.2; DB 6; Length 3673778;
Best Local Similarity 43.5%; Pred. No. 0.0096;
Matches 467; Conservative 0; Mismatches 596; Indels 8; Gaps 2;

QY 1386 TATCCTTTTCTCTCCAAACAAATCATTCACAGAGAAATCTGCTGATCACTT 1445
Db 1132183 TATACGTGTGATAGTAGGTTTAAATTTTATTTAAATTTTATAGTTTTTTT 1132242
QY 1446 CAGCAGAAATTAATCTAATTTTGTATTTTGTCAAGTCTTGCTTTAAGTCAT 1505
Db 1132243 TTTAAAAATATAAATTTATAGTGTATAGTATTTTATATTTTATATTTAT 1132302
QY 1506 TATTGGTACTATATATGTGTGATATACATCCAGTCAAGTCAATCAATATGATCTCCT 1565
Db 1132303 GTTTATATTTAAATATATGTAAATATAGTATATGTAGAAATTTTATTTAAATATAGGG 1132362
QY 1566 TCTGCTATCAATTAATATACACCATTAAGTCAAGTCAATTAATTAACACCATTC 1625
Db 1132363 TTAATTTATATATATATTTTGTATTTTGTGTTTAAATATATATATATATGCGTAA 1132422
QY 1626 TCTTATCAATTTTATATGTATATTAATTAACAAACGATATAGGCTACAGATTGGTAT 1685
Db 1132423 TATATTAATTTAATATTTTATATAGTATATAGTATAGTGTGATGATATATGTTTAT 1132482
QY 1686 TAAAGCATTAATGCTCTCTAGTCAGAGAAATTTTGTATATGATTAACATCGTGGGAA 1745
Db 1132483 TTAATTAATTTTAAAGATATGATATTTAGTTGTTTTTAAATTTTGTGTTTAA 1132542
QY 1746 AATATCCAGCTATATATGCTATTTAAAGATATGATATTAATGCTTATCATTTAA 1805
Db 1132543 TGAATTTGTATTTGTAAATGATATGTAAATATATTTTATATATATATATATGATTTGA 1132602
QY 1806 ATAAAGGTTTTGCTTTAAAGGTAAACACCGCTTAATCATTAAGGAAATATTTAA 1865
Db 1132603 TTTTTTAAAGATATTTTAAAGTAAATGTTAATTAAGAAATGTTATTTTAA 1132662
QY 1866 CTTTGATCGAAATCCAAATATCTTTTAAACATTAAGAAATTTTCAGATTTTAAA 1925
Db 1132663 TGTAAATGATATATATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAAG 1132722
QY 1926 TAAAGGTATATTTATGGGTCAATTAATATGTTCCACGTAAAGTTTGAGGTTTAA 1985
Db 1132723 GAAATATGAGATTTTATTTTATTTTATATTTGTATGCTGTGGAACGGTATGTTATTT 1132782
QY 1986 CACATGAATGTTTTTGAATTTAAACACATTAATTTTCTAGTATATTAACATTTTAA 2045
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Db 1132783 TTAATTTTGTATTTTGAAGAAATGGTATTTATTTTATTTTATATTTTGA 1132842
QY 2046 CCGTCATCCAGATTTGATATATAGTACAAATCTGAAACATTTTCTTGAATCT 2105
Db 1132843 TTATATGAGATTTGAATTTTATTTTAAATTTTAAATTTTAAATTTTGAATTTTGA 1132902
QY 2106 TGTTTAAATTTCTCTGCTGATATCTTGACGACATTTGACCAAGCATTAACA----TA 2160
Db 1132903 TGAATTTATGTTTTTAAATTTGCTGTTGTTTTGTTTTTATTTAGTTTAAATGCTGTT 1132962
QY 2161 TTGAACAGAAATATTCACACGAGATATGCGTTAGATCCCATCAATCATCTTTGT 2220
Db 1132963 TTGATATTAAGTTTTTATTTTATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 1133022
QY 2221 CTTTGTATTTTAAAGAAACAAATATTTTATCAAGGAAATTAACGTTCTCTCTAGGTA 2280
Db 1133023 TTTTATATATTTTATTTTATTTTATTTTATTTTAAATTTATTTTGAATTTGATTAATTA 1133082
QY 2281 TAAATATATATTAATTAACAAATTTAATTAATTAATTAATTAATTAATTAATTAATTA 2340
Db 1133083 TTTATTTTATTTTATTAAGAAATTTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1133142
QY 2341 ACATCTTCACATTTATATATGATCAATTTTATTTTATTTTATTTTATTTTATTTTATTT 2400
Db 1133143 ---GTTTTAAATTAAGCTTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1133199
QY 2401 AAAAAATGCAAAAGAGATATATATTTAATTAAGTCAAGTATTAAGATGAT 2453
Db 1133200 AATATATTAATTAATTAAGTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 1133252

RESULT 10
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication NO. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/MO
; CURRENT APPLICATION NUMBER: US/10/312, 841
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3324164)
US-10-312-841-1

Query Match 1.9%; Score 79.4; DB 6; Length 3673778;
Best Local Similarity 41.6%; Pred. No. 0.013;
Matches 1013; Conservative 0; Mismatches 1401; Indels 23; Gaps 7;

QY 1124 TTTGCGGCTGTGACTTTTCTTATGTCGTTTGTGACTAATTTTTCAGAGTGAGA 1183
Db 1712880 TTTTGGATTTTAAAGTGTGTTTTTGTGTTTGTGATGATGTTTATATGTAATTT 1712939
QY 1184 GTGTATCAAGAAATCAATATTTGAAAGAAAGAAAGAAAGCAAGAAATATTTGTC 1243
Db 1712940 TTGTGATGTGTATGATTTGATTTTAAATGATATATATATATATATATATATATATTT 1712999
QY 1244 GAAAGACATTAATGACATTAATTTGATTTTAAATATGATATATATGTTTGGTGA 1303
Db 1713000 TTAATATATTAATATATATATATATATATATATATATATATATATATATATAT 1713059
QY 1304 TTTATAT -CATTAACAAATCAAGAGAGAGAGGACCTTCTGCTGATATGATTT 1362
Db 1713060 TTAATTAATTAATTTTGTATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1713119
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QY 1363 CCTCTAAACAACGCTGCTCCCACTATCCCTTTTACTTCCACAAACATCTACAGAG 1422
DB 1713120 AATATATATATAACGATTAATTTATATTTTGTGTGTGTATATATATTTTATATAT 1713179
QY 1423 AAAATCTGTCTGTATGACTCTTCATGCAAAATTAACCTAAATTTTGGATTTTGTCA 1482
DB 1713180 AAT 1713239
QY 1483 AGTTCTGCTGTTTAAAGTGAATTTTGGTAAATACATATATGTGTGATATACACATCCA 1542
DB 1713240 TTTATTTTAAAT 1713299
QY 1543 AGCTAAATCAATATATGATCTCTTCTGCTATCAATTAATTTACACCACTATAGCTATCA 1602
DB 1713300 TTTAT 1713359
QY 1603 AGCTAAATTAATTAACACCACTCTCTTATCAATTTTATATGATATATATATATATAT 1662
DB 1713360 AAT 1713419
QY 1663 ACATATAGCTACAGAGTGGTATTAAGGCTATATGCTCTTACGAGAGAAATTTT 1722
DB 1713420 TAT 1713479
QY 1723 GTATATGATTAACACTCGTGGGAAAAAATCCAGCTAATATGCTCATTTAAAG-GATPAT 1781
DB 1713480 AT 1713539
QY 1782 GATTTAATGCTTTAATCAT-----TAAATTAAGGTTTTTGTCTTTAAAGGTTAC 1833
DB 1713540 TAT 1713599
QY 1834 CACCGCTAATCATCATTAAGGAATTTAACTTTGATCGAAATTCGAAATTCCTTTT 1893
DB 1713600 ATTTTAT 1713659
QY 1894 TAACACATGAAGAAATTTTCCAGCTTTTAAATGAAGGATCTTATGCGTCAATTA 1953
DB 1713660 AT 1713719
QY 1954 ATATGTTTCCAGTAAGTTTGAGGTTTAACCATGAATGTTTTTGAATTTAAAAAAC 2013
DB 1713720 AT 1713779
QY 2014 ACATTAATTTCTATGATATATACATTTTAAACCGTCCATCCGATTTGTAATAGGACA 2073
DB 1713780 TTAAT 1713839
QY 2074 AATCTGAAAAATTTTCTTCTGAAATCTGTTTAAATCTCTGCTGACATCTTG 2133
DB 1713840 TATTTAT 1713899
QY 2134 CAGGCAATTTGACCAACGACTATACATATTTGAAAGCAAAATATCCACGAGGATAGAGG 2193
DB 1713900 TAT 1713959
QY 2194 TTGATCCCACTCAATATCTTTGTCTTTGT-TATTTATGAAAACAAAATTTATATCA 2252
DB 1713960 ATATTTAT 1714019
QY 2253 GGAABAAAAAGTTCTCTCTAGGCTATAGTATAGATTAAGATTAACAAATTAATCTT 2312
DB 1714020 TATTTAT 1714079
QY 2313 AGTTAATGATATATATCTTCAAACTTACCATC---CTTCAACATTAATATGATCAAT 2369
DB 1714080 ATTTTAT 1714139
QY 2370 TTTTATTTTTTTTACTAACTACTTCACTTAAAAAAATGCAAAAGAGATATATATTT 2429
DB 1714140 TTTTAT 1714199

QY 2430 AAGTCAAGTAATTAAGAATGATGGGTATCTTCCAGCAAAAGCGCCGCTAGAGGTGT 2489
DB 1714200 TAT 1714259
QY 2490 CTATATCTTACATTAACGCTGGGTTGTGGCAGACATCATAGGCGCTACGATATTTGAGCT 2549
DB 1714260 ATTTTAT 1714319
QY 2550 TTACCTGACGAAAGCTTTAAACATATCTATGTTAGTCTGACCTGACAAACAAAT 2609
DB 1714320 AT 1714379
QY 2610 CCAATTCGTAACATATATCAAAATCTACTAGTACTAGT-----TACGCTAGCTAT 2661
DB 1714380 TAT 1714439
QY 2662 ACATGCTTTTTCGCAAAATTTCTAACTATCTATCAACAACTGAAATGTTGTGTTG 2721
DB 1714440 AT 1714499
QY 2722 TATTTATCTTAAACCAAGTTTGAATGTGCAATGGGAGCTACACTAGTCCCCTT 2781
DB 1714500 TAT 1714559
QY 2782 TTTCCCAAAATATATCTCTTACATGACCGGTTAAAGTATTTTAAACCAAAATTTTAA 2841
DB 1714560 ATGAT 1714619
QY 2842 TTTGTGCTGAAGGTAACAACATGTCAATATATAGACAGCATGCTTATATCAAAATTA 2901
DB 1714620 ATATATTTTAAAT 1714679
QY 2902 TGTTCGATGTTATGGAATTCAAATATTAATTCGAATTTAGCGACTGCTGTTTAAATAG 2961
DB 1714680 TAT 1714739
QY 2962 TTGGAAGATTAATGAATTAATAAATGAATTCAAAGGATACAGACTATATATGCGGCTC 3021
DB 1714740 TATTTAT 1714799
QY 3022 ATTTAGACCGTGACCAAAAGTTTGGTGGTATTTCTACGCTCGGTCAATGAAGAAATTTG 3081
DB 1714800 ATATATTTTAAAT 1714859
QY 3082 GACTTTCTTCAACCTTATATGAACTTCTGATAGTTTTTCGGAATATATATTTGAT 3141
DB 1714860 TATATTTTAAAT 1714919
QY 3142 TCGTATATATTTTGTCTTAAATATGATACGTAAATTCAGATTAAGAAAGACTTCTTTT 3201
DB 1714920 ATATATATTTTGTATATATATATATATATATATATATATATATATATATAT 1714979
QY 3202 ATTTA-ATTTGATTTAAACTTTGTTTTTGAATATGACTCATATCAAGGTTAAAGTTT 3260
DB 1714980 ATATATATTTTAAAT 1715039
QY 3261 GATGATATCAATTTACAAAAATGTTTCGAGAGTGGGTTGCAATGTCCTACCAACATCGT 3320
DB 1715040 ATATATTTTAAAT 1715099
QY 3321 ACCAATCTGATGGGTTATATATATAGTTTTCTTCTTTTCCAAATGCTTATATAT 3380
DB 1715100 ATATATATTTTAT 1715159
QY 3381 GAAACATCTAAATTTCTTTTAAATAGTTAAGAACTTGAATTTTCTGTGATTT 3440
DB 1715160 TTTAT 1715219
QY 3441 TAAACCAAGGTTTCAATTTCTTTGACACAAAAAAGGTTTCAATTAATTA 3500
DB 1715220 TATATATATTTTAAAT 1715279
QY 3501 AGAATCTAAATTTTGTGAGTTCAAGGTTTAAATGATA 3537

Qy 3817 GTCCTTAGCCATATAGTCTTAAGTTTAAATGTTTCAGAAAGCTTTACAAAATTAAT 3876
 Db 240 ATTTAAATTTGNAAAAAATTAATTAATAAATTTATTTATTAATAACNATGCTATAAAA 181
 Qy 3877 AATTAATAGGTGAATTTGTAGGGCTAAAGCGAAAAATTAATAATTAAGTAAG 3936
 Db 180 NNTTAAANAATAGNATNTTGAANTTTAAATTTTAAATCTTTTAAATTAATAANTAT 121
 Qy 3937 AAGCTCTTCTCAATAGAACAGATCCCAAGGATTTCAACGCAAT 3987
 Db 120 TNAATTTAAAAAAGAAAAAAGAAAAAAGCGNNGNCGNAGTACNT 70

RESULT 13

US-10-311-455-1842
 : Sequence 1842, Application US/10311455
 : Publication No. US20030143606A1
 : GENERAL INFORMATION:
 : APPLICANT: OLEK, Alexander
 : APPLICANT: PISENBROCK, Christian
 : APPLICANT: BERLIN, Kurt
 : TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Detect
 : FILE REFERENCE: 5013.1014
 : CURRENT APPLICATION NUMBER: US/10/311,455
 : PRIOR FILING DATE: 2002-12-16
 : PRIOR APPLICATION NUMBER: PCT/EP01/07537
 : PRIOR FILING DATE: 2001-07-02
 : PRIOR APPLICATION NUMBER: DE 10032529.7
 : PRIOR FILING DATE: 2000-06-30
 : PRIOR APPLICATION NUMBER: DE 10043826.1
 : PRIOR FILING DATE: 2000-09-01
 : NUMBER OF SEQ ID NOS: 2424
 : SEQ ID NO 1842
 : LENGTH: 13573
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 US-10-311-455-1842

Query Match 1.7%; Score 73.2; DB 6; Length 13573;
 Best Local Similarity 46.2%; Pred. No. 0.017;
 Matches 243; Conservative 0; Mismatches 283; Indels 0; Gaps 0;
 Qy 3042 GTTTCGTGTAATTTCTAGCGTGCATTAAGAAATTTTGACCTTTCTGACCCCTTTTA 3101
 Db 3742 GTGAGTATATTTTATTAACGATCGTAGTGAATTTTATGATATGTTGTAATTTTA 3801
 Qy 3102 TGAACCTCTGATAGTTTGTGCGATTAATATTTGATTCGATATTTTGTGCTA 3161
 Db 3802 TATTAATATTTGTTTATTTTATTTGATTTATGATGAGAGTCCGTTTTTTTTTTA 3861
 Qy 3162 ATATAGATGTAATTCAGATTAAGAAAGCTCTTTTATTTATTTGATTTAAACT 3221
 Db 3862 AATTTTAAATTAATTTTGTAGTTTATTTTATTTTGTAGTTTATTTTATTTT 3921
 Qy 3222 TTGTTTGGAAATGACTACATACACAAGTTAAAGTTGATGATCAATTTTACAAA 3281
 Db 3922 TTAATTTTATAGATTAAGAAAGATTAAGATTTTGTGATTAAGTTTGTGATTAAG 3981
 Qy 3282 ATGTTTGAAGAGTCGTTGAGTGTCTCAACACATGTCACCACTGATGAGTTTAT 3341
 Db 3982 GAAATGTTGGTGTAGTTGATTTTATTTATAGATTAATTAATTTTATTTATAGTA 4041
 Qy 3342 ATTAGTTTTTTCTCTTTTCCATATGCTTTATTAATTAAGCACTTAATTTCTTT 3401
 Db 4042 ATTAGTTTGTATTTTATTTTATTTATTTAGTATTAATGAGATTAATTTTATTTT 4101
 Qy 3402 TTTAAATAGGTAAAGATCTGAATTTTCTGTGATTTTAAACCAAGTTTCAATTC 3461
 Db 4102 AAAAATTTTTTTTTTATTTATTAATTTGTTAAATGTTTATTTGATTTTGAATGCT 4161

Qy 3462 TCTTAGCAGAAAAAAGGTTTCAATATTAAAGATCTAAATTTTGGAGT 3521
 Db 4162 TTTTATAGTATGATTAATTTATTTTATTTTGTATTTTGAATTAAGTATGATATGCTTT 4221
 Qy 3522 CAAGATTTAATGATAGCTGAAAAGTTATGATGATTCAGATTG 3567
 Db 4222 TTGTTTATTTGAATATTTAGAGTTATTTGATGATTTATTAATGG 4267

RESULT 14

US-10-239-676-54/c
 : Sequence 54, Application US/10239676
 : Publication No. US2003082609A1
 : GENERAL INFORMATION:
 : APPLICANT: OLEK, Alexander
 : APPLICANT: PISENBROCK, Christian
 : APPLICANT: BERLIN, Kurt
 : TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
 : FILE REFERENCE: 5013.1003
 : CURRENT APPLICATION NUMBER: US/10/239,676
 : PRIOR FILING DATE: 2002-09-24
 : PRIOR APPLICATION NUMBER: PCT/EP01/03968
 : DE 10019173.8
 : DE 10032529.7
 : DE 10043826.1
 : PRIOR FILING DATE: 2001-04-06
 : 2000-04-06
 : 2000-04-07
 : 2000-06-30
 : 2000-09-01
 : NUMBER OF SEQ ID NOS: 228
 : SEQ ID NO 54
 : LENGTH: 17421
 : TYPE: DNA
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
 : FEATURE:
 : NAME/KEY: unsure
 : LOCATION: (167, 1832..1833, 1836..1837, 1842, 1848, 1852, 1857, 1859..1860)
 : NAME/KEY: unsure
 : LOCATION: (9147, 9153, 9168, 9170, 9173, 10243, 10340, 10394, 11996)
 : NAME/KEY: unsure
 : LOCATION: (12002, 12005, 12012, 12102, 13715, 13717, 16077, 16097, 16907)
 US-10-239-676-54

Query Match 1.7%; Score 71.6; DB 5; Length 17421;
 Best Local Similarity 44.9%; Pred. No. 0.036;
 Matches 311; Conservative 0; Mismatches 379; Indels 2; Gaps 1;
 Qy 3271 AATTTACAAAATGTTTCGAGAGTGCCTGAGTGTCTCAACACATGTAACCACTGT 3330
 Db 9128 AATATTAATTAATTCACATATCTTCAAGCTTATTAATTAATCACTTTTAACTTTA 9069
 Qy 3331 ATGGTTTATTAATGATTTTCTTTCTTTTCAATGCTTTATTAATTAAGCACTCT 3390
 Db 9068 ACCATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 9009
 Qy 3391 AATATCTTTTAAATTAAGTTAAGATCTGAATTTCTGTGATTTTAAACCAAG 3450
 Db 9008 AATATCTTTATCATATTTCTTAATCAATTCATATCATCTTTTATTAATAATTAATTC 8949
 Qy 3451 TTTTCAATCTCTTACACAAAAAAGGTTTCAATTAATTAAGATCTTAA 3510
 Db 8948 AATATCATATTCACATTAATAAATAAATCAATTAATTAATTAATTAATTAATAA 8889
 Qy 3511 TTTTGTAGTCAAGAGTTTAATGATAGCTGAAA--GTTATGATGATTTCAAGTTGC 3568


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Db 8888 ATTTATTTTAAABAACTAAATTCCTAATACAAACCTTACCAAAATCTATTTTTC 8829
Qy 3569 AACAGATGTCATGTAGTACATACAAACATGCATCAAAATTAATTCGTCTTA 3628
Db 8828 AATATATTTTCCAAATTTTAAATCTTAATCTCAACATTTAAATTAACAAAAA 8769
Qy 3629 GCAAGAGAAACGATGAAATTAACAGAACATGTTACACCTTAATAATCTTAGATA 3688
Db 8768 AAAACAAAATTAATTAATAAAATTAATTAATTAATTAATTAATTAATTAAT 8709
Qy 3689 TTTTGTAGTATATTTCTGTAGAGAGATCATATCTTAACAAAAAACTCAT 3748
Db 8708 AAAATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8649
Qy 3749 TCAGATTAATTAATGTTGTCATCGTTACCAAGATGTTTGTCTCATCGTTGTAT 3808
Db 8648 TAATTAACCTACAACTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8589
Qy 3809 TGTAACTCGTCTTACCATATAGTCTTAAGTTTAAATGTTTCAAGACTTACAA 3868
Db 8588 AAAAAAATCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8529
Qy 3869 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3928
Db 8528 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8469
Qy 3929 AAGTAAGAAACGCTTTCTCATTAAGAACAC 3960
Db 8468 AATTAACCAAACTAATCAAAAAATTAATTAAC 8437

RESULT 15
US-10-240-453-56/c
; Sequence 56, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIERENBROCK, Christian
; TITLE OF INVENTION: Berlin, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240.453
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 56
; LENGTH: 17421
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (167, 1832, 1833, 1836..1837, 1842, 1848, 1852, 1857,
; LOCATION: 1859..1860)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (2953, 4024, 4630, 4733, 4767, 8161, 8189, 8200, 9142..9143)
; FEATURE:
; NAME/KEY: unsure
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; LOCATION: (9147, 9153, 9168, 9170, 9173, 10243, 10340, 10394, 11996)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12002, 12005, 12012, 12102, 13715, 13717, 16077, 16097, 16907)
US-10-240-453-56
Query Match
Best Local Similarity 44.9%; Pred. No. 0.036;
Matches 311; Conservative 0; Mismatches 379; Indels 2; Gaps 1;
1.7%; Score 71.6; DB 6; Length 17421;
Qy 3271 AATTACAAAATGTTTTCAGAGTGGCTTGCAGTGTCTTACCAACCATTCGATCACTCGT 3330
Db 9128 AATTAATCTTATCATATTTCTTACTTAACATTTCAATGATCTTCTTTTAAATACTATTC 9069
Qy 3331 ATGCGTTATTAATAGTATTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 3390
Db 9068 ACCATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 9009
Qy 3391 AATTTCTTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3450
Db 9008 AATATCTTATCATATTTCTTACTTAACATTTCAATGATCTTCTTCTTCTTCTTCTTCT 8949
Qy 3451 TTTCAATCTTCTTACCAAAAAAATTAATTAATTAATTAATTAATTAATTAATTAAT 3510
Db 8948 AATCATCTATCCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8889
Qy 3511 TTTTGTAGTCAAGTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3568
Db 8888 AATTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8829
Qy 3569 AACAGATGTCATGTAGTACATATCAAAAATCATCATCAAAAATTAATTAATTAATTAAT 3628
Db 8828 AATATATTTTCCAAATTTTAAATCTTAATCTTAATTTCAACATTAATTAATTAATTAAT 8769
Qy 3629 GCAAGAGAAACGATGAAATTAACAGAACATGTTTACCACTTAATAATCTTAGATA 3688
Db 8768 AAAACAAAATTAATTAATAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8709
Qy 3689 TTTTGTAGTATATTTCTGTAGAGAGATCATATCTTAACAAAAAACTCAT 3748
Db 8708 AAAATCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8649
Qy 3749 TCAGATTAATTAATGTTGTCATCGTTACCAAGATGTTTGTCTCATCGTTGTAT 3808
Db 8648 TAATTAACCTACAACTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8589
Qy 3809 TGTAACTCGTCTTACCATATAGTCTTAAGTTTAAATGTTTCAAGACTTACAA 3868
Db 8588 AAAAAAATCAATCAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 8529
Qy 3869 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 3928
Db 8528 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 8469
Qy 3929 AAGTAAGAAACGCTTTCTCATTAAGAACAC 3960
Db 8468 AATTAACCAAACTAATCAAAAAATTAATTAAC 8437
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Search completed: February 27, 2006, 20:09:19
Job time : 2131 secs

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 19:33:52 ; Search time 743 Seconds
(without alignments)
12134.115 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtgcgactctgcctcactg.....agaaccacaaagaacc 4228

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7209121 seqs, 1066183437 residues

Total number of hits satisfying chosen parameters: 14418242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*
Listing first 45 summaries

Database :

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2: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB_seq.*
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5: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB_seq.*
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13: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB_seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	75.4	1.8	171486	12 US-11-121-086-105	Sequence 105, App
2	69.6	1.6	171486	12 US-11-121-086-105	Sequence 105, App
3	63.6	1.5	39794	12 US-11-098-686-8737	Sequence 8737, App
4	62.8	1.5	173602	12 US-11-121-086-25	Sequence 25, App1
5	62.6	1.5	5152	8 US-10-240-708-73	Sequence 73, App1
6	62.2	1.5	173602	12 US-11-121-086-25	Sequence 25, App1
7	60.2	1.4	119036	8 US-10-995-561-13314	Sequence 13314, A
8	59.6	1.4	5562	8 US-10-240-708-63	Sequence 63, App1
9	58.8	1.4	26772	8 US-10-995-561-13313	Sequence 13313, A
10	58.8	1.4	54946	8 US-10-995-561-13479	Sequence 13479, A
11	58.2	1.4	139054	12 US-11-121-086-96	Sequence 96, App1
12	58	1.4	5360	8 US-10-240-708-65	Sequence 65, App1
13	58	1.4	139054	12 US-11-121-086-96	Sequence 96, App1
14	57.4	1.4	6499	12 US-11-011-332A-91	Sequence 91, App1
15	56.6	1.3	6070	8 US-10-240-708-10	Sequence 10, App1
16	56.6	1.3	6669	8 US-10-240-708-6	Sequence 6, App1
17	56.4	1.3	5152	8 US-10-240-708-74	Sequence 74, App1
18	56.4	1.3	26772	8 US-10-995-561-13313	Sequence 13313, A
19	56.4	1.3	54946	8 US-10-995-561-13479	Sequence 13479, A
20	55.8	1.3	6499	12 US-11-011-332A-77	Sequence 77, App1

21	55	1.3	49979	8 US-10-995-561-13443	Sequence 13443, A
22	54.8	1.3	28536	12 US-11-011-332A-151	Sequence 151, App
23	54.8	1.3	28536	12 US-11-011-332A-155	Sequence 155, App
24	54.8	1.3	49979	8 US-10-995-561-13443	Sequence 13443, A
25	54.8	1.3	194553	12 US-11-098-686-8738	Sequence 8738, App
26	54.4	1.3	1230	6 US-09-925-065A-77681	Sequence 77681, A
27	54.4	1.3	1230	6 US-09-925-065A-77682	Sequence 77682, A
28	53.2	1.3	611	6 US-09-925-065A-7768158	Sequence 7768158, A
29	53.2	1.3	1230	6 US-09-925-065A-77683	Sequence 77683, A
30	53.2	1.3	1230	6 US-09-925-065A-77684	Sequence 77684, A
31	53.2	1.3	6113	8 US-10-240-708-13	Sequence 13, App1
32	53.2	1.3	6306	8 US-10-240-708-49	Sequence 49, App1
33	52.8	1.2	582	6 US-09-925-065A-726874	Sequence 726874, A
34	52.8	1.2	6866	8 US-10-240-708-20	Sequence 20, App1
35	52.6	1.2	6317	8 US-10-240-708-11	Sequence 11, App1
36	52.4	1.2	20317	8 US-10-995-561-13460	Sequence 13460, A
37	52.2	1.2	11049	8 US-10-240-708-22	Sequence 22, App1
38	52.2	1.2	105550	8 US-10-995-561-13235	Sequence 13235, A
39	52	1.2	600	8 US-10-750-185-305	Sequence 305, App
40	52	1.2	600	8 US-10-750-185-305	Sequence 305, App
41	52	1.2	1528	8 US-10-750-185-50461	Sequence 50461, A
42	52	1.2	1528	8 US-10-750-623-50461	Sequence 50461, A
43	52	1.2	6306	8 US-10-240-708-50	Sequence 50, App1
44	51.6	1.2	677	6 US-09-925-065A-667264	Sequence 667264, A
45	51.6	1.2	10467	8 US-10-240-708-1	Sequence 1, App1

ALIGNMENTS

RESULT 1									
US-11-121-086-105									
Sequence 105, Application US/11121086									
Publication No. US20050266459A1									
GENERAL INFORMATION:									
APPLICANT: POULSEN, TIM S.									
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES									
FILE REFERENCE: 09138.6000-00000									
CURRENT APPLICATION NUMBER: US/11/121,086									
CURRENT FILING DATE: 2005-05-04									
PRIOR APPLICATION NUMBER: 60/567,570									
PRIOR FILING DATE: 2004-05-04									
NUMBER OF SEQ ID NOS: 107									
SOFTWARE: PatentIn version 3.3									
SEQ ID NO 105									
LENGTH: 171486									
TYPE: DNA									
ORGANISM: Homo sapiens									
US-11-121-086-105									
Query Match 1.8%; Score 75.4; DB 12; Length 171486;									
Best Local Similarity 43.0%; Pred. No. 0.039;									
Matches 894; Conservative 0; Mismatches 1161; Indels 22; Gaps 10;									
QY	1785	TTAATGCTTAAATCAATTAATAAAGTTTGGCTTTAAAGTTACACCGCTTAAT	1844						
DB	15684	TAAATTAATATGTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	15743						
QY	1845	TCATCATTAAGAAATTTAACTTGATCGAAATTCGAAATCTTTTAAACATGAG	1904						
DB	15744	ATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	15803						
QY	1905	AAATTTTCAGCATTTTAAATAAAGGTACATTATGGGTCATTAATATGTTTCA	1964						
DB	15804	ATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	15859						
QY	1965	CGTAAAGTTGAGGTTTAAACATGATGTTTGTGATTTAAATAAACAATTAATTT	2024						
DB	15860	CATTAATTTTAAATTAATTAATTAATTAATTAATTAATTTGATTAATTAATTAAT	15919						
QY	2025	CTAGTAATTAACATTTTAAACGTCATCACTGATTTGTAATGACAAATCGAAAC	2084						

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RESULT 2
US-11-121-086-105/C
; Sequence 105, Application US/11121086
; Publication No. US20050266459x1
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138.6000-00000
; CURRENT APPLICATION NUMBER: US/11/121,086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 105
; LENGTH: 171486
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-105

Query Match      1.6%; Score 69.6; DB 12; Length 171486;
Best Local Similarity 43.3%; Pred. No. 0.3;

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Oy	2589	ACTGTACAAACAAAACAAAATCCAAATTCCGTAACATATATACAAATCTACTAGTACTAGA	2648
Db	16675	TATATTAATATNGTAATATATATTTACTATATATAATTAATATATATATATATATAT	16616
Oy	2649	TTACGCTACGTATATCATCGCTTTTGCGCAAAATTCCTAACCTAATCTATACCAAACTGG	2708
Db	16615	ATTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	16556
Oy	2709	AATGTTGTTTGGTAATTTATCTTAAACCAAAGTTTTGAATGGCATTTGGAGGCATCAC	2768
Db	16555	ATATTATGATTTATATATATTAATTTGTTTATATATATAT--ATATATATATATTAATA	16498
Oy	2769	TCTAGTCCCCCTTTTTTCCCCAAAATATCTCCTTAGATGACCGGTAAAGTATTTAAAC	2828
Db	16497	TGTAAATTAATTTATTAATTAATTAATTAATCTATATTAATTTATATATATTAATTAAT	16438
Oy	2829	CACAATAATTTAATTTGTTGCTGAGAGGTACAAACATGTCATATATAGACACAGCATCG	2888
Db	16437	ATTATTAATTTATATATATTTATTAATTAATTTATTAATTAATTAATTAATTAAT	16379
Oy	2889	TTTATACAAPATATNGTCCATGTTATTTGGAATCAATTAATTAATACGAATTAACGACTCA	2948
Db	16378	ATTATTAATTTATATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	16315
Oy	2949	CTTGCTTTAATAGTTGGAGAGATATGAATAAAAAAT	2986
Db	16318	ATATGTTATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT	16281

RESULT 3
US-11-098-686-8737/c
Sequence 8737, Application US/11098686
Publication No. US20060024696A1
GENERAL INFORMATION:
APPLICANT: Kapur, Vivek and Gebhart, Connie J.
TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
FILE REFERENCE: 09531-128001
CURRENT APPLICATION NUMBER: US/11/098, 686
CURRENT FILING DATE: 2005-04-04
PRIOR APPLICATION NUMBER: PCT/US03/31318
PRIOR FILING DATE: 2003-10-01
PRIOR APPLICATION NUMBER: US 60/416,395
PRIOR FILING DATE: 2002-10-04
NUMBER OF SEQ ID NOS: 11433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8737
LENGTH: 39794
TYPE: DNA
ORGANISM: Lawsonia intracellularis
US-11-098-686-8737

Query Match	1.5%; Score 63.6; DB 12; Length 39794;
Best Local Similarity	45.1%; Pred. No. 1.8;
Matches 399; Conservative 0; Mismatches 474; Indels 11; Gaps 4;	

Oy	2881	CAGCATGCTTTATACAAATATATGTCATGATTTATGGAATCAATATATATACGAATTA	2940
Db	33848	CAGATCTTTTGTATTTATTTATCAAAAAAGCAATTTGTATTAACATTAAGAAATAGAAAA	33789
Oy	2941	GCGACTCACTTGCTTTAATATGTTTGGAAAGATATAGAAATTAATTAATTAATTAATTA	3000
Db	33788	TAGATTAATATAGCTATATTTAATTAACATCTTTTATATTAATTAATTAATTAATTAAT	33729
Oy	3001	CAGAGCTATATATAGTGGGGTCATTATAGACCGGTGACCAAAAGTTTCGTATTTCTAC	3060
Db	33728	TATATGTGATATTTAAACATAATGTAAAAAANGTTTATATATCTTTAATTAATAGATGA	33669
Oy	3061	GGTGGTCATPAAGAAATTTGACCTTTTCTCAACCCTTTATGAACCTTGTATAGTTTT	3120
Db	33668	TCAATCTATATATAGATTTAATTAATCTTAACCTAGTTTTTATAAAAAANAATGTATATAT	33609

[illegible]

```

RESULT 4
US-11-121-086-25/c
; Sequence 25, Application US/11121086
; Publication No. US20050266459A1
; GENERAL INFORMATION:
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138, 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121, 086
; PRIORITY FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
; LENGTH: 173602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-25

```

[illegible][illegible][illegible]

Query Match	1.5%	Score 62.6	DB 8	Length 5152
Best Local Similarity	43.5%	Pred. No. 1.6		
Matches 398	Conservative	0	Mismatches 504	Indels 13
				Gaps 2

Qy	3052	AAATTCTACGGTCGGTCATPAAGAAATTTTGGACCTTTCTCACCCCTTTATGAACTTCG	3111
Db	3973	AATTAACAAGCCATCATTAATACTATATTAACCTTAATTAATAAATCTTTAAATTTT	3914
Qy	3112	TAAAGTTTTGTCCGATTAATPAATTTGTATTGTAATATTTTTGTTCATTAATGATAC	3171
Db	3913	TTTATTTTTTATTTTTTATTTTTTAAATTTTAACTATTTTAAATTCAAAAATATATAT	3854
Qy	3172	GTAATATCACATPAAGAAAGACTCTTTATATTAATTTGATTTAAACTTTTGTTTTG	3231
Db	3853	ACAAATTTATTTACACGAACATPAATATCAATTTTTCTTTAACCTTAATTAATAAATTA	3794
Qy	3232	GAAATGACTCATACACAAGTTTAAAGTTGATGATCCAAATTTACAAAAATGTTGCG	3291
Db	3793	AAATATTTCTTTAAACTAATTTCTTTAACACACTTTTAATTTAATAAATTTTCCC	3734
Qy	3292	AGTGCCTTCGAGTCTCTACACACATCGAACCTCGATGGTTATTTATTAAGTTTT	3351
Db	3733	ATT--TTTAAAAAAATCTCTAAATACCTAAATATTAATAAACAACACTACTACATATA	3676
Qy	3352	TTTCTCTCTTTCCAAATCTTTAATTAATGAACACTAATTTCTTTTAAATTAATAG	3411
Db	3675	TTTCTAATCTTCAACAACTAATATATTTTACTATTTTCTTTACATTTACAAAAATCAAAAT	3616
Qy	3412	GTTAAGATCTTGAATTTTCTGTGATTTTAAACAAAGTTTCAATCTCTTAGACACA	3471
Db	3615	TTTTTAACGATTAATTTCCAACTCTTATTTAAAAATTAATAATAAATCTCTTTAAACT	3556
Qy	3472	AAAAAAGTTTCAATTTAATTAAGAATCTAAATTTTTTGAGTTCAAGATTTA	3531
Db	3555	AAAAAATATAAAACACTTATTTTCTAAATPACATATATATTTAATTAATAATPAACTTT	3486
Qy	3532	ATGATAGTGAAAGTTATGAATGATTGCACACTTTGCAACGAATGCGATGATGATCA	3591
Db	3495	AAATATCACTTTAATTAATCTTATCTTTTCTTTTTT-----TTCTTTTCTAAT	3447

RESULT 6
US-11-121-086-25

```

; sequence 25, Application US/11121086
; Publication No. US20050266459A1
;
; GENERAL INFORMATION:
; APPLICANT: POULSEN, TIM S.
; APPLICANT: NIELSEN, KIRSTEN V.
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
; FILE REFERENCE: 09138 6000-00000
; CURRENT APPLICATION NUMBER: US/11/121, 086
; CURRENT FILING DATE: 2005-05-04
; PRIOR APPLICATION NUMBER: 60/567,570
; PRIOR FILING DATE: 2004-05-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 25
;
; LENGTH: 173602
;
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-121-086-25

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[illegible]


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QY 2820 TATTTAAACCAAAATTTTAAATTTTGGTGAAGGTGACAAACATGTCACATATATAGAG 2879
    |||||
DB 136339 TATTTATATATATATATATATATATATATATATATATATATATATATATATATAT 136398
QY 2880 ACAGCATCGTTTATACAAATATATGT-TCGATGTATTTGGAATCAATATATATATACGAT 2938
    |||||
DB 136399 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136458
QY 2939 TAGCGACTGCTGGTTTATAGTTTGAAGATATAGCAATATATATATATATATATATATAT 2998
    |||||
DB 136459 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136518
QY 2999 TACAGAGCTATATATGCGGTCATTTAGACCGGTGACAAAGTTTCGTCGTATATTC 3058
    |||||
DB 136519 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136571
QY 3059 ACGGTGCTATATAGAAATTTTGGACTTTTCTTCAACCTTTTATGAACTTCTGTATAGTT 3118
    |||||
DB 136572 AATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136631
QY 3119 TTTGTGCGATATATATTTGTATTCGTATATTTTGTTCATATATATATATATATATATAT 3178
    |||||
DB 136632 TGTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136691
QY 3179 CACGATAGAAAGACTTCTTTTATTTTAAATTTGATTTTAAACCTTTTGTGGAATGCA 3238
    |||||
DB 136692 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136751
QY 3239 CTCATACACAAAGTTTAAAGTTTGAAGTATCCAATTTTCAAAAGTTTTCGAGAGTGCCT 3298
    |||||
DB 136752 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136811
QY 3299 TCGAGTGTCTACACACATGTCACAACTGTATGAGTTTATATATATATATATATATATAT 3358
    |||||
DB 136812 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136871
QY 3359 TTTTTCCAATGTCCTTATATATATGACCACTTAAATTTCTTTTAAATTTAGGTTAAGA 3418
    |||||
DB 136872 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136931
QY 3419 ATCTGAAATTTCTGTGATTTTAAACCAAGTTTCAATCTTCTTACGACAAACAAAAA 3478
    |||||
DB 136932 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 136991
QY 3479 AAAAAAGTTTCAATATATATATATATATATATATATATATATATATATATATATATAT 3538
    |||||
DB 136992 ATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 137051
QY 3539 CTGAAAAGTTAT-GAATGATTGCAAGTTTGCAACAGAAAGTGTGAGTAGTACATATCA 3597
    |||||
DB 137052 GTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 137111
QY 3598 AAACATGATCAAAATATATATATGTCGTGACAGAGAAACGATGAAATATATATATATAT 3657
    |||||
DB 137112 CATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 137171
QY 3658 AATCGTTAACCACTTAAATATCTTGAATATTTTGTAGATATATTTCTGTGAAGAG 3717
    |||||
DB 137172 TATATATATATATATATATATATATATATATATATATATATATATATATATATAT 137231
QY 3718 AGGTATCATCTTCAAAACAAAAAAGCTTTCAGATTAATA 3760
    |||||
DB 137232 TATGTATATATATATATATATATATATATATATATATATATATATATATATATATAT 137274

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RESULT 7

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US-10-995-561-13314
; Sequence 13314, Application US/10995561
; Publication No. US20050272054AI
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH

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; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF
; TITLE OF INVENTION: DETECTION AND USES THEREOF
; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561
; CURRENT FILING DATE: 2004-11-24
; NUMBER OF SEQ ID NOS: 85702
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13314
; LENGTH: 119036
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(119036)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-;
US-10-995-561-13314

Query Match 1.4%; Score 60.2; DB 8; Length 119036;
Best Local Similarity 43.8%; Pred. No. 7,6;
Matches 263; Conservative 0; Mismatches 338; Indels 0; Gaps 0;

QY 3331 ATGGGTTATATATAGTATTTTCTTCTTCCATGCTTATATATATGAAACACTCT 3390
    |||||
DB 31272 ATGGCTGATTAATAGATTTTATATATATATATATATATATATATATATATATATATATAT 31331
QY 3391 AAATTTCTTTTAAATATAGTTAAGATCTGAATTTTCGTGATTTTAAACCAAG 3450
    |||||
DB 31332 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 31391
QY 3451 TTTTCAATCTTCTTACGACAAACAAAAAAGTTTTCATTTATTAAGATCTTAA 3510
    |||||
DB 31392 TTTTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 31451
QY 3511 TTTTGGAGTCAAGGTTTATATGATGAGTGAAGAACTTATGATGATTTGCA 3570
    |||||
DB 31452 AAATAGATTTTATATATATATATATATATATATATATATATATATATATATATATATAT 31511
QY 3571 CAGAATGTCGATGTAGTACATATCAAAACATGCAATCAAAATATATATATGTCGCTTACG 3630
    |||||
DB 31512 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 31571
QY 3631 AAGAGAAAGATTTGAATATATATATATATATATATATATATATATATATATATATATAT 3690
    |||||
DB 31572 AAATAGATTTTATATATATATATATATATATATATATATATATATATATATATATATAT 31631
QY 3691 TTGTATGATTAATTTCTGTAGAGAGATATCATATCTTACAAACAAAAATCTCTTTC 3750
    |||||
DB 31632 AAATATGATTTTATATATATATATATATATATATATATATATATATATATATATATAT 31691
QY 3751 AGATTAATATATATGTCGATCGTTACCAAGATGTTTGTGTCATCAGTTGATTG 3810
    |||||
DB 31692 TATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 31751
QY 3811 TAACGTGCTCTTACGATATAGTTCTAAAGTTTAAAGTTTCAAGACTTATACAAA 3870
    |||||
DB 31752 GATTTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 31811
QY 3871 TAAATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 3930
    |||||
DB 31812 AGATTAATCTTAATATATATATATATATATATATATATATATATATATATATATATAT 31871
QY 3931 G 3931
    |||||
DB 31872 G 31872

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RESULT 8

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US-10-240-708-63
; Sequence 63, Application US/10240708
; Publication No. US20050282157AI
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian

```


Query Match	1.4%	Score 59.6	DB 8	length 5562
Best Local Similarity	48.5%	Pred. No. 4.8		
Matches 164, Conservative	0	Mismatches 174	Indels 0	Gaps 0

RESULT 9
US-10-995-561-13313

US-10-995-561-13313

157 TTATTCATTTAATGAGTTAGCATTAAATATATATACGTCGACATTACCAACCAAGTTT 216
: ||| ||| | : ||||| | | : | | | |
21131 WTATATTTAATTTATATATAAATTTTATATATATTTTATATWAAAAATTTATATATAT 2119

Oy	514TTTACGCGCTACATAAACAATGTATCGATCAAAATCAAATTATTATAGACTAGAATC	573
Db	21491TTTTATCATTAATTTATTTATATATATATATATATATCTTATACATTAATATA	2155

Db 21851 ATATTTTATAGCATTTATATATATAATAATATATATTTTATATAGCAATTATATAT 2191

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; FILE REFERENCE: CL001559
; CURRENT APPLICATION NUMBER: US/10/995,561

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Qy 2313 AGTAAATGATTTACTATCTTCAAACTTACCATCTTCAACATTAATATGATCAATTT 2372
Db 43561 TTTAATTAATACTATATCTTCAATTTTATTAATTTAAATTTAAATGATTTAAATATA 43502
Qy 2373 TATTTTCTTACTAATCTACTTCCATMAAAATGCAAAAGAGATATATATTAAG 2432
Db 43501 TAAATTTATATGCTGATTTAAATTAATTAAGTATATGGAATGATTAATTAATATATAT 43442
Qy 2433 TCAAAATTAATTAAGATGAT 2453
Db 43441 TTTATATATTTTAAATTAATCAT 43421

RESULT 12
US-10-240-708-65
Sequence 65, Application US/10240708
Publication No. US20050282157A1
GENERAL INFORMATION:
APPLICANT: OLEK, Alexander
APPLICANT: PIERENBROCK, Christian
APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
FILE REFERENCE: 5013.1012
CURRENT APPLICATION NUMBER: US/10/240.708
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: PCT/EP01/03971
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR APPLICATION NUMBER: DE 10019173.8
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: DE 10043826.1
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 98
SEQ ID NO 65
LENGTH: 5360
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-65

Query Match 1.4%; Score 58; DB 8; Length 5360;
Best Local Similarity 50.6%; Pred. No. 8.4; Indels 5; Gaps 1;
Matches 169; Conservative 0; Mismatches 160; Indels 5; Gaps 1;
Qy 3071 AAGAAATTTGACCTTTCTTCCACCTTTTATGAAGTTCTGTATGATTTTGTGCGAATTA 3130
Db 1580 AAGAAATTTTGTGTTTATGATTTTGTGTTTGTGTTTATTAATTAAGATGA 1639
Qy 3131 TATAATTTGATTCGTAATTTTGTGTTCTAATAATGATACGTAATTCACGATPAGAA 3190
Db 1640 GATATGCTATTTTGTGTTTGTGTTTGTGTTAAGAAAGTAAATTTGAGATA 1699
Qy 3191 GACTCTTTTATTAATTTGATTTAAAGTTTGTGTTTGAATGACGATACAGAG 3250
Db 1700 TTTTGTGTTTGTGTTTGTGTTTATTAATTAATTAATTTGAAATTTATTTTATGATG 1759
Qy 3251 GTTAAAGTTGATGATCACTTATTAACAAAATGTTTGAAGTGGTTCGATGCTCTTA 3310
Db 1760 TATAGAGTTTGTGTTTATTTTGTGTTGATGTTATAGGTTTATTTTGTGTA 1814
Qy 3311 CCACCATGTAACAACGTAAGGTTTATTAATTAAGTTTGTGTTTCTTTTCCATGT 3370
Db 1815 GTGCTGATTTGTTTATTTTATTTTATGATTAATTAATTAAGTTTATTTTAAAGATT 1874
Qy 3371 CTTTATTAATGAACACTTAATTTCTTTT 3404
Db 1875 TGTATTAATAATTAATTAATTTGTTTATTTT 1908

RESULT 13
US-11-121-086-96
Sequence 96, Application US/11121086
Publication No. US20050266459A1
GENERAL INFORMATION:
APPLICANT: POULSEN, TIM S.
APPLICANT: NIELSEN, KIRSTEN V.
TITLE OF INVENTION: NUCLEIC ACID PROBES AND NUCLEIC ACID ANALOG PROBES
FILE REFERENCE: 09138.6000-00000
CURRENT APPLICATION NUMBER: US/11/121.086
CURRENT FILING DATE: 2005-05-04
PRIOR APPLICATION NUMBER: 60/567,570
PRIOR FILING DATE: 2004-05-04
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn version 3.3
SEQ ID NO 96
LENGTH: 139054
TYPE: DNA
ORGANISM: Homo sapiens
US-11-121-086-96

Query Match 1.4%; Score 58; DB 12; Length 139054;
Best Local Similarity 43.4%; Pred. No. 17; Indels 12; Gaps 3;
Matches 424; Conservative 0; Mismatches 540; Indels 12; Gaps 3;
Qy 2833 AATTTTAATTTTGTGCTGAAGTACAAAGTGCATATATATAGACAGCATCGTTTA 2892
Db 43405 AATTAATTAATTTTAATGTAATTTAATAATTAATTAATTAATTAATTAATTAATTA 43464
Qy 2893 TACAAATTAATGTCGATGTTATTTGAAATCAATATTAATTAATTAATTAATTAATTA 2952
Db 43465 CATATCTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43524
Qy 2953 GTTAAATGTTTGGAGATATGAATTAATAATTAATTAATTAATTAATTAATTAATTA 3012
Db 43525 TTAATTAATTAATAATGAAGATATGTTATTAATTAATTAATTAATTAATTAATTAATTA 43584
Qy 3013 TGTCGGTCATTTAGACCGGTGACCAAAAGTTTGTGTAATTTCTACGGTGGTCATTA 3072
Db 43585 ATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 43644
Qy 3073 GAAATTTGACCTTTCTTCACTTTTATGAAGTTCTGTATGATTTTGTGCGATTA 3132
Db 43645 TAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43704
Qy 3133 TATTTGATTCGTAATTTTGTGTTCTAATTAATTAATTAATTAATTAATTAATTAATTA 3192
Db 43705 TATGTAATA--ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43761
Qy 3193 CTCTTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3252
Db 43762 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43821
Qy 3253 TAAAGTTGATGATCAATTTAATAAAATGTTTGAAGTGGTTCGATGCTTACC 3312
Db 43822 CATATTAATGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAC 43881
Qy 3313 ACCATGTAACCACTGTAAGGTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 3372
Db 43882 ATATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 43941
Qy 3373 TTAATTAATGAACCACTTAATTTCTTTTATTAATTAATTAATTAATTAATTAATTTCT 3432
Db 43942 TTAATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTA 43996
Qy 3433 GTTGAATTTAAACCAAGTTTCAATTTCTTTGCAAAAAAAGGTTTCA 3492
Db 43997 ATAGACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 44056
Qy 3493 ATTAATTAAGATTAATTTTGTGAGTTCAAGGTTTATTAATTAATTAATTAATTAATTAAT 3552

; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 10
; LENGTH: 6070
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-708-10

Query Match 1.3%; Score 56.6; DB 8; Length 6070;

Best Local Similarity 47.4%; Pred. No. 14;
Matches 232; Conservative 0; Mismatches 254; Indels 3; Gaps 2;

```
QY 3453 TTCAATCTTCTTGACACAAAAAAGTTTCAATTATTAAGATCTAAATT 3512
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2169 TCCATTATATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2110
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3513 TTTGAGTTCAGATTATGATAGTGAAGTTGAAATGATGCAAGTTGCAACA 3572
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2109 TTAACCTCAAAAAAATTTCTAATCACTACACATTAATCTCTTAACACA 2050
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3573 GAATGTCAGTAGT--ACATATCAAAACATGATCAAAATTAATTCGTGCTTAGC 3630
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 2049 TTATACATAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1990
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3631 AAGAGAACGATTGAATTAACAGACATGCTTAACACTTAATAATCTTAGAATAAT 3690
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1989 ACGATACCTCGACTTCAAAACAAAAATACATATCGACTATTAATAATTAATAAAC 1930
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3691 TTGATGATTAATTTCTGTAGAGAGATGATCATATCTTACAAAAAACTCATTC 3750
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1929 GAATACGAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1870
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3751 AGATTAATTAATGTTGTCATCGTTACCAAGTATGTTTGTGTCATCGATGATG 3810
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1869 TAAAAATA-AATATATTAATTAATTTGACACATTAATTAATTAATTAATTAAC 1811
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3811 TAACTGCTCTTAGCCATATAGTTCTTAAGTTTAATGTTTCAAGACTTTACAAAA 3870
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1810 TATACACTTAATAATAATTAATTAATTAATTAATTAATTAATTAATTAAT 1751
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3871 TAAATATATTAATGATGGAATTTGTAGGCTAAAGCAAAATTAATAATTAATA 3930
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1750 AAAAAACGAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1691
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 3931 GTAAAGAAA 3939
    ||| |||
DB 1690 AAAAAAAA 1682
```

Search completed: February 27, 2006, 20:21:32
Job time : 752 secs

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 16:24:53 : Search time 10413 Seconds
(without alignments)
18960.585 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228

Sequence: 1 gtgcagctctggcctcactcctg.....agaacccaataaagaacc 4228

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 41078325 seqs, 23393541228 residues

Total number of hits satisfying chosen parameters: 82156650

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100*

Listing first 45 summaries

Database :

EST:*
1: gb_est1.*
2: gb_est2.*
3: gb_est3.*
4: gb_hlc.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_est7.*
9: gb_g881.*
10: gb_g882.*
11: gb_g883.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	590.4	14.0	652	9	B62389
2	551.4	13.0	581	10	BX290871
3	394	9.3	437	9	CC056828
4	387.8	9.2	415	9	BZ379137
5	276.4	6.5	323	9	CC797115
6	252	6.0	276	11	CR402298
7	249	5.9	300	11	CR402297
8	240.4	5.7	2106	4	CNS0A4GJ
9	226	5.3	418	10	AL769556
10	214	5.1	2315	4	CNS0A2BQ
11	212	5.0	796	9	BH510257
12	200.8	4.7	268	10	AL756782
13	193	4.6	234	10	AL936239
14	157.2	3.7	162	10	AL759737
15	156.4	3.7	192	10	AL759736
16	147.2	3.5	698	9	BH936859
17	142.6	3.4	381	9	BH481919
18	142.4	3.4	673	9	BH676371
19	134.6	3.2	424	3	BP561373
20	124.2	2.9	594	6	CB260786
21	112	2.6	112	9	CC455690
22	110.8	2.6	694	9	BH934314

23	107	2.5	793	9	BH510250
24	104	2.5	318	8	BH451271
25	102.4	2.4	1007	8	DN566957
26	102	2.4	969	10	CL484870
27	98.6	2.3	1101	10	CNS00EVL
28	97.4	2.3	418	10	AL769556
29	97	2.3	1896	10	CG753083
30	93.8	2.2	110	10	AL769557
31	93.8	2.2	1112	1	AJ926321
32	93.2	2.2	1101	10	CNS00EVL
33	92.2	2.2	1101	10	CNS017V2
34	91.6	2.2	1092	10	CNS020K7
35	91	2.2	92	10	AL769520
36	89.8	2.1	1896	10	CG753083
37	87.8	2.1	92	10	AL754990
38	87	2.1	1101	10	CNS0039G
39	86.6	2.0	1101	10	CNS0039G
40	85.6	2.0	1103	1	AJ926366
41	85.4	2.0	1007	8	DN566957
42	85.2	2.0	1214	10	CL646783
43	85	2.0	1101	10	CNS00EVL
44	84.8	2.0	96	10	AL754991
45	84.6	2.0	1201	10	CNS0167M

ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION T21110TR TMMU Arabidopsis thaliana genomic clone T21110, genomic survey sequence.
ACCESSION B62389
VERSION B62389.1 GI:2629151
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE 1 (bases 1 to 652)
Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Linher, K., Golden, K., Berry, K., Granger, D., Sun, E., Wible, C., Adams, M.D. and Venter, J.C.
A BAC End Sequence Database for Identifying Minimal Overlaps in Arabidopsis Genomic Sequencing. Update 3
JOURNAL Unpublished (1997)
COMMENT Contact: Steve Rounsley
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0200
Email: rounsley@tigr.org
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 652.
FEATURES
source
Location/Qualifiers
1..652
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Columbia"
/db_xref="taxon:3702"
/clone="T21110"
/sex="hermaphrodite"
/clone_id="TMMU"
/note="Vector: BelobAC11; Site 1: HindIII; Site 2: HindIII; Produced by Rod Wing"
ORIGIN
Query Match 14.0%; Score 590.4; DB 9; Length 652;

Best Local Similarity 97.7%; Pred. No. 3.7e-92;
Matches 643; Conservative 0; Mismatches 6; Indels 9; Gaps 4;

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QY 1907 AATTTTCAGATTTTAAATGAAGGACATTT-ATTGGTTCATTAATTAATTTCCAC 1965
DB 652 ATTTTCAGATTTTAAATGAAGGACATTTAAATGGGTTCAATTAATTTTCCAC 593
QY 1966 GTAAAGTTTGAGAGTTTAA-CCACATGAATGTTTTTGAATTTAAACACATTAATTTT 2024
DB 592 GTAAAGTTTGAGAGTTTAAACCCACATGAATGTTGTTGATTTAAACACATTAATTTT 533
QY 2025 C-TAGTAATTTACATTTTAAACCGTCCATCCAGATTTGAATTAAGTACAAATCTGAAA 2083
DB 532 CTAGTAATTTACATTTTAAACCGTCCATCCAGATTTGAATTAAGTACAAATCTGAAA 473
QY 2084 CATTTTCTTTCTGTAATCTGTTTAAATTTCTCTGCTGCACTCTGACGACATTTG 2143
DB 472 CATTTTCTTTCTGTAATCTGTTTAAATTTCTCTGCTGCACTCTGACGACATTTG 413
QY 2144 ACCAAGACTATACATATTGAAGCAAAATATCCACAGGAGATGATGAGGTTAGATCCCA 2203
DB 412 ACCAAGACTATACATATTGAAGCAAAATATCCACAGGAGATGATGAGGTTAGATCCCA 353
QY 2204 CATTCATATCTTTGCTTTGTTTATTAAGAAAACAAATATTTATCAAGAAAACG 2263
DB 352 CATTCATATCTTTGCTTTGTTTATTAAGAAAACAAATATTTATCAAGAAAACG 293
QY 2264 TTTCTTCTGAGTGATTAAGTAAATTAACAAATTTAAATCTTAATGAT 2323
DB 292 TTTCTTCTGAGTG-----GTAATGAATTAATTAACAAATTTAAATGAT 239
QY 2324 TTACTATCTTCAACTTACATCTTCAACATTAATTTGATCAATTTTATTTT 2383
DB 238 TTACTATCTTCAACTTACATCTTCAACATTAATTTGATCAATTTTATTTT 179
QY 2384 CTAAACTACTTCCATTAATAAAGAGAGAGATATATTTTAAGTCAAGTAT 2443
DB 178 CTAAACTACTTCCATTAATAAAGAGAGATATATTTTAAGTCAAGTAT 119
QY 2444 AAAGATGATGGGTATTTCTTCAGCAAAACGCGCGGTAGAGGTCTTATCTCAATTA 2503
DB 118 AAAGATGATGGGTATTTCTTCAGCAAAACGCGCGGTAGAGGTCTTATCTCAATTA 59
QY 2504 CAGCTGGGTTTGCGAGACATCATAGGCGCTAGATATTTGAGCTTTACTGATGA 2561
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RESULT 2
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DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-440G05-018216,
genomic survey sequence.
ACCESSION BX290871
VERSION BX290871.1 GI:28889867
KEYWORDS GSS
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
REFERENCE 1 Li,Y., Rosso,M.G., Strizhov,N., Viehoever,P. and Weisshaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2 Rosso,M.G., Li,Y., Strizhov,N., Reis,B., Dekker,K. and
Weisshaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics

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JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3 Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and
AUTHORS Weisshaar,B.
TITLE High-throughput generation of sequence indexes from T-DNA
JOURNAL mutagenized Arabidopsis thaliana lines
PUBMED Biotechniques 35 (6), 1164-1168 (2003)
REFERENCE 4 (bases 1 to 581)
AUTHORS Strizhov,N., Li,Y., Rosso,M.G. and Weisshaar,B.
TITLE Direct Submision
JOURNAL Submitted (31-MAR-2004) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT This sequence has been recovered from the left border of the T-DNA.
It indicates an insertion within the locus defined by BAC clone
T28119. Details on the protocols used for generation of the
sequence are described in References 1-3. The sequences are
generated at the MPI for Plant Breeding Research in the context of
the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
program designated 'GABI'. Information on line availability can be
found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
source
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-440G05-018216"
/clone_1fb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector pAC161 (Genbank accession number: M537514). The
lines contain one or more T-DNA insertions. The DNA
fragment(s) resulting from the PCR were directly sequenced
to determine the genomic sequence flanking the insertion.
T-DNA derived sequences were removed."

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ORIGIN

Query Match 13.0%; Score 551.4; DB 10; Length 581;
Best Local Similarity 99.5%; Pred. No. 2.2e-85;
Matches 563; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

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QY 1095 CGTTTACGTTTCCGTTCCGTCGCACTTTGGGCGTTTGTGACTTTTCTTAATGC 1154
DB 581 CGTTTACGTTTCCGTTCCGTCGCACTTTGGGCGTTTGTGACTTTTCTTAATGC 522
QY 1155 GTTGTGACTAATTTTCTCAGAGTGAGAGTGAATCAAGAAAACTAATTTGAAAAGA 1214
DB 521 GTTGTGACTAATTTTCTCAGAGTGAGAGTGAATCAAGAAAACTAATTTGAAAAGA 462
QY 1215 AAGAAAAAAGGCAAGAAAACTAATTTGCAAAAGACATTAATGAACATAATTTGAT 1274
DB 461 AAGAAAAAAGGCAAGAAAACTAATTTGCAAAAGACATTAATGAACATAATTTGAT 402
QY 1275 ATTAATAAATGATTAATGTTGGTGAATTTATATCTTACCAAAATTAAGAAAGA 1334
DB 401 ATTAATAAATGATTAATGTTGGTGAATTTATTAATCAATTAACAAATTAAGAAAGA 342
QY 1335 GAGAGGAGCTCTGCGTGTATGATTTCCCTCCATAACAGCTCCGACTATCTTTT 1394
DB 341 GAGAGGAGCTCTGCGTGTATGATTTCCCTCCATAACAGCTCCGACTATCTTTT 282
QY 1395 TTACTTCAACAAATCATTCACAGAGAAATCTGTCGTGATCATTTTCAGAAA 1454
DB 281 TTACTTCAACAAATCATTCACAGAGAAATCTGTCGTGATCATTTTCAGAAA 222
QY 1455 TTAACTAATTTTGGTATTTTGTCAAGTTCTTGCTGTTTAAGTCATTAATTTGTA 1514
DB 221 TTAACTAATTTTGGTATTTTGTCAAGTTCTTGCTGTTTAAGTCATTAATTTGTA 162
QY 1515 ATACTATATGATGATATACATCAAGGATTAATGAATGATCTCTGCTGAT 1574

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Db 161 ATACTATATGTGTGATATACATCCAGTAATCAATATGATCTCTTCT-CTTAT 103

Qy 1575 CAATTAATTTACACCACTTAGCTATATCAAGTATTAATTTACACCACTTTCTTATCA 1634

Db 102 CAATTAATTTACACCACTTAGCTATATCAAGTATTAATTTACACCACTTTCTTATCA 43

Qy 1635 TTTTATATGTGTATTAATTAACAC 1660

Db 42 TTTTATATGTGTATTAATTAACAC 17

RESULT 3
CC056828
LOCUS 437 bp DNA linear GSS 02-APR-2003
DEFINITION SALK_111232.51.45.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_111232.51.45.x, genomic survey sequence.

ACCESSION CC056828
VERSION CC056828.1 GI:29476492
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 437)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES
Location/Qualifiers
1..437
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_111232.51.45.x"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 9.3%; Score 394; DB 9; Length 437;
Best Local Similarity 95.4%; Pred. No. 4.3e-58;
Matches 417; Conservative 0; Mismatches 16; Indels 4; Gaps 1;

Qy 2334 CAATCTACATCTTCAACATTAATATGATCAATTTTATTTTCTAACTACT 2393

Db 1 CAATCTACATCTTCAACATTAATATGATCAATTTTATTTTCTAACTACT 60

Qy 2394 TCCTCTAAAAATGCAAAAGAGATATATTAATGCAAGTAATTAAGTGAT 2453

Db 61 TCCTCTAAAAATGCAAAAGAGATATATTAATGCAAGTAATTAAGTGAT 120

Qy 2454 GGGGATTTCTTACGCAAAAGCGCGGTAGAGGTCTTATCCATTAAGCTGGGT 2513

Db 121 GGGGATTTCTTACGCAAAAGCGCGGTAGAGGTCTTATCCATTAAGCTGGGT 180

Qy 2514 GTGGCAGACATCATAGGGCCCTACGTATATTGAGCTTTACTGTAAGCTTAACT 2573

Db 181 GTGGCAGACATCATAGGGCCCTACGTATATTGAGCTTTACTGTAAGCTTAACT 240

Qy 2574 ----ATCTAGTTAGTTCTACCTGTACAAACAAATTCATTCGTATATATAC 2629

Db 241 TCGCAGAGTTTACGCAACACCTGTACAAACAAATTCATTCGTATATATAC 300

Qy 2630 AATATCTACTAGTACTGATTAAGTATGCTATACATGCTTTTGGCAATTTCTAACT 2689

Db 301 AATATCTACTAGTACTGATTAAGTATGCTATACATGCTTTTGGCAATTTCTAACT 360

Qy 2690 AATATCTACTAGTACTGATTAAGTATGCTATACATGCTTTTGGCAATTTCTAACT 2749

Db 361 AATCTATACAAACAACTGTAATGTTGTTGTAATTAATCTTAACCAAGTTTGAT 420

Qy 2750 TGTGATTTGGAGCTAC 2766

Db 421 TGTGATTTGGAGCTAC 437

RESULT 4
B2379137
LOCUS 415 bp DNA linear GSS 26-NOV-2002
DEFINITION SALK_112909.37.05.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_112909.37.05.x, genomic survey sequence.

ACCESSION B2379137
VERSION B2379137.1 GI:25470664
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 415)
Alonso,J.M., Leisbe,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
Unpublished (2001)
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
Class: TDNA tagged.

FEATURES
Location/Qualifiers
1..415
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
/clone="SALK_112909.37.05.x"
/clone_1lb="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

ORIGIN
Query Match 9.2%; Score 387.8; DB 9; Length 415;
Best Local Similarity 96.9%; Pred. No. 5.2e-57;
Matches 408; Conservative 0; Mismatches 7; Indels 6; Gaps 1;

QY 2146 CAACGACTATACATATGTAAGCAAAATATCCACGAGGATGATAGGTTAGATCCACA 2205
DB 1 CAACGACTATACATATGTAAGCAAAATATCCACGAGGATGATAGGTTAGATCCACA 60
QY 2206 TTCAATATCTTTTGTCTTTTGTATTTATGAAAAAATAATTTATCAGAAAAAAGCTT 2265
DB 61 TTCAATATCTTTTGTCTTTTGTATTTATGAAAAAATAATTTATCAGAAAAAAGCTT 120
QY 2266 TCTTCTAGTGGATATAGTATAGATTAACAAAATTTTAATCTAGTAAATGATTT 2325
DB 121 TCTTCTAGTGGATATAG-----ATAATTAACAAAATTTTAATCTAGTAAATGATTT 174
QY 2326 ACTATCTTCAAACTTACATCTTCAACATTAATATGATCAATTTTATTTTACT 2385
DB 175 ACTATCTTCAAACTTACATCTTCAACATTAATATGATCAATTTTATTTTACT 234
QY 2386 AAACACTTCCACTAAAAAATGCAAAAGAGATATATTTAACTCAAGTAATTA 2445
DB 235 AAACACTTCCACTAAAAAATGCAAAAGAGATATATTTAACTCAAGTAATTA 294
QY 2446 AGATGATGGGTATCTTCAAGAAAACGGCGCTGAGGTCTTATCTACATTA 2505
DB 295 AGATGATGGGTATCTTCAAGAAAACGGCGCTGATAGGTCTTATCTTACATTA 354
QY 2506 GCTGGGTGGGACATCATAGGCGCTATATTTAGCTTTACTGTAGTAAGC 2565
DB 355 GCTGGGTGGGACATCATAGGCGCTATATTTAGCTTTACTGTAGTAAGC 414
QY 2566 T 2566
DB 415 T 415

RESULT 5
LOCUS CC797115 323 bp DNA linear GSS 01-JUL-2003
DEFINITION SALK_144490.54.40.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_144490.54.40.x, genomic
survey sequence.
ACCESSION CC797115
VERSION CC797115.1 GI:32392338
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1 (bases 1 to 323)
Alonso,J.M., Leisner,T.J., Barajas,P., Chen,H., Cheuk,R.,
Gadriab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
Shim,P., Zimmerman,J. and Ecker,J.R.
A Sequence-indexed Library of Insertion Mutations in the
Arabidopsis Genome
Unpublished (2001)
JOURNAL Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
TDNA.
FEATURES
source
1. .323
Location/Qualifiers
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/ecotype="Col-0"
/db_xref="taxon:3702"
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/clone_1bp="Arabidopsis thaliana TDNA insertion lines"
/notes="PCR was performed on Arabidopsis thaliana lines"

each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html

ORIGIN
Query Match 6.5%; Score 276.4; DB 9; Length 323;
Best Local Similarity 89.5%; Pred. No.1,1e-37;
Matches 289; Conservative 0; Mismatches 34; Indels 0; Gaps 0;
QY 2524 TCATAGGGCTACGATATTTAGCTTTACTGACGTAAGCTTTACATATCTAGTTAG 2583
DB 1 TCATAGGGCTACGATATTTAGCTTTACTGACGTAAGCTTGACGCCGACCGTCAA 60
QY 2584 TTTCACCTGTACAAACAAATCCAAATTCGATATATATACAAATCTACTAGTA 2643
DB 61 CCACACNTGTAC 120
QY 2644 CTGATTTACGCTACGATATCTTACGCTTTTTCGCAATTTCTAACTATCTATACACAA 2703
DB 121 CTGATTTACGCTACGATATCTTACGCTTTTTCGCAATTTCTAACTATCTATACACAA 180
QY 2704 ACTTGATGTTGTTTGTATATTTATCTTAAACCAAGTTTGAATTTGCATTGGAGC 2763
DB 181 ACTTGATGTTGTTTGTATATTTATCTTAAACCAANTTTGAATTTGCATTGGAGC 240
QY 2764 TACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAATTT 2823
DB 241 TACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATGACCGGTTAAATTT 300
QY 2824 TAAACCAACAAATTTAATTTGT 2846
DB 301 TAAACCAACAAATTTAATTTGT 323

RESULT 6
LOCUS CR402298/c 276 bp DNA linear GSS 02-MAY-2004
DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-853H05-025845,
genomic survey sequence.
ACCESSION CR402298
VERSION CR402298.1 GI:46943026
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
REFERENCE 1
Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
the identification of T-DNA insertion mutants in Arabidopsis
thaliana
Bioinformatics 19 (11), 1441-1442 (2003)
JOURNAL PubMed 12874060
REFERENCE 2
Rosso,M.G., Li,Y., Strizhov,N., Reis,B., Dekker,K. and
Weishaar,B.
An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
flanking sequence tag-based reverse genetics
Plant Mol. Biol. 53 (1-2), 247-259 (2003)
JOURNAL PubMed 14756321
REFERENCE 3
Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
Weishaar,B.
High-throughput generation of sequence indexes from T-DNA
mutagenized Arabidopsis thaliana lines
Biotechniques 35 (6), 1164-1168 (2003)
JOURNAL PubMed 14682050
REFERENCE 4 (bases 1 to 276)
Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B.
Direct Submission

JOURNAL Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany. This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
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1. .276
/organism="Arabidopsis thaliana"
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/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 6.04; Score 252; DB 11; Length 276;
Best Local Similarity 96.1%; Pred. No. 1.9e-33;
Matches 271; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 2075 ATCGAAGAACTTTTCTTGAATCTGTTAAATCTCTGTCGATACCTTGC 2134
Db 276 ATCGAAGAACTTTTCTTGAATCTGTTAAATCTCTGTCGATACCTTGC 217

Qy 2135 AGCGATTGACCAAGCATATATGAAAGCAAAATATCCACGAGATGATGGGT 2194
Db 216 AGCGATTGACCAAGCATATATGAAAGCAAAATATCCACGAGATGATGGGT 157

Qy 2195 TAGATCCCACTGATATATCTTTGTCTTTGTTATTTATGAAAAACAATATTTATCAGG 2254
Db 156 TAGATCCCACTGATATATCTTTGTCTTTGTTATTTATGAAAAACAATATTTATCAGG 97

Qy 2255 AAAAAACGTTTCTTCTAGTGTATGATTAAGATTAATACAAATTTAATCTTAG 2314
Db 96 AAAAAACGTTTCTTCTAGTGTATGATTAAGATTAATACAAATTTAATCTTAG 43

Qy 2315 TTAATGATTTACTATCTTCAAACTTACACTCTTCAACATT 2356
Db 42 TTAATGATTTACTATCTTCAAACTTACACTCTTCAACATT 1

RESULT 7
CR402297/c 300 bp DNA linear GSS 02-MAY-2004
LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-853H05-025756,
DEFINITION genomic survey sequence.
ACCESSION CR402297
VERSION CR402297.1 GI:46943025
KEYWORDS GSS.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana

REFERENCE
AUTHORS Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P. and Weishaar, B.
TITLE GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED 12874060
REFERENCE 2

AUTHORS Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
TITLE An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
PUBMED 14756321
REFERENCE 3

AUTHORS Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
TITLE High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
PUBMED 14682050
REFERENCE 4 (bases 1 to 300)
AUTHORS Li, Y., Rosso, M.G., Strizhov, N. and Weishaar, B.
TITLE Direct Submision
JOURNAL Submitted (01-MAY-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforshung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany. This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.

FEATURES
source
1. .300
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"
/clone="GK-853H05-025756"
/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"
/ecotype="Col-0"
/note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."

ORIGIN
Query Match 5.94; Score 249; DB 11; Length 300;
Best Local Similarity 96.1%; Pred. No. 6.2e-33;
Matches 268; Conservative 0; Mismatches 5; Indels 6; Gaps 1;

Qy 2082 AAGCTTTTCTTCTTGAATCTGTTAAATCTCTGTCGATACCTTGCAGGCAATT 2141
Db 300 AAGCTTTTCTTCTTGAATCTGTTAAATCTCTGTCGATACCTTGCAGGCAATT 241

Qy 2142 TGACCAAGCACTATACATATTTGAAGCAAAATATCCACGAGATGATGGGTAGATCC 2201
Db 240 TGACCAAGCACTATACATATTTGAAGCAAAATATCCACGAGATGATGGGTAGATCC 181

Qy 2202 CACATTCATATCTTTGTCTTTGTTATTTATGAAAAACAATATTTATCAGGAAAAAA 2261
Db 180 CACATTCATATCTTTGTCTTTGTTATTTATGAAAAACAATATTTATCAGGAAAAAA 121

Qy 2262 CGTTTCTTCTTGTGTATGATTAAGATTAATACAAATTTAATCTTAGTATATGT 2321
Db 120 CGTTTCTTCTTGTGTATGATTAAGATTAATACAAATTTAATCTTAGTATATGT 67

Qy 2322 ATTACTATCTTCAAACTTACCAATCTTCAACATTATA 2360
Db 66 ATTACTATCTTCAAACTTACCAATCTTCAACATTAGA 28

RESULT 8
CNS0A4GJ 2106 bp mRNA linear HTC 06-FEB-2004
LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone GSRFB372E02 of flowers and buds of strain col-0 of Arabidopsis

thaliana (thale cress) .
 BX826541
 VERSION BX826541.1 GI:42462514
 KEYWORDS HTC; GSUT_cDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1 (bases 1 to 2106)
 Castell, V., Aury, J.-M., Jallou, O., Wincker, P., Clepet, C., Menard, M., Craud, C., Quetier, F., Scarpelli, C., Schachter, V., Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences: A Combined Approach to Evaluate and Improve Arabidopsis Genome Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2106)
 Genoscope.
 JOURNAL Direct Submission
 TITLE Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage : BP 131 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads. The sequences are based on single pass reads. Life Technologies (a division of Invitrogen) members carried out full-length libraries construction : Temple G. Genoscope members carried out sequencing and annotation : Castell, V., Aury J.-M., Jallou O., Wincker P., Menard M., Craud C., Schachter V., Weissenbach J., Salanoubat M. URV INRA : Clepet C., Caboche M. Annotation is based on the June 2003 version of the Arabidopsis genome released by MIPS (Munich Information center for Protein Sequences). 5 prime and 3 prime are assembled with Phrap. http://www.genoscope.cns.fr/externe/sequences/Barque_Projet_FullLength
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.location/Qualifiers
 FEATURES
 source
 1. 2106
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="GSLTFRB372E02"
 /cistype="flowers and buds"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"
 1. 2106
 /gene="At4g37750"
 gene
 ORIGIN
 Query Match 5.7%; Score 240.4; DB 4; Length 2106;
 Best Local Similarity 97.3%; Pred. No. 1.6e-31;
 Matches 255; Conservative 0; Mismatches 6; Indels 1; Gaps 1;
 Oy 3968 AACGATTCAAGCAAAATTTGCTTCTCTCTCTTATTATATCTCTCA 4027
 Db 1 AAGGATTCAAGCAAAATTTGCTTCTCTCTCTTATTATATCTCTCA 60
 Oy 4028 AAACCTCTCTATATCTCTTAAGCCCCCTTCTTTTCTTACCGCAACAAAG 4087
 Db 61 AAACCTCTCTATATCTCTTAAGCCCCCTTCTTTTCTTACCGCAACAAAG 120
 Oy 4088 AAAACAAATTTGAGAAAATG-GTGTGTTCTGTGTATACCAATATTTGGGTTTAC 4146
 Db 121 AAAACAAATTTGATTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 180
 Oy 4147 TTACTACTGAGAGATTATAGAAAGAGTAAAGATACATTATAGAAAGAGAA 4206
 Db 181 TTACTACTGAGAGATTATAGAAAGAGTAAAGATACATTATAGAAAGAGAA 240
 Oy 4207 GCAGAAACCAAAAAGAAAC 4228
 Db 241 GCAGAAACCAAAAAGAAAC 262

RESULT 9
 AL769556/c
 LOCUS AL769556
 DEFINITION Arabidopsis thaliana T-DNA flanking sequence GK-087D01-012260.
 ACCESSION AL769556
 VERSION AL769556.1 GI:21531758
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 1
 Li, Y., Rosso, M.G., Strizhov, N., Viehoever, P., and Weishaar, B.
 GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
 JOURNAL Bioinformatics 19 (11), 1441-1442 (2003)
 REFERENCE 12874060
 PUBMED
 JOURNAL
 TITLE Rosso, M.G., Li, Y., Strizhov, N., Reiss, B., Dekker, K. and Weishaar, B.
 An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for flanking sequence tag-based reverse genetics
 JOURNAL Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 REFERENCE 14756321
 PUBMED
 JOURNAL
 TITLE Strizhov, N., Li, Y., Rosso, M.G., Viehoever, P., Dekker, K.A. and Weishaar, B.
 High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
 JOURNAL Biotechniques 35 (6), 1164-1168 (2003)
 REFERENCE 14682050
 PUBMED
 JOURNAL
 TITLE 4 (bases 1 to 418)
 Strizhov, N., Rosso, M.G., Li, Y. and Weishaar, B.
 Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50629, Germany
 COMMENT This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone T28119. Details on the protocols used for generation of the lines are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpi-zkoeln.mpg.de/GABI-Kat/.location/Qualifiers
 FEATURES
 source
 1. 418
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-087D01-012260"
 /clone_lib="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pAC161 (Genbank accession number: A0537514). The lines contain one or more T-DNA insertions. The DNA fragment (s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
 ORIGIN
 Query Match 5.3%; Score 226; DB 10; Length 418;
 Best Local Similarity 77.6%; Pred. No. 5.9e-29;
 Matches 250; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
 Oy 1717 TTTTGTGATGATACCTCGTGGGAAAAATCCAGCTATATGCTATTAAAGCA 1776
 Db 418 TTTTGTGATGATACCTCGTGGGAAAAATCCAGCTATATGCTATTAAAGCA 359

QY 1777 TAATGATTAAATGCTTAAATCAATTAATAAAGGTTTTGCTTTAAAGGTTACAC 1836
 |||||
 DB 358 AATGATTTTAAAGCTTTTATCTTAAATTAAGTTTTGTTTTAAAGGTTCCCC 299
 |||||
 QY 1837 CGCTTAATCATCATTAAGAGAAATTAATCACTTATGCAAAATTCCTTTTAA 1896
 |||||
 DB 298 CGGTTTATTATCTTGGGGAATATTAACTTTGTTGGAATCCCAAAACCTTTTTTA 239
 |||||
 QY 1897 CACTAAGAAAATTTTCAAGCTTTTAAATTAAGGTCATTTTGGGTTCAATAATA 1956
 |||||
 DB 238 CCAATTAAGAAAATTTTCAAGCTTTTAAATTAAGGTCATTTTGGGTCCTAATA 179
 |||||
 QY 1957 TGTTCACGTAAGATTGAGGTTTAAACCATGAATGTTTTGATTTAAATAACA 2016
 |||||
 DB 178 TGTTCCTCCGTAAGATTGAGGTTTAAACCATGAATGTTTTGATTTAAATAACA 119
 |||||
 QY 2017 TAAATTTCTAGTAATTAACACA 2038
 |||||
 DB 118 NNNNNNNNNNNNNNNNNNNNTA 97
 |||||
 RESULT 10
 CNS0A2BQ 2315 bp mRNA linear HTC 06-FEB-2004
 LOCUS Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 DEFINITION GSIUTS902C06 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).
 BX827650.1 GI:42459424
 HTC; GSIUTS902C06
 Arabidopsis thaliana (thale cress)
 Arabidopsis thaliana
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2315)
 REFERENCE
 AUTHORS Castelli V., Aury J.M., Jallion O., Wincker P., Clepet C.,
 Menard M., Crnaud C., Querier F., Scarpelli C., Schachter V.,
 Temple G., Caboche M., Weissenbach J. and Salanoubat M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2315)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 Web : www.genoscope.cns.fr)
 COMMENT The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli
 V., Aury J.M., Jallion O., Wincker P., Menard M., Crnaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 URGV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich information center for Protein
 Sequences). 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_EF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.
 Location/Qualifiers
 1..2315
 /organism="Arabidopsis thaliana"
 /mol_type="mRNA"
 /db_xref="taxon:3702"
 /clone="GSIUTS902C06"
 /csize="Adult vegetative tissue"
 /ecotype="Col-0"
 /plasmid="pCMVSPORT_6"
 1..2315
 /gene="At4g37750"

ORIGIN
 Query Match 5.1%; Score 214; DB 4; Length 2315;
 Best Local Similarity 95.7%; Pred. No. 6.1e-27;
 Matches 220; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
 QY 3999 TCTTCTCTTAAATTAATATCCCTCAAAACCCCTGCTATATCTCTTAAAGCCCC 4058
 |||||
 DB 1 TCTTCTCTTAAATTAATATCCCTCAAAACCCCTGCTATATCTCTTAAAGCCCC 60
 |||||
 QY 4059 CTTCCTGTTTCTCTACCGACAAAGAAAAAAGTTTGAAGAAAAATGTTGTTTC 4118
 |||||
 DB 61 CTTCCTGTTTCTCTACCGACAAAGAAAAAAGTTTGAAGAAAAATGTTGTTTC 120
 |||||
 QY 4119 GTTGTGTAACCAATGATTGGGTTTACCTTACTTCTGAGAGATTATAAGAAAGAA 4178
 |||||
 DB 121 GTTGTGTAACCAATGATTGGGTTTACCTTACTTCTGAGAGATTATAAGAGAGA 180
 |||||
 QY 4179 GTGAGATACATTATTAAGAAAGAGAGAGAAACCAAGAAAAAGAAAC 4228
 |||||
 DB 181 GTGAGATACATTATTAAGAAAGAGAGAGAAACCAAGAAAAAGAGAAC 230
 |||||

RESULT 11
 LOCUS BH510257 796 bp DNA linear GSS 13-DEC-2001
 DEFINITION BOHKU78TR BOHK Brassica oleracea genomic clone BOHKU78, genomic
 survey sequence.
 ACCESSION BH510257
 VERSION BH510257.1 GI:17718347
 KEYWORDS GSS.
 SOURCE Brassica oleracea
 ORGANISM Brassica oleracea
 Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 796)
 REFERENCE
 AUTHORS Aylee M., Haas B.J., Kumar N., Wu H., Xiao Y., Van Aken S.,
 Utechtack T.R., Wortman J.R., White O.R. and Town C.D.
 Whole genome shotgun sequencing of Brassica oleracea and its
 application to gene discovery and annotation in Arabidopsis
 JOURNAL Genome Res. 15 (4), 487-495 (2005)
 PUBMED 15805490
 COMMENT Other_GSSs: BOHKU78TF
 Contact: Chris Town
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA.
 Tel: 301-838-3523
 Fax: 301-838-0208
 Email: cdtown@tigr.org
 DNA is from a doubled haploid provided by Tom Osborn.
 Seq primer: TR
 Class: sheared ends.
 Location/Qualifiers
 1..796
 /organism="Brassica oleracea"
 /mol_type="genomic DNA"
 /strain="TO100DH3"
 /db_xref="taxon:3712"
 /clone="BOHKU78"
 /csize="BOHK"
 /note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared
 genomic DNA inserted into pHOS1 using BstXI linkers"
 ORIGIN
 Query Match 5.0%; Score 212; DB 9; Length 796;
 Best Local Similarity 76.1%; Pred. No. 1.5e-26;
 Matches 303; Conservative 0; Mismatches 85; Indels 10; Gaps 3;
 QY 2822 TTTAAACCAACAATTTTATTTGTTGCTGAAGTCAACATGTCAATATATAGAC 2881
 |||||
 DB 677 TATTAACCTTGAATACATGTCTCTGGAAGTCAACATGTCAATATATAGAC 618
 |||||

QY 2882 AGCATGCTTTATAC-AAATATGTCGATGTTATGGAATCAATATTAATGCAATTA 2940
 |||||
 Db 617 AGCATGCTGTCGATGTTATGTTGATGTTGGAATCAATATTAATGCAATTA 559
 |||||
 QY 2941 GCCATCCTGCTGTTATATGTTGGAAGTAATGAATATTAATGCAATGCAATTA 3000
 |||||
 Db 558 GCCATCCTGCTGTTATATGTTGGAAGTAATGAATATTAATGCAATGCAATTA 499
 |||||
 QY 3001 CAGAGCTATATGTCGCTGCTATTTAGAGCGTGACCAAAAGTTGCTGTAATTTCTAC 3060
 |||||
 Db 498 CAGAGCTATATGTCGCTGCTATTTAGAGCGTGACCAAAAGTTGCTGTAATTTCTAC 439
 |||||
 QY 3061 GGTGCTGCTATGAAATTTTGAAGCTTTCTTCAACCTTTTGAAGCTTCTGTAATGTTT 3120
 |||||
 Db 438 GGTGCTGCTATGAAATTTTGAAGCTTTCTTCAACCTTTTGAAGCTTCTGTAATGTTT 379
 |||||
 QY 3121 TGTGCTGCTATGAAATTTTGAAGCTTTCTTCAACCTTTTGAAGCTTCTGTAATGTTT 3172
 |||||
 Db 378 TGTGCTGCTATGAAATTTTGAAGCTTTCTTCAACCTTTTGAAGCTTCTGTAATGTTT 319
 |||||
 QY 3173 TAAATTCAGATAGAAAGCTCTTTTATTTATTTT 3210
 |||||
 Db 318 TACTTACGATTAGAAACAGCTTTCATTCATTTT 281
 |||||

RESULT 12
 AL756782 268 bp DNA linear GSS 01-APR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-113A12-012505,
 DEFINITION genomic survey sequence.
 ACCESSION AL756782
 VERSION AL756782.1 GI:21489280
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
 AUTHORS GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 TITLE the identification of T-DNA insertion mutants in Arabidopsis
 JOURNAL thaliana
 PUBMED Bioinformatics 19 (11), 1441-1442 (2003)
 REFERENCE 2 12874060
 AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 TITLE Weishaar,B.
 JOURNAL An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 PUBMED flanking sequence tag-based reverse genetics
 REFERENCE 3 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 AUTHORS 14756321
 TITLE Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
 JOURNAL Weishaar,B.
 PUBMED High-throughput generation of sequence indexes from T-DNA
 REFERENCE 4 mutagenized Arabidopsis thaliana lines
 TITLE Biotechniques 35 (6), 1164-1168 (2003)
 JOURNAL 14682050
 PUBMED 4 (bases 1 to 268)
 REFERENCE Li,Y., Rosso,M.G., Strizhov,N. and Weishaar,B.
 TITLE Direct Submission
 JOURNAL Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer
 PUBMED Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
 REFERENCE This sequence has been recovered from the left border of the T-DNA.
 TITLE It indicates an insertion within the locus defined by BAC clone
 JOURNAL T28119. Details on the protocols used for generation of the
 PUBMED sequence are described in References 1-3. The sequences are
 REFERENCE generated at the MPI for Plant Breeding Research in the context of
 TITLE the GABI-Kat project. GABI-Kat is part of the German Plant Genomics
 JOURNAL program designated 'GABI'. Information on line availability can be
 REFERENCE found at: <http://www.mpiz-koeln.mpg.de/GABI-Kat/>.
 TITLE location/Qualifiers

source
 1..268
 /organism="Arabidopsis thaliana"
 /mol_type="genomic DNA"
 /db_xref="taxon:3702"
 /clone="GK-113A12-012505"
 /clone_11b="Arabidopsis thaliana T-DNA insertion lines"
 /ecotype="Col-0"
 /note="PCR was performed on DNA from Arabidopsis thaliana
 plants (T1) which were transformed with the T-DNA from
 vector pAC161 (Genbank accession number: AJ537514). The
 lines contain one or more T-DNA insertions. The DNA
 fragment(s) resulting from the PCR were directly sequenced
 to determine the genomic sequence flanking the insertion.
 T-DNA derived sequences were removed."

Query Match 4.7%; Score 200.8; DB 10; Length 268;
 Best Local Similarity 84.3%; Pred. No. 1.4e-24;
 Matches 226; Conservative 0; Mismatches 42; Indels 0; Gaps 0;

QY 1998 TTTTGAATTAATAACACATTAATTTCTGATATACATTTTACCGTCATCCAG 2057
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 Db 1 TTTTGAATTAATAACACATTAATTTCTGATATACATTTTACCGTCATCCAG 60
 |||||
 QY 2058 ATTTGATTAAGTACAAATCTGAAACATTTTCTTGAATCTGTTAAATCT 2117
 |||||
 Db 61 ATTTGATTAAGTACAAATCTGAAACATTTTCTTGAATCTGTTAAATCT 120
 |||||
 QY 2118 CTCTGCTGATCTTGACGACATTTGACCAAGACATATGTAAGCAAAATATCC 2177
 |||||
 Db 121 CTTGCGCGCATCTGCGCGGCTTTGGACCAAGCATCTTCTTTGGAAGCAAAATTTTC 180
 |||||
 QY 2178 ACCAGGATGATAGGTTGATGCCCATTCATATCTTTGCTGTTATTAAGAA 2237
 |||||
 Db 181 CCCAGGATGATAGGTTGATGCCCATTCATATCTTTGCTGTTATTAAGAA 240
 |||||
 QY 2238 AACAAATATTATTCAGAAATAACGTT 2265
 |||||
 Db 241 AACAAATTTTTCAGAAATAACGTT 268
 |||||

RESULT 13
 AL936239 234 bp DNA linear GSS 01-APR-2004
 LOCUS Arabidopsis thaliana T-DNA flanking sequence GK-047A09-016076,
 DEFINITION genomic survey sequence.
 ACCESSION AL936239
 VERSION AL936239.1 GI:24367864
 KEYWORDS GSS.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 REFERENCE 1 Li,Y., Rosso,M.G., Strizhov,N., Viehoveer,P. and Weishaar,B.
 AUTHORS GABI-Kat SimpleSearch: a flanking sequence tag (FST) database for
 TITLE the identification of T-DNA insertion mutants in Arabidopsis
 JOURNAL thaliana
 PUBMED Bioinformatics 19 (11), 1441-1442 (2003)
 REFERENCE 2 12874060
 AUTHORS Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and
 TITLE Weishaar,B.
 JOURNAL An Arabidopsis thaliana T-DNA mutagenized population (GABI-Kat) for
 PUBMED flanking sequence tag-based reverse genetics
 REFERENCE 3 Plant Mol. Biol. 53 (1-2), 247-259 (2003)
 AUTHORS 14756321
 TITLE Strizhov,N., Li,Y., Rosso,M.G., Viehoveer,P., Dekker,K.A. and
 JOURNAL Weishaar,B.
 PUBMED High-throughput generation of sequence indexes from T-DNA
 REFERENCE mutagenized Arabidopsis thaliana lines
 TITLE

JOURNAL	BioTechniques 35 (6), 1164-1168 (2003)
PUBMED	14682050
REFERENCE	4 (bases 1 to 234)
AUTHORS	Ll.Y., Strizhov,N., Rosso,M.G. and Weishaar,B.
TITLE	Direct Submision
JOURNAL	Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT	This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by Bac clone T2819. Details on the protocols used for generation of the sequences are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-kat project. GABI-Kat is part of the German Plant Genomic program designated "GABI". Information on line availability can be found at: http://www.mpiz-koeln.mpg.de/GABI-Kat/ .
FEATURES	location/Qualifiers
source	1..234 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /clone="GK-047A09-016076" /clone_1fb="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Col-0" /note="PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector PAC161 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
ORIGIN	
Query Match	4.6%; Score 193; DB 10; Length 234;
Best Local Similarity	100.0%; Pred. No. 3.2e-23;
Matches 193; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	1092 TAGCGTTACGCTTGCGCTTCGCCGAACCTTGGCGGTGTGACTTTTTCTTAT 1151
Db	213 TAGCGTTACAGTTTGCGCTTCGCCCACTTGGCGGTGTGACTTTTTCTTAT 154
OY	1152 GTCCGTTGGACATAATTCTCAGAGGAGAAGCTATCAAGAAACTTAATATTCGAA 1211
Db	153 GTCCGTTGGACATAATTCTCAGAGGAGAAGCTATCAAGAAACTTAATATTCGAA 94
OY	1212 AGAAGAAAAAAAAGGCAGAAAACCTATTGTCAAAAGACATTAATGACACTAAATTGG 1271
Db	93 AGAAGAAAAAAAAGGCAGAAAACCTATTGTCAAAAGACATTAATGACACTAAATTGG 34
OY	1272 ATTATTAATAATG 1284
Db	33 ATTATTAATAATG 21
RESULT 14	
LOCUS	AL759737 162 bp DNA linear GSS 01-APR-2004
DEFINITION	Arabidopsis thaliana T-DNA flanking sequence GK-190B10-014641,
ACCESSION	AL759737
VERSION	AL759737.1 GI:21498085
KEYWORDS	GSS.
SOURCE	Arabidopsis thaliana (chale cress)
ORGANISM	Arabidopsis thaliana
REFERENCE	Eukaryote Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; eudicotyledons; core eudicotyledons; rosoids; eurosoid II; Brassicales; Brassicaceae; Arabidopsi.
AUTHORS	Ll.Y., Rosso,M.G., Strizhov,N., Vliehever,P. and Weishaar,B.
TITLE	GABI-Kat Simplesearch: a flanking sequence tag (FST) database for the identification of T-DNA insertion mutants in Arabidopsis thaliana
JOURNAL	Bioinformatics 19 (11), 1441-1442 (2003)
PUBMED	12874060

	REFERENCE	
AUTHORS	2	Rosso,M.G., Li,Y., Strizhov,N., Reiss,B., Dekker,K. and Weishaar,B.
TITLE		An Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag-based reverse genetics
JOURNAL PUBMED		Plant Mol. Biol. 53 (1-2), 247-259 (2003)
REFERENCE AUTHORS	3	Strizhov,N., Li,Y., Rosso,M.G., Viehoever,P., Dekker,K.A. and Weishaar,B.
TITLE		High-throughput generation of sequence indexes from T-DNA mutagenized Arabidopsis thaliana lines
JOURNAL PUBMED		BioTechniques 35 (6), 1164-1168 (2003)
REFERENCE AUTHORS	4	(bases 1 to 162) Rosso,M.G., Strizhov,N., Li,Y. and Weishaar,B. Direct Submission Submitted (31-MAR-2004) Weishaar B., Max-Planck-Institut fuer Zuechtungsforchung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
COMMENT		This sequence has been recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by BAC clone TB819. Details on the protocols used for generation of the sequence are described in References 1-3. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at: http://www.mpilz-koeln.mpg.de/GABI-Kat/. location/Qualifiers 1..162 /organism="Arabidopsis thaliana" /mol_type="genomic DNA" /db_xref="taxon:3702" /cclone="GK-190B10-0146d1" /clone_1fb="Arabidopsis thaliana T-DNA insertion lines" /ecotype="Col-0" /note=PCR was performed on DNA from Arabidopsis thaliana plants (T1) which were transformed with the T-DNA from vector pACT61 (GenBank accession number: AJ537514). The lines contain one or more T-DNA insertions. The DNA fragment(s) resulting from the PCR were directly sequenced to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed."
FEATURES	SOURCE	
ORIGIN		
Query Match		3.7%; Score 157.2; DB 10; Length 162;
Best Local Similarity		98.1%; Pred. No. 5,4e+17;
Matches 159; Conservative 0; Mismatches 3; Indels 0; Gaps 0;		
Gy	2113	ATTCTCTGTCTGCATCTTCAGCAGCATTTGACCACAAGCATATACATATTGAAGCAAAA 2172
Db	1	ACTTCTCTGTGCATCTTCAGCAGCATTTGACCACAAGCATATACATATTGAAGCAAAA 60
Gy	2173	TATCCACCGAGTGATAGGGTTAAGATGCCAACATTCATAATCTTTGTCTTGTATTTA 2232
Db	61	TATCCACCGAGTGATAGGGTTAAGATGCCAACATTCATAATCTTTGTCTTGTATTTA 120
Gy	2233	TGA AAAACA ATATTAT TCAGA AAAAA AG GTT CTCTCT CA 2274
Db	121	TGA AAAACA ATATTAT TCAGA AAAAA AG GTT CTCTCT CA 162
RESULT 15		
LOCUS		AL759736 .192 bp DNA linear GSS 01-Apr-2004
DEFINITION		Arabidopsis thaliana T-DNA flanking Sequence GK-190B10-0146d0,
ACCESSION		AL759736
VERSION		AL759736.1 GI:21498084
KEYWORDS		GSS.
ORGANISM		Arabidops thaliana (thale cress)
		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

GenCore version 5.1.7
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OM nucleic - nucleic search, using bw model1

Run on: February 27, 2006, 07:56:28 ; Search time 2341 Seconds
(without alignments)
12036.873 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtcgactcagcctcactg.....agaaacccaaaaaagaacc 4228

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 496397 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : N_Geneseq_21:*

- 1: geneseqn19808:*
- 2: geneseqn19908:*
- 3: geneseqn20008:*
- 4: geneseqn20018:*
- 5: geneseqn20018:*
- 6: geneseqn20028:*
- 7: geneseqn20028:*
- 8: geneseqn20038:*
- 9: geneseqn20038:*
- 10: geneseqn20038:*
- 11: geneseqn20048:*
- 12: geneseqn20048:*
- 13: geneseqn20048:*
- 14: geneseqn20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4228	100.0	4228	10	ADG25137 Thalecres
2	4228	100.0	4228	14	AEAI7182 A. thalia
3	4216	99.7	4227	3	AAAS9221 Promoter
4	4203.4	99.4	4228	10	ADG88432 Arabidops
5	268	6.3	2148	3	AAAS9220 Aa559220
6	268	6.3	2148	8	ABX13437 A. thalia
7	268	6.3	2148	10	ADG88430 Arabidops
8	268	6.3	2148	10	ADG88430 Arabidops
9	268	6.3	2148	10	ADG88430 Arabidops
10	147	3.5	8056	8	ABZ10246 Haematopo
11	107.8	2.5	8056	8	ABZ10246 Haematopo
12	106.8	2.5	8056	8	ABZ10246 Haematopo
13	99.4	2.4	8056	8	ABZ10246 Haematopo
14	96.6	2.3	2482	14	ADZ71091 Human chr
15	92.6	2.2	7306	6	ABN80291 Human chr
16	88.2	2.1	2131	14	ADZ71009 Human chr
17	84.6	2.0	2482	14	ADZ71091 Human chr
18	81.4	1.9	2131	14	ADZ71009 Human chr
19	77.4	1.8	4660	14	ADZ70902 Human chr

C	20	77.2	1.8	1524	14	ADZ70897	Adz70897 Human mat
C	21	75	1.8	1554	14	ADZ70999	Adz70999 Human chr
C	22	74.2	1.8	883	14	AA115210	AA115210 Human bre
C	23	74.2	1.8	960	11	ACN85231	ACN85231 Breast ca
C	24	73.2	1.7	1428	14	ADZ70899	Adz70899 Human mat
C	25	73.2	1.7	13573	6	ABL33869	ABL33869 Human chr
C	26	72	1.7	5286	13	ADS89278	ADS89278 Human chr
C	27	72	1.7	5286	13	ADS89552	ADS89552 Human chr
C	28	71.6	1.7	1524	14	ADZ70897	Adz70897 Human chr
C	29	71.6	1.7	4660	14	ADZ70902	Adz70902 Human chr
C	30	71.6	1.7	17421	4	AA545349	AA545349 Chemical1
C	31	71.6	1.7	17421	6	ABK28182	ABK28182 DNA trans
C	32	71.4	1.7	115218	8	ACA64845	ACA64845 Human HNR
C	33	70.8	1.7	1340	14	ADZ71035	Adz71035 Human chr
C	34	70.6	1.7	158001	12	ADL17884	ADL17884 Human chr
C	35	69.8	1.7	6881	6	ABL33380	ABL33380 Human chr
C	36	69.8	1.7	6881	6	ABK28249	ABK28249 DNA trans
C	37	69.2	1.6	2000	11	ACL35887	ACL35887 Rice stre
C	38	69.2	1.6	110000	13	ABD32968_6	ABD32968_6 Human chr
C	39	69	1.6	1554	14	ADZ70999	Adz70999 Human chr
C	40	68.8	1.6	679	14	ADZ70998	Adz70998 Human chr
C	41	68.6	1.6	4590	1	AA60472	AA60472 Sequence
C	42	68.6	1.6	15548	6	ABL34155	ABL34155 Human chr
C	43	68.4	1.6	110000	13	ABD32968_6	ABD32968_6 Human chr
C	44	68.2	1.6	5286	13	ADS89551	ADS89551 Oligonuci
C	45	68	1.6	17703	6	ABK39953	ABK39953 Human chr

ALIGNMENTS

RESULT 1	ADG25137	ADG25137 standard; DNA; 4228 BP.	
ID	ADG25137		
AC	ADG25137		
XX	26-FEB-2004	(first entry)	
XX	Thalecress Aintegumenta, ANT, gene promoter.		
XX	Thalecress; ds; promoter; Aintegumenta; ANT; AP2 domain; plant;		
KW	seed mass; asexual reproduction; reduced fertility.		
XX	Arabidopsis thaliana.		
OS	US6639128-B1.		
PN	XX		
XX	28-OCT-2003.		
PD	XX		
XX	07-JAN-2000; 2000US-00479855.		
PF	XX		
XX	08-JAN-1999; 99US-00227421.		
PR	XX		
XX	(NASC-) NAT SCI FOUND.		
PA	XX		
XX	Fischer RL, Mizukami Y;		
PI	XX		
XX	WPI; 2003-842795/78.		
DR	XX		
XX	New nucleic acid, useful in conferring desired traits on plants, such as		
PT	increased seed mass, asexual reproduction or reduced fertility.		
XX	Disclosure; SEQ ID NO 3; 25pp; English.		
PS	XX		
XX	The invention relates to an isolated nucleic acid comprising a		
CC	polynucleotide encoding a polypeptide having at least 90% identity with a		
CC	Canola Aintegumenta, ANT, (appearing as ADG25139) as determined using a		
CC	BLAST algorithm and comprising two AP2 domains. Also included are an		
CC	expression cassette comprising a plant promoter operably linked to a		
CC	heterologous polynucleotide encoding the polypeptide, a vector comprising		
CC	the expression cassette, a plant comprising the plant promoter operably		
CC	linked to the heterologous polynucleotide, a method of asexually		

reproducing a plant and a method of reducing fertility in a plant. The nucleic acid is useful in conferring desired traits on plants, such as increased seed mass, asexual reproduction or reduced fertility. The present sequence is the promoter region of the *Thalassia* *Ain* gene.

Sequence 4228 BP; 1489 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;

Query Match 100.0%; Score 4228; DB 10; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCTGAGGCTGACCTGACCTAATGACACTCACTATGAGGAGCTGAGAGATCCCTTA 60
DB 1 GTGACCTGAGGCTGACCTGACCTAATGACACTCACTATGAGGAGCTGAGAGATCCCTTA 60
QY 61 GTTGAAGAAAACTTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 GTTGAAGAAAACTTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ACATGTGATTCACATATATATATATGAAATTTGCAATTTATGATGATGAT 180
DB 121 ACATGTGATTCACATATATATATATGAAATTTGCAATTTATGATGATGAT 180
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DB 181 TATATATATAGCTGACATTAACAACCAATGTTCTGCTTTATGAGATGCTATAT 240
QY 241 GTTGCACTGATTAATGATACATATATATATATATATATATATATATATATATATAT 300
DB 241 GTTGCACTGATTAATGATACATATATATATATATATATATATATATATATATATAT 300
QY 301 AAAAGTGACCAAAAGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 AAAAGTGACCAAAAGAGATCCATGTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 ATGATTAATGAGATTAATTAATCTTACTAATTAATTAATTAATTAATTAATTAATTAAT 420
DB 361 ATGATTAATGAGATTAATTAATCTTACTAATTAATTAATTAATTAATTAATTAATTAAT 420
QY 421 ATATGTGAGTGTCTTCAAGTCTCACTGTCAAGAAATTAATCTGATTAATCTTCACTTGA 480
DB 421 ATATGTGAGTGTCTTCAAGTCTCACTGTCAAGAAATTAATCTGATTAATCTTCACTTGA 480
QY 481 CTGAAAGTTGATTAACAACAGTGAATTTTAAACGACCTGATTAATTAATTAATTAATTA 540
DB 481 CTGAAAGTTGATTAACAACAGTGAATTTTAAACGACCTGATTAATTAATTAATTAATTA 540
QY 541 CGATCAAAATCAAAATTAATTAATGAGATCAAGATGAGGATGCTGATGAGATTA 600
DB 541 CGATCAAAATCAAAATTAATTAATGAGATCAAGATGAGGATGCTGATGAGATTA 600
QY 601 TACAGAGCTAAGATTTGTAACAAGAGTCAAGAAATTAATTAATTAATTAATTAATTA 660
DB 601 TACAGAGCTAAGATTTGTAACAAGAGTCAAGAAATTAATTAATTAATTAATTAATTA 660
QY 661 TATGATTTGATGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
DB 661 TATGATTTGATGATGATGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 720
QY 721 TGTGTTTGTGTTTCCGATTAATGAAATGTTGTGTTTAAATTAATTAATTAATTAATTA 780
DB 721 TGTGTTTGTGTTTCCGATTAATGAAATGTTGTGTTTAAATTAATTAATTAATTAATTA 780
QY 781 AACTGCTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
DB 781 AACTGCTTATGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 840
QY 841 TACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
DB 841 TACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 900
QY 901 TATGTTAAGCTACAAATTTTCTCTTGAATTAATTAATTAATTAATTAATTAATTA 960

DB 901 TATGTTAATCTACAAATTTTCTCTTGAATTAATTAATTAATTAATTAATTAATTAATTA 960
QY 961 CCTTGACGGGATTAAGGATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
DB 961 CCTTGACGGGATTAAGGATCTGATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1020
QY 1021 TGTGCTTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
DB 1021 TGTGCTTAAAGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1080
QY 1081 GAGATCCATTAAGCTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 1140
DB 1081 GAGATCCATTAAGCTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTTCAAGTTT 1140
QY 1141 TTTTTCCTTAATGCTGTTGTTTGAATTTTCTGAGATGAGATGATTAATTAATTAATTA 1200
DB 1141 TTTTTCCTTAATGCTGTTGTTTGAATTTTCTGAGATGAGATGATTAATTAATTAATTA 1200
QY 1201 AATATTCGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1260
DB 1201 AATATTCGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGGAAAGG 1260
QY 1261 ACTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
DB 1261 ACTAAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1320
QY 1321 AATCAAG 1380
DB 1321 AATCAAG 1380
QY 1381 CCACATATCTTTTACTTCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
DB 1381 CCACATATCTTTTACTTCAACAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1440
QY 1441 ACTTTCATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
DB 1441 ACTTTCATCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1500
QY 1501 TCGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
DB 1501 TCGATTAATTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1560
QY 1561 CTCCTTCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
DB 1561 CTCCTTCGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1620
QY 1621 CATTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
DB 1621 CATTCCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1680
QY 1681 GGTATTAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
DB 1681 GGTATTAAGGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1740
QY 1741 GGAAGAAATTCAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
DB 1741 GGAAGAAATTCAGGCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1800
QY 1801 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
DB 1801 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1860
QY 1861 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
DB 1861 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1920
QY 1921 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
DB 1921 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1980
QY 1981 TTAACCATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2040

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Db 1981 TTAACACATGATGTTTTTGTATTTAAAAACATTAATTTCTAGTATTAACACTT 2040
Qy TTTAACCGTCCATCCAGATTGTATTAAGTGAACAAATCGAAAAAATTTTTTTTCTTG 2100
Db 2041 TTTAACCGTCCATCCAGATTGTATTAAGTGAACAAATCGAAAAAATTTTTTTTCTTG 2100
Qy 2101 AATCTGTTAAATTTCTCTGCTGCATACCTTGAGGCAATTGACCAACGACTATACATA 2160
Db 2101 AATCTGTTAAATTTCTCTGCTGCATACCTTGAGGCAATTGACCAACGACTATACATA 2160
Qy 2161 TTGAAGCAAAATATCCACGAGGATGATAGGTTAGATCCCACTTCAATATCTTTTGT 2220
Db 2161 TTGAAGCAAAATATCCACGAGGATGATAGGTTAGATCCCACTTCAATATCTTTTGT 2220
Qy 2221 CTTTGTATTTATGAAAAAATAATTTATGAGAAAAAAGTTTCTTCTGATGAGTA 2280
Db 2221 CTTTGTATTTATGAAAAAATAATTTATGAGAAAAAAGTTTCTTCTGATGAGTA 2280
Qy 2281 TAACTATAGATATATAAATAATTTAACTATGATTAATGATTAATCTTCAAACTT 2340
Db 2281 TAACTATAGATATATAAATAATTTAACTATGATTAATGATTAATCTTCAAACTT 2340
Qy 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTCTTAAACTACTTCCACTA 2400
Db 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTCTTAAACTACTTCCACTA 2400
Qy 2401 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAAGTAAATTAAGATGAGTGGTAT 2460
Db 2401 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAAGTAAATTAAGATGAGTGGTAT 2460
Qy 2461 TCTTACGCAAAAAGGCGCCGAGAGGCTCTTATCCATCAATTAAGCTGGGTTGCGAG 2520
Db 2461 TCTTACGCAAAAAGGCGCCGAGAGGCTCTTATCCATCAATTAAGCTGGGTTGCGAG 2520
Qy 2521 ACATCATAGAGGCTCATATATTTAGCTTTAAGCTTAACTGTAAGCTTTAACAATCTAGT 2580
Db 2521 ACATCATAGAGGCTCATATATTTAGCTTTAAGCTTAACTGTAAGCTTTAACAATCTAGT 2580
Qy 2581 TAGTCTCACTGTAACAAACAAACAAATTCATTCGTAATATATATACAAATCTACTA 2640
Db 2581 TAGTCTCACTGTAACAAACAAACAAATTCATTCGTAATATATATACAAATCTACTA 2640
Qy 2641 GTATCATATTAACGTAAGTATACATCGCTTTTTCGCAAAATTTCTAAACTATCTATCAA 2700
Db 2641 GTATCATATTAACGTAAGTATACATCGCTTTTTCGCAAAATTTCTAAACTATCTATCAA 2700
Qy 2701 CAAACTGGAATGTTTGTGTGTAATTTATCTTAAACCAAGTTTGAATGTGCAATGGG 2760
Db 2701 CAAACTGGAATGTTTGTGTGTAATTTATCTTAAACCAAGTTTGAATGTGCAATGGG 2760
Qy 2761 AGCTACACTGTAAGTCCCTTTTCCCAAAATATATCTCTTACATGACCGGTTAAAGT 2820
Db 2761 AGCTACACTGTAAGTCCCTTTTCCCAAAATATATCTCTTACATGACCGGTTAAAGT 2820
Qy 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGGTACAAACATGTCAATATATAGAGA 2880
Db 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGGTACAAACATGTCAATATATAGAGA 2880
Qy 2881 CAGATCGTTATATCAAAATATGTTGATGTTATGSAATCAAAATTAATATGSAATTA 2940
Db 2881 CAGATCGTTATATCAAAATATGTTGATGTTATGSAATCAAAATTAATATGSAATTA 2940
Qy 2941 GCGACTCACTGTTTAAATATGTTTGAAGATTAATGAATTAATTAATGAAGATA 3000
Db 2941 GCGACTCACTGTTTAAATATGTTTGAAGATTAATGAATTAATTAATGAAGATA 3000
Qy 3001 CAGAGCTATATATGTGGGCTATTTAGAGCGGTGACCAAAAGTTTGTCTGTAATTTCTAC 3060
Db 3001 CAGAGCTATATATGTGGGCTATTTAGAGCGGTGACCAAAAGTTTGTCTGTAATTTCTAC 3060
Qy 3061 GGTGCGCTATATGAAATTTTGAAGCTTTTCAACCCCTTTATGAACTTCTGTATAGTTTT 3120
Db 3061 GGTGCGCTATATGAAATTTTGAAGCTTTTCAACCCCTTTATGAACTTCTGTATAGTTTT 3120
```

QY 4201 AGAAGACGAGAAACCAAAAAAGAAACC 4228
DB 4201 AGAAGACGAGAAACCAAAAAAGAAACC 4228

RESULT 2

ID ABA17182

ABA17182 standard; cDNA; 4228 BP.

ABA17182;

25-AUG-2005 (first entry)

A. thaliana aintegumenta (ANT) 5' promoter, seq id 3.

XX plant engineering; growth; cell proliferation; organ mass; fertility;
KW asexual reproduction; aintegumenta; ANT; plant; promoter; ds.

Arabidopsis thaliana.

US2005132445-A1.

16-JUN-2005.

18-JUL-2003; 2003US-00623477.

07-JAN-2000; 2000US-00479855.

(REGC) UNIV CALIFORNIA.

Fischer RL, Mizukami Y;

WPI; 2005-424635/43.

XX Modulating growth and cell proliferation in a plant, useful in plant
PT genetic engineering, comprises modulating aintegumenta (ANT) gene
PT activity and selecting plants with altered cell number.

Claim 52; SEQ ID NO 3; 27bp; English.

XX The invention relates to modulating growth and cell proliferation in a
CC plant comprising modulating aintegumenta (ANT) gene activity and
CC selecting plants with altered cell number. Further disclosed is a method
CC for directing expression of a heterologous nucleic acid in meristematic
CC cells of a plant. The method is useful in plant genetic engineering,
CC specifically for altering organ mass, controlling fertility and enhancing
CC asexual reproduction in plants. The current sequence represents the A.
CC thaliana ANT promoter sequence.

SQ Sequence 4228 BP; 1489 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;

Query Match 100.0%; Score 4228; DB 14; Length 4228;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGACCTTAGGCTCACTGCGCTAATAGACTCACTATAGGAGCTCGAGATCCCTTA 60
DB 1 GTGACCTTAGGCTCACTGCGCTAATAGACTCACTATAGGAGCTCGAGATCCCTTA 60
QY 61 GTTAGAAAAAACTTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
DB 61 GTTAGAAAAAACTTTCTTTGTAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
QY 121 ACATGTGATATCAACAATATATATATATGAAATTGGAATTATTCATATATAGAGTACAT 180
DB 121 ACATGTGATATCAACAATATATATATATGAAATTGGAATTATTCATATATAGAGTACAT 180
QY 181 TAATATATATAGCTGATTAACCAACCAATGTTTCTGCTTTATAGATATATATATATAT 240
DB 181 TAATATATATAGCTGATTAACCAACCAATGTTTCTGCTTTATAGATATATATATATAT 240
QY 241 GTTGACCTTAGATATAGAT 300
DB 241 GTTGACCTTAGATATAGAT 300

DB 241 GTTGACCTTAGATATAGAT 300
QY 301 AAAAGTGAGCAAAACGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
DB 301 AAAAGTGAGCAAAACGATCCATGCTTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 360
QY 361 ATGATATATAGAAATTAATCTTTACTAATATATATATATATATATATATATATATATAT 420
DB 361 ATGATATATAGAAATTAATCTTTACTAATATATATATATATATATATATATATATATAT 420
QY 421 ATATGTGTAGTGTCTTCACTGCTCACTGTTCAAGAAATATCTGTGTATCTTACTTGA 480
DB 421 ATATGTGTAGTGTCTTCACTGCTCACTGTTCAAGAAATATCTGTGTATCTTACTTGA 480
QY 481 CTAGAGTGTAT 540
DB 481 CTAGAGTGTAT 540
QY 541 CGATCAAAATACAAATTTATATAGACTAGATATCCAAAGATGAGATGCTTACAGAAATA 600
DB 541 CGATCAAAATACAAATTTATATAGACTAGATATCCAAAGATGAGATGACTTACAGAAATA 600
QY 601 TACACAGCTAAGATTTGTACAAAGAGCTCGAAAAATAGATTCTATCATTTAAAAAGA 660
DB 601 TACACAGCTAAGATTTGTACAAAGAGAGCTCGAAAAATAGATTCTATCATTTAAAAAGA 660
QY 661 TATGATTTCACTGCTCGATGATATATATATATATATATATATATATATATATATATAT 720
DB 661 TATGATTTCACTGCTCGATGATATATATATATATATATATATATATATATATATATAT 720
QY 721 TGT 780
DB 721 TGT 780
QY 781 AACTGTTTATGTAT 840
DB 781 AACTGTTTATGTAT 840
QY 841 TACAATTTATGTAT 900
DB 841 TACAATTTATGTAT 900
QY 901 TATGTATATGTAT 960
DB 901 TATGTATATGTAT 960
QY 961 CTTGCAAGGAGTAT 1020
DB 961 CTTGCAAGGAGTAT 1020
QY 1021 TCTGTCTTAAAGATATCTACAGCTGCTTGCCTGTGAATATGAAAGAAATGATATGTA 1080
DB 1021 TCTGTCTTAAAGATATCTACAGCTGCTTGCCTGTGAATATGAAAGAAATGATATGTA 1080
QY 1081 GAGATCCCATCTAGCGCTTCACTGCTTGCCTGTGCAACTTTGGCGGCTTGTGACT 1140
DB 1081 GAGATCCCATCTAGCGCTTCACTGCTTGCCTGTGCAACTTTGGCGGCTTGTGACT 1140
QY 1141 TTTTCTTATATGT 1200
DB 1141 TTTTCTTATATGT 1200
QY 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAAACATATGTGAAAAAGCATTAATGAC 1260
DB 1201 AATATTCGAAAAAGAAAAAGAAAAAGCAAAACATATGTGAAAAAGCATTAATGAC 1260
QY 1261 ACTTAAATTTGAT 1320
DB 1261 ACTTAAATTTGAT 1320
QY 1321 AATCAAG 1380
DB 1321 AATCAAG 1380

QY 1381 CCCAGTACCTTTTCTTACTTCGACAAATCATTCACAGGAAATCTGTCTGTATC 1440
 DB 1381 CCCAGTACCTTTTCTTACTTCGACAAATCATTCACAGGAAATCTGTCTGTATC 1440
 QY 1441 ACTTCATGCAAAATTAACATAATTTTGGTATTTTGTCAAGTCTGTCTGTAG 1500
 DB 1441 ACTTCATGCAAAATTAACATAATTTTGGTATTTTGTCAAGTCTGTCTGTAG 1500
 QY 1501 TCGATTAATTTGGTAATCTATAATGTGTGATATACATCCAGCTAATCATTAATGAT 1560
 DB 1501 TCGATTAATTTGGTAATCTATAATGTGTGATATACATCCAGCTAATCATTAATGAT 1560
 QY 1561 CTCCTTGTGCTTATCAATTAATTAACACATTAAGCTAATCAAGCTAATTAACCA 1620
 DB 1561 CTCCTTGTGCTTATCAATTAATTAACACATTAAGCTAATCAAGCTAATTAACCA 1620
 QY 1621 CATTCCTTATCAATTTTATATGTATGTAATTAATAACAACGATATAGCTACAGATT 1680
 DB 1621 CATTCCTTATCAATTTTATATGTATGTAATTAATAACAACGATATAGCTACAGATT 1680
 QY 1681 GGTATTAAGCATTAATGCTCTAGTCGAAGGAATTTTGTATGATTAACATCTGTG 1740
 DB 1681 GGTATTAAGCATTAATGCTCTAGTCGAAGGAATTTTGTATGATTAACATCTGTG 1740
 QY 1741 GGAATAAAATCCAGCCCTAATATGCTCATTTAAAGGATTAATGCTTAAATCA 1800
 DB 1741 GGAATAAAATCCAGCCCTAATATGCTCATTTAAAGGATTAATGCTTAAATCA 1800
 QY 1801 TTAATAATAAAGGTTTGTCTTAAAGGTACCAACGCTTAATTCATCATTAAGAGAT 1860
 DB 1801 TTAATAATAAAGGTTTGTCTTAAAGGTACCAACGCTTAATTCATCATTAAGAGAT 1860
 QY 1861 ATTAACCTTATGCAAAATTCGAAATTAATCTTTTAAACATTAAGAAATTTTCAGATTT 1920
 DB 1861 ATTAACCTTATGCAAAATTCGAAATTAATCTTTTAAACATTAAGAAATTTTCAGATTT 1920
 QY 1921 TTAATAATAAAGGTTATTAATGCTTCAATTAATGCTTCCAGTAAATTTGGAGT 1980
 DB 1921 TTAATAATAAAGGTTATTAATGCTTCAATTAATGCTTCCAGTAAATTTGGAGT 1980
 QY 1981 TTAACCATGATATGTTTGTATTAATAAACAATTAATTTCTAGTATTAACATTT 2040
 DB 1981 TTAACCATGATATGTTTGTATTAATAAACAATTAATTTCTAGTATTAACATTT 2040
 QY 2041 TTTAACCGTCATTCAGATTTGTAATAGTGAACAATCTGAAAACATTTTCTGTG 2100
 DB 2041 TTTAACCGTCATTCAGATTTGTAATAGTGAACAATCTGAAAACATTTTCTGTG 2100
 QY 2101 AATCTGTTTAAATTCCTCTGCTGCAATCTTGAGGATTAATCCATTCATTAATCTTTGT 2160
 DB 2101 AATCTGTTTAAATTCCTCTGCTGCAATCTTGAGGATTAATCCATTCATTAATCTTTGT 2160
 QY 2161 TTTAAAGCAAAATATCCAGAGGATGATAGGTTAGATCCCATTCATTAATCTTTGT 2220
 DB 2161 TTTAAAGCAAAATATCCAGAGGATGATAGGTTAGATCCCATTCATTAATCTTTGT 2220
 QY 2221 CTTTGTATTTATGAAAAAATAATTTATCAGGAAAAAAACGTTCTCTAGTGTGA 2280
 DB 2221 CTTTGTATTTATGAAAAAATAATTTATCAGGAAAAAAACGTTCTCTAGTGTGA 2280
 QY 2281 TAAATATAGATTAATAAATAATTTAATCTAGTAAATGATTAATCTTCAAACTT 2340
 DB 2281 TAAATATAGATTAATAAATAATTTAATCTAGTAAATGATTAATCTTCAAACTT 2340
 QY 2341 ACCATCTTGAACATTAATTAATGATCAATTTTATTTTCTTAACTAATCTTCACTA 2400
 DB 2341 ACCATCTTGAACATTAATTAATGATCAATTTTATTTTCTTAACTAATCTTCACTA 2400
 QY 2401 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAATTAATTAAGATGATGGTAT 2460
 DB 2401 AAAAAATGCAAAAGAGATATATATTTAAGTCAAAATTAATTAAGATGATGGTAT 2460

QY 2461 TCTTCAGCAAAAAGGCGCCGTAGAGGTGCTTATCCATTAACATTAACAGTGGTTGTGAG 2520
 DB 2461 TCTTCAGCAAAAAGGCGCCGTAGAGGTGCTTATCCATTAACATTAACAGTGGTTGTGAG 2520
 QY 2521 ACATCAATAGGCGCTACGTATATTTGAGCTTACTGTACGTAAGCTTTAAATCATATCTAGT 2580
 DB 2521 ACATCAATAGGCGCTACGTATATTTGAGCTTACTGTACGTAAGCTTTAAATCATATCTAGT 2580
 QY 2581 TAGTTCCTACTGTACAAAACAAAATCCAAATTCGTAACATTAATTAACATTAATCTA 2640
 DB 2581 TAGTTCCTACTGTACAAAACAAAATCCAAATTCGTAACATTAATTAACATTAATCTA 2640
 QY 2641 GTACTAGATTAACGCTACGTATACATGCTTTTGTGCAAAATTTCTAAATCTATCTAACA 2700
 DB 2641 GTACTAGATTAACGCTACGTATACATGCTTTTGTGCAAAATTTCTAAATCTATCTAACA 2700
 QY 2701 CAAACTGGAATGTTTGTATTAATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
 DB 2701 CAAACTGGAATGTTTGTATTAATTTATCTTAAACCAAGTTTGAATGTGATGGG 2760
 QY 2761 AGCTACCTCTAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTTAAAGT 2820
 DB 2761 AGCTACCTCTAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTTAAAGT 2820
 QY 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGGTACAAACATGTCATATATAGAGA 2880
 DB 2821 ATTTAAACCAACAAATTTTAAATTTGTGCTGAAGGTACAAACATGTCATATATAGAGA 2880
 QY 2881 CAGCATGCTTATTAACAAATTAATGTCATGTTATGGAATTCAAATTAATAATGCAATTA 2940
 DB 2881 CAGCATGCTTATTAACAAATTAATGTCATGTTATGGAATTCAAATTAATAATGCAATTA 2940
 QY 2941 GCGACTCACTGCTTATTAATGTTTGAAGATTAATGAATTAATAATGAATTCAGAGATA 3000
 DB 2941 GCGACTCACTGCTTATTAATGTTTGAAGATTAATGAATTAATAATGAATTCAGAGATA 3000
 QY 3001 CAGAGCTATTAATGCTGGGCTCATTTAGAGCGGAGCAACAAAGTTTGTGCTAAATTTCTAC 3060
 DB 3001 CAGAGCTATTAATGCTGGGCTCATTTAGAGCGGAGCAACAAAGTTTGTGCTAAATTTCTAC 3060
 QY 3061 GGTGCGTCATTAAGAAATTTTGAATTTCTTCAACCCCTTTATGAACTTCTGTATAGTTT 3120
 DB 3061 GGTGCGTCATTAAGAAATTTTGAATTTCTTCAACCCCTTTATGAACTTCTGTATAGTTT 3120
 QY 3121 TGTGGAATTAATTAATTTGATTCGTATATTTTGTCTTAATTAATGATAGTAATTTCA 3180
 DB 3121 TGTGGAATTAATTAATTTGATTCGTATATTTTGTCTTAATTAATGATAGTAATTTCA 3180
 QY 3181 CGATTAAGAAAGACTTCTTTTATTTAATTTGAATTTAAACCTTTTGTGGAATGACT 3240
 DB 3181 CGATTAAGAAAGACTTCTTTTATTTAATTTGAATTTAAACCTTTTGTGGAATGACT 3240
 QY 3241 CATACCAAGGTTAAAGTTGATGATATCCAAATTTTACAAAATGTTTCAAGAGTCTTC 3300
 DB 3241 CATACCAAGGTTAAAGTTGATGATATCCAAATTTTACAAAATGTTTCAAGAGTCTTC 3300
 QY 3301 GAGTGTCTTAACAACATCGTACCAACTCGTATGAGGTTATTAATGAGTTTCTTCTT 3360
 DB 3301 GAGTGTCTTAACAACATCGTACCAACTCGTATGAGGTTATTAATGAGTTTCTTCTT 3360
 QY 3361 TTTTCGAATGCTTATTAATTTGAACCACTTAATTTCTTTTAAATTAATGATTAAGAT 3420
 DB 3361 TTTTCGAATGCTTATTAATTTGAACCACTTAATTTCTTTTAAATTAATGATTAAGAT 3420
 QY 3421 CTTGAATTTCTGTGATTTTAAACCAAGGTTTCAATCTTCTTGAACAATAAAAAAAA 3480
 DB 3421 CTTGAATTTCTGTGATTTTAAACCAAGGTTTCAATCTTCTTGAACAATAAAAAAAA 3480
 QY 3481 AAAAAATGCAATTAATTAAGATTAATTTTGAAGTCAAGATTTAATGATGCT 3540
 DB 3481 AAAAAATGCAATTAATTAAGATTAATTTTGAAGTCAAGATTTAATGATGCT 3540
 QY 3541 GAAAAATGATTAATGATGCAAGTTTGAACCAAGATGCTGAATGATATCAAAAA 3600

Db 3541 GAAAAGTTAATGATGATGCAAGTTTGCAACAGAAATGATGATGATCATATCAAAA 3600
 Qy 3601 CATGCATCAAAAATTAATATTCGTGCTTAGCAAGAAAGCAATGAATAACGAACAT 3660
 Db 3601 CATGCATCAAAAATTAATATTCGTGCTTAGCAAGAAAGCAATGAATAACGAACAT 3660
 Qy 3661 CGTTAACCACTTAAATCTTAGAATAATTTGATGATGAATTTCTGTAAGAGAGAG 3720
 Db 3661 CGTTAACCACTTAAATCTTAGAATAATTTGATGATGAATTTCTGTAAGAGAGAG 3720
 Qy 3721 TATCATATCTTCAAAAATACTCATTTGATGATGAATAATATGATGATGATGATGAT 3780
 Db 3721 TATCATATCTTCAAAAATACTCATTTGATGATGAATAATATGATGATGATGATGAT 3780
 Qy 3781 AGATATGTTTGTGCTGATCATGTTGATGATGATGATGATGATGATGATGATGATGAT 3840
 Db 3781 AGATATGTTTGTGCTGATCATGTTGATGATGATGATGATGATGATGATGATGATGAT 3840
 Qy 3841 TTTTAAATGTTTCAAAAGACTTACAAAATAATAATAATAATAATAATAATAATAATA 3900
 Db 3841 TTTTAAATGTTTCAAAAGACTTACAAAATAATAATAATAATAATAATAATAATAATA 3900
 Qy 3901 CTAAAAAGCAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3960
 Db 3901 CTAAAAAGCAAAAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 3960
 Qy 3961 AGATCCCAAGGATTCAAACAGCAAAATTTGCTGCTTCTTCTTCTTCTTCTTCTTCTT 4020
 Db 3961 AGATCCCAAGGATTCAAACAGCAAAATTTGCTGCTTCTTCTTCTTCTTCTTCTTCTT 4020
 Qy 4021 CTCTCAAAAACCTCTCTATATCTCTTAAAGCCCCCTTCTCTGTTCTCAACGCGAA 4080
 Db 4021 CTCTCAAAAACCTCTCTATATCTCTTAAAGCCCCCTTCTCTGTTCTCAACGCGAA 4080
 Qy 4081 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4140
 Db 4081 CAAAGAAAAAACAAGTTTGAGAAAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4140
 Qy 4141 TTTAGCTTACTTCTGAGATTTATTAAGAAAGAAAGATGATGATGATGATGATGATGAT 4200
 Db 4141 TTTAGCTTACTTCTGAGATTTATTAAGAAAGAAAGATGATGATGATGATGATGATGAT 4200
 Qy 4201 AGAGAGCAAGAAACCAAAAAGAAACC 4228
 Db 4201 AGAGAGCAAGAAACCAAAAAGAAACC 4228

RESULT 3
 AAAS9221
 ID AAAS9221 standard, cDNA; 4227 BP.

AC AAAS9221;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Promoter sequence of the Arabidopsis aintegumenta (ANT) gene.
 XX
 KW Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;
 KW asexual reproduction; plant; male sterile plant; female sterile plant;
 KW early flowering; promoter; ss.
 XX
 OS Arabidopsis sp.
 XX
 PN MO200040694-A2.
 XX
 PD 13-JUL-2000.
 XX
 PF 07-JAN-2000; 2000MO-US000465.
 XX
 PR 08-JAN-1999; 99US-00227421.
 XX
 PA (REGC) UNIV CALIFORNIA.

XX
 PI Fischer RL, Mizukami Y;
 XX
 DR MPI, 2000-465969/40.
 XX
 PT Modulating growth and cell proliferation in a plant used to alter organ
 PT mass, control fertility and enhance asexual reproduction in plants
 PT comprises modulating ANT activity and selecting plants with altered cell
 PT number.
 XX
 PS Claim 4; Page 41-43; 54pp; English.
 XX
 CC The present sequence represents a promoter of an aintegumenta (ANT) gene.
 CC The ANT gene is expressed and functions not only in developing ovules but
 CC also in various developing organs. Growth and cell proliferation in plant
 CC can be modulated by modulating ANT activity. Modulation of ANT activity
 CC is used to alter organ mass, control fertility and enhance asexual
 CC reproduction in plants. Increased ANT activity can be used to produce
 CC male or female sterile plants. Inhibition of ANT activity can be used to
 CC truncate vegetative growth, resulting in early flowering
 XX
 SQ Sequence 4227 BP; 1488 A; 651 C; 641 G; 1447 T; 0 U; 0 Other;
 Query Match 99.7%; Score 4216; DB 3; Length 4227;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 4227; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 GTGCACTTAGAGCCCTCACTGCGCTTAATACGACTCACTAATAGGAGCTCGAGATCCTTAA 60
 Db 1 GTGCACTTAGAGCCCTCACTGCGCTTAATACGACTCACTAATAGGAGCTCGAGATCCTTAA 60
 Qy 61 GTTAGAAAAAAGCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Db 61 GTTAGAAAAAAGCTTCTTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
 Qy 121 ACATGATATCAAT 180
 Db 121 ACATGATATCAAT 180
 Qy 181 TAATATATATAGCTGATCACTTACCAACCAAAAGTTTCTGCTTATATATATATATATATAT 240
 Db 181 TAATATATATAGCTGATCACTTACCAACCAAAAGTTTCTGCTTATATATATATATATATAT 240
 Qy 241 GTTGCACTTAT 300
 Db 241 GTTGCACTTAT 300
 Qy 301 AAAAGTGAACAAACGAGATCCATGTTTGTGTTTACTTGTGTTTAAACCAATAT 360
 Db 301 AAAAGTGAACAAACGAGATCCATGTTTGTGTTTACTTGTGTTTAAACCAATAT 360
 Qy 361 ATGATATATGAAAGATTAATCTTCTTATATATATATATATATATATATATATATATATAT 420
 Db 361 ATGATATATGAAAGATTAATCTTCTTATATATATATATATATATATATATATATATATAT 420
 Qy 421 ATATGTTGATGCTTCAAGTCACTGTTCAAGAAATAATCTGCTTATCTTACTTGA 480
 Db 421 ATATGTTGATGCTTCAAGTCACTGTTCAAGAAATAATCTGCTTATCTTACTTGA 480
 Qy 481 CTAGAAATGAT 540
 Db 481 CTAGAAATGAT 540
 Qy 541 CGATCAATATCAAT 600
 Db 541 CGATCAATATCAAT 600
 Qy 601 TACACAGCTAAGATTTGTAACAAGAGTCAAGAAATAGATTTATATATATATATATATATATAT 660
 Db 601 TACACAGCTAAGATTTGTAACAAGAGTCAAGAAATAGATTTATATATATATATATATATATAT 660
 Qy 661 TATGATTTCAAGTATGAT 720

Db 661 TATGATTTTCAGTTACGGATTGATATTACATTAACGAGTAGTACATACATATTTTT 720
Qy 721 TGTTTTGTTTTACGGATTAATAGAAATGATGTTTAAATAATGGTTTTTACTTA 780
Db 721 TGTTTTGTTTTACGGATTAATAGAAATGATGTTTAAATAATGGTTTTTACTTA 780
Qy 781 AACTCGTTTTATGTTAACTATATATGCTTCCGCACTGTAATTTGAAACAAACCTGTA 840
Db 781 AACTCGTTTTATGTTAACTATATATGCTTCCGCACTGTAATTTGAAACAAACCTGTA 840
Qy 841 TACAAATTAATGTTAAGCCATTGCAATTAATAAATCCAAGGTAGTAAATCTCAGAAAT 900
Db 841 TACAAATTAATGTTAAGCCATTGCAATTAATAAATCCAAGGTAGTAAATCTCAGAAAT 900
Qy 901 TAGTTTAAGTCTACAAATTTTCTCTTATGATTAAGTTTGAACAATAATTAATTA 960
Db 901 TAGTTTAAGTCTACAAATTTTCTCTTATGATTAAGTTTGAACAATAATTAATTA 960
Qy 961 CTTTGACAGGGGTATTAAGTCACTGCAATGTCAGACTCAGCATGAGCCAAAGATGCTC 1020
Db 961 CTTTGACAGGGGTATTAAGTCACTGCAATGTCAGACTCAGCATGAGCCAAAGATGCTC 1020
Qy 1021 TCTGTCTTAAGAATATCTACAGCTGCTCCCTGTGAATAGAGAATAATGTAATGA 1080
Db 1021 TCTGTCTTAAGAATATCTACAGCTGCTCCCTGTGAATAGAGAATAATGTAATGA 1080
Qy 1081 GAATGCCATCTAGCGTTTCACTGCTTCCCTGCGCACTTTGGCGGTTGTGACT 1140
Db 1081 GAATGCCATCTAGCGTTTCACTGCTTCCCTGCGCACTTTGGCGGTTGTGACT 1140
Qy 1141 TTTTCTTATGATGCTGTTTGACTAATTTTCTCAGAGTAGAGTGAATCAAGAAACT 1200
Db 1141 TTTTCTTATGATGCTGTTTGACTAATTTTCTCAGAGTAGAGTGAATCAAGAAACT 1200
Qy 1201 AATATTCGAAAGAGAAAGAAAGAAAGCAAGAAACTATTTGCGAAAGACATTAATGAC 1260
Db 1201 AATATTCGAAAGAGAAAGAAAGAAAGCAAGAAACTATTTGCGAAAGACATTAATGAC 1260
Qy 1261 ACTTAAATTTGATTTAATAAATGATTAATATGTTTGTGGAATTTAATCAATTACAA 1320
Db 1261 ACTTAAATTTGATTTAATAAATGATTAATATGTTTGTGGAATTTAATCAATTACAA 1320
Qy 1321 AATCAAGAGAGAGAGAGGAGCCTCTGCTGCTTAATGATTTCCCTCTTAAACAACCTGCT 1380
Db 1321 AATCAAGAGAGAGAGAGGAGCCTCTGCTGCTTAATGATTTCCCTCTTAAACAACCTGCT 1380
Qy 1381 CCCACTATCTCTTTTAACTTCAACAATAATCATTCACACGAGAAATCTGCTCGTATC 1440
Db 1381 CCCACTATCTCTTTTAACTTCAACAATAATCATTCACACGAGAAATCTGCTCGTATC 1440
Qy 1441 ACTTTCATGCAAAATTAACATAATTTGGTATTTTGTCAAGTTCTGCTGTTTTAG 1500
Db 1441 ACTTTCATGCAAAATTAACATAATTTGGTATTTTGTCAAGTTCTGCTGTTTTAG 1500
Qy 1501 TCGATTAATTTGATTAATCTATATGCTGATGATTAACACATCCAGCTAATCAATTAATGAT 1560
Db 1501 TCGATTAATTTGATTAATCTATATGCTGATGATTAACACATCCAGCTAATCAATTAATGAT 1560
Qy 1561 CTCCTCTGCTTATCAATAATTAACACATTAAGCTAATCAAGCTAATTAATTAACCA 1620
Db 1561 CTCCTCTGCTTATCAATAATTAACACATTAAGCTAATCAAGCTAATTAATTAACCA 1620
Qy 1621 CATCTCTTATCAATTTTATATGATTAATAAACAACCGACTATAGGCTACAGATT 1680
Db 1621 CATCTCTTATCAATTTTATATGATTAATAAACAACCGACTATAGGCTACAGATT 1680
Qy 1681 GGTATTAAGGCAATTAATGCTTCTAGTCGAGAGAAATTTTGTGATAGTAACACCTGCTG 1740
Db 1681 GGTATTAAGGCAATTAATGCTTCTAGTCGAGAGAAATTTTGTGATAGTAACACCTGCTG 1740
Qy 1741 GGAATAAATAATCCAGCTTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTTAATCA 1800
Db 1741 GGAATAAATAATCCAGCTTAATATGCTCATTTAAAGATTAATGATTTAAATGCTTTAATCA 1800

Qy 1801 TTAATAAATAAGGTTTTGCTTTTAAAGTTACACCGCTTAATATCATATAGAGAAAT 1860
Db 1801 TTAATAAATAAGGTTTTGCTTTTAAAGTTACACCGCTTAATATCATATAGAGAAAT 1860
Qy 1861 ATTAACTTTGATCGAAATTTCAAAATCTTTTAAACATTAAGAAATTTTACAGATTT 1920
Db 1861 ATTAACTTTGATCGAAATTTCAAAATCTTTTAAACATTAAGAAATTTTACAGATTT 1920
Qy 1921 TTAATAAAGGGTACATTTATGCGTTCAATTAATAATGTTTCAAGTAAAGTTGAGGT 1980
Db 1921 TTAATAAAGGGTACATTTATGCGTTCAATTAATAATGTTTCAAGTAAAGTTGAGGT 1980
Qy 1981 TTAACCAATGATATGTTTTTGAATTTAAATAACATTAATTTTCTATGTAATTAACATT 2040
Db 1981 TTAACCAATGATATGTTTTTGAATTTAAATAACATTAATTTTCTATGTAATTAACATT 2040
Qy 2041 TTTAACCGTCCATCCAGATTTGTAATAGTGAACAAATCTGAATAATTTTTTTTTCTTG 2100
Db 2041 TTTAACCGTCCATCCAGATTTGTAATAGTGAACAAATCTGAATAATTTTTTTTTCTTG 2100
Qy 2101 AATCTGTTTAAATCTCTGCTGCAATCTTGCAAGCAATTTGACCAACGACTATACATA 2160
Db 2101 AATCTGTTTAAATCTCTGCTGCAATCTTGCAAGCAATTTGACCAACGACTATACATA 2160
Qy 2161 TTTGAAGCAAAATATCCACAGAGATATGAGGTATGATCCCATTAATCTTTTGT 2220
Db 2161 TTTGAAGCAAAATATCCACAGAGATATGAGGTATGATCCCATTAATCTTTTGT 2220
Qy 2221 CTTTGTATTTAAGAAACAAATATTTTACAGAAACAAACGTTTCTCTAGAGGTA 2280
Db 2221 CTTTGTATTTAAGAAACAAATATTTTACAGAAACAAACGTTTCTCTAGAGGTA 2280
Qy 2281 TAAATATAGATTAATAACAAATTTAATCTATGTAATGATTTTATCTTCAAACTT 2340
Db 2281 TAAATATAGATTAATAACAAATTTAATCTATGTAATGATTTTATCTTCAAACTT 2340
Qy 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTAACTTAACATCTTCCACTA 2400
Db 2341 ACCATCTTCAACATTAATATGATCAATTTTATTTTAACTTAACATCTTCCACTA 2400
Qy 2401 AAAAAATGCAAAAGAGATATATATTAATGAAGCAAGTAAATGAAGTGAAGGAT 2460
Db 2401 AAAAAATGCAAAAGAGATATATATTAATGAAGCAAGTAAATGAAGTGAAGGAT 2460
Qy 2461 TCTTACGAAAGCGGCGGTAGAGGTCTTATCTCACTACATCACTGGGTGTGGCAG 2520
Db 2461 TCTTACGAAAGCGGCGGTAGAGGTCTTATCTCACTACATCACTGGGTGTGGCAG 2520
Qy 2521 ACATCAATAGGGCTTACGTATATTTGAGCTTACGTAAAGCTTAAACATCTAAGT 2579
Db 2521 ACATCAATAGGGCTTACGTATATTTGAGCTTACGTAAAGCTTAAACATCTAAGT 2579
Qy 2581 TAGTTCTCATGTAACAAACAAACAAATCCAAATTCGTAACATATATACAAATCTACTA 2640
Db 2581 TAGTTCTCATGTAACAAACAAACAAATTCGTAACATATATACAAATCTACTA 2640
Qy 2641 GTACTAGATTAACGCTACGTATACATGCTTTTCCGAAATTTCTAATCTATATACAA 2699
Db 2641 GTACTAGATTAACGCTACGTATACATGCTTTTCCGAAATTTCTAATCTATATACAA 2699
Qy 2701 CAAACTTGAATGTTGTTTGTATTAATCTTAACCAAAGTTTGAATTTGCAATGAG 2760
Db 2701 CAAACTTGAATGTTGTTTGTATTAATCTTAACCAAAGTTTGAATTTGCAATGAG 2760
Qy 2761 AGCTACATCTAGTCCCTTTTCCGAAATTAATCTCTTAACGACGCGTTAAAGT 2820
Db 2761 AGCTACATCTAGTCCCTTTTCCGAAATTAATCTCTTAACGACGCGTTAAAGT 2820
Qy 2821 ATTTAAACCAACAAATTTTATTTGTTGCTGAAGTGAACCAATGCAATATATAGAA 2880
Db 2821 ATTTAAACCAACAAATTTTATTTGTTGCTGAAGTGAACCAATGCAATATATAGAA 2880
Qy 2880 ATTTAAACCAACAAATTTTATTTGTTGCTGAAGTGAACCAATGCAATATATAGAA 2880
Db 2880 ATTTAAACCAACAAATTTTATTTGTTGCTGAAGTGAACCAATGCAATATATAGAA 2880

QY 2881 CAGCATGTTTATACAAATTAATGTCATGTTATTTGAAATCAATATTAATCAATTA 2940
 DB 2880 CAGCATGTTTATACAAATTAATGTCATGTTATTTGAAATCAATATTAATCAATTA 2939
 QY 2941 GCGACTCAGTGGTTTAATAGTTTGAAGATAATGAATTAATAATGAATTCAGAGATA 3000
 DB 2940 GCGACTCAGTGGTTTAATAGTTTGAAGATAATGAATTAATAATGAATTCAGAGATA 2999
 QY 3001 CAGAGCTAATATATGTCGGGTCTTTAGACCCGACCAAAAGTTGTCGTATTTCTAC 3060
 DB 3000 CAGAGCTAATATATGTCGGGTCTTTAGACCCGACCAAAAGTTGTCGTATTTCTAC 3059
 QY 3061 GGTGGCTCAATGAATTTTGAATTTCTTCACTTATTAAGTCTGTATAGTTT 3120
 DB 3060 GGTGGCTCAATGAATTTTGAATTTCTTCACTTATTAAGTCTGTATAGTTT 3119
 QY 3121 TGTGGATTATATATTTGTAATTTGTAATTTTGTCTAATATGATACGTAATTTCA 3180
 DB 3120 TGTGGATTATATATTTGTAATTTGTAATTTTGTCTAATATGATACGTAATTTCA 3179
 QY 3181 CCAATAAGAAAGCTTCTTTTATTTTAAATTTGAATTTTGAATTTTGAATGACT 3240
 DB 3180 CCAATAAGAAAGCTTCTTTTATTTTAAATTTGAATTTTGAATTTTGAATGACT 3239
 QY 3241 CATACACAAGTTAAAGTTGATGATATCAATTTTCAAAAAATGTTTCAGAGTGGCTC 3300
 DB 3240 CATACACAAGTTAAAGTTGATGATATCAATTTTCAAAAAATGTTTCAGAGTGGCTC 3299
 QY 3301 GAGTGTCTTACCAACATCGTACCAACTCGTATGAGTTTATTAATTAAGTTTCTTCTT 3360
 DB 3300 GAGTGTCTTACCAACATCGTACCAACTCGTATGAGTTTATTAATTAAGTTTCTTCTT 3359
 QY 3361 TTTCCAAATGCTTTAATTAATGAACAATCTAATTTCTTTTAAATTAAGTTAAGT 3420
 DB 3360 TTTCCAAATGCTTTAATTAATGAACAATCTAATTTCTTTTAAATTAAGTTAAGT 3419
 QY 3421 CTGTAATTTCTGTTAATTTTAAACCAAGTTTCAATTTCTTGAACAATAAAAAA 3480
 DB 3420 CTGTAATTTCTGTTAATTTTAAACCAAGTTTCAATTTCTTGAACAATAAAAAA 3479
 QY 3481 AAAAGTTTCAATTTTAAAGATCTAATTTTGTGAGTTCAAGTTTATGATAGCT 3540
 DB 3480 AAAAGTTTCAATTTTAAAGATCTAATTTTGTGAGTTCAAGTTTATGATAGCT 3539
 QY 3541 GAAAAATTAATGAATGATGCAAGTTTGAACAAGATGCTGATATCAATTA 3600
 DB 3540 GAAAAATTAATGAATGATGCAAGTTTGAACAAGATGCTGATATCAATTA 3599
 QY 3601 CATGCAATCAAAATTAATTTCTGCTTAGCAAGAAACGATTGAATTAACAGAAAT 3660
 DB 3600 CATGCAATCAAAATTAATTTCTGCTTAGCAAGAAACGATTGAATTAACAGAAAT 3659
 QY 3661 CGTTAACCAATTAATTTCTGCTTAGCAAGAAACGATTGAATTTCTGTAAGAGAGG 3720
 DB 3660 CGTTAACCAATTAATTTCTGCTTAGCAAGAAACGATTGAATTTCTGTAAGAGAGG 3719
 QY 3721 TATCAATATCTTAACAAAAAACTCATTTGATGATTAATATGTCCTCAATGTTACCA 3780
 DB 3720 TATCAATATCTTAACAAAAAACTCATTTGATGATTAATATGTCCTCAATGTTACCA 3779
 QY 3781 AGTATGTTTTGCTGATCATGATGTTGTAATGCTGCTCTAGGCAATATGTTCTAAG 3840
 DB 3780 AGTATGTTTTGCTGATCATGATGTTGTAATGCTGCTCTAGGCAATATGTTCTAAG 3839
 QY 3841 TTTTAAATGTTTTCAAGACTTTACAAAAATTAATATATAGGTTGTAAGG 3900
 DB 3840 TTTTAAATGTTTTCAAGACTTTACAAAAATTAATATATAGGTTGTAAGG 3899
 QY 3901 CTAAAAAGCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3960
 DB 3900 CTAAAAAGCAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
 QY 3961 AGATCCCAAGGATTCAGCAAAATTTGTGCTTGTCTCTCTTATTAATATATC 4020

DB 3960 AGATCCCAAGGATTCAGCAAAATTTGTGCTTGTCTCTCTTATTAATATATC 4019
 QY 4021 CTCTCAAAAACTCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTTCTACCGCA 4080
 DB 4020 CTCTCAAAAACTCTCTCTATATCTCTCTAAAGCCCCCTTCTGTTTCTACCGCA 4079
 QY 4081 CAAAGAAAAACAAAGTTTGAAGAAAAATGTTGTTCTGTTGTAACCAATGAGGT 4140
 DB 4080 CAAAGAAAAACAAAGTTTGAAGAAAAATGTTGTTCTGTTGTAACCAATGAGGT 4139
 QY 4141 TTTAGCTTACTACTTCTGAGAGATTATTAAGAAAAAGTGAAGATACATTATAGAAGA 4200
 DB 4140 TTTAGCTTACTACTTCTGAGAGATTATTAAGAAAAAGTGAAGATACATTATAGAAGA 4199
 QY 4201 AGAGAGCGAAGAACCAAAAAAGAAACC 4228
 DB 4200 AGAGAGCGAAGAACCAAAAAAGAAACC 4227

RESULT 4

ADG88432 standard; DNA; 4228 BP.

ADG88432;

11-MAR-2004 (first entry)

Arabidopsis thaliana alnbugmenta (ANT) promoter DNA.

Plant; Genetic engineering; cell proliferation; alnbugmenta; ANT;

transgenic; transgenic plant; organ mass alteration; fertility;

asexual reproduction; de.

Arabidopsis thaliana.

US2003159180-A1.

21-AUG-2003.

28-JAN-2002; 2002US-00059911.

28-JAN-2002; 2002US-00059911.

(REGC) UNIV CALIFORNIA OFFICE TECHNOLOGY.

Fischer RL, Mizukami Y;

WPI; 2003-787370/74.

Increasing cell proliferation in a plant by introducing into the plant an

expression cassette containing a plant promoter operably linked to a

nucleic acid encoding a modified ANT polypeptide and selecting plants

with increased mass.

Disclosure; SEQ ID NO 3; 51bp; English.

The present invention relates to plant genetic engineering. The invention

particularly relates to a method of increasing cell proliferation in a

plant. The method involves introducing into the plant an expression

cassette containing a plant promoter operably linked to a nucleic acid

encoding a modified alnbugmenta (ANT) polypeptide comprising an ANT AP2

domain and selecting plants the with increased size or mass. The

invention is useful to generate transgenic plants. The method is useful

for increasing cell proliferation in a plant for altering organ mass,

controlling fertility or enhancing asexual reproduction. The present

sequence is Arabidopsis thaliana ANT promoter DNA.

Sequence 4228 BP; 1488 A; 651 C; 643 G; 1446 T; 0 U; 0 Other;

Query Match 99.4%; Score 4203.4; DB 10; Length 4228;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 4226; Conservative 0; Mismatches 1; Indels 2; Gaps 2;

QY	1	GTGCACTCTAGGCTCTCACTGCGCTTAATACGACTCATATAGGAGCTCGAGAGCTCTTTA	60
DB	1	GTGCACTCTAGGCTCTCACTGCGCTTAATACGACTCATATAGGAGCTCGAGAGCTCTTTA	60
QY	61	GTTAATAAAAACTTTCTTTGTACGATGCTGTGTGTGTGTAACTTAACTTAATCTAGTC	120
DB	61	GTTAATAAAAACTTTCTTTGTACGATGCTGTGTGTGTGTAACTTAACTTAATCTAGTC	120
QY	121	ACATGTGATATCACAATATATATATTGAAAATTGGAATTAATCATATTAATAGTAGAGAT	180
DB	121	ACATGTGATATCACAATATATATATTGAAAATTGGAATTAATCATATTAATAGTAGAGAT	180
QY	181	TAAATATATATACGCTGACATTAACAACCAATGTTTCTGCTTTATGATAGTCTATAT	240
DB	181	TAAATATATATACGCTGACATTAACAACCAATGTTTCTGCTTTATGATAGTCTATAT	240
QY	241	GTTCGACTTGATTAATAGATACATATATMAAACCTGGGTTTATTTAAATCCGTACCATAC	300
DB	241	GTTCGACTTGATTAATAGATACATATATMAAACCTGGGTTTATTTAAATCCGTACCATAC	300
QY	301	AAAATGAGCCAAAACGAGATCCAGATGTTTGTGTTCCTTGTTGTTAACCAATAT	360
DB	301	AAAATGAGCCAAAACGAGATCCAGATGTTTGTGTTCCTTGTTGTTAACCAATAT	360
QY	361	ATGATTAATGAGAAGATTAAATCTTTACTAAATATATATAATTTGGAATAAACAACTTAA	420
DB	361	ATGATTAATGAGAAGATTAAATCTTTACTAAATATATATAATTTGGAATAAACAACTTAA	420
QY	421	ATATGTGAGTGTCTTCAGTGTCTCACTGTTCAAGAAATATCTCGTTATCTCACTTAA	480
DB	421	ATATGTGAGTGTCTTCAGTGTCTCACTGTTCAAGAAATATCTCGTTATCTCACTTAA	480
QY	481	CTAGAAGTGAATATACATPAAACGATGAATNTTTAAGACCGATCATPAAACACTGAT	540
DB	481	CTAGAAGTGAATATACATPAAACGATGAATNTTTAAGACCGATCATPAAACACTGAT	540
QY	541	CGATCAAAATACAAATTAATTAAGACTAGATCCAAAGATGAGATGACTAGCAGATA	600
DB	541	CGATCAAAATACAAATTAATTAAGACTAGATCCAAAGATGAGATGACTAGCAGATA	600
QY	601	TACACAGCTAAAGATTGTGACAGAGAGTCGAAAAATAGATTCTAATCATTTAAAAAGA	660
DB	601	TACACAGCTAAAGATTGTGACAGAGAGTCGAAAAATAGATTCTAATCATTTAAAAAGA	660
QY	661	TATGAGTTTCACTTACGATGATATTAACAATACGAGTAGTACATACATATATTTT	720
DB	661	TATGAGTTTCACTTACGATGATATTAACAATACGAGTAGTACATACATATATTTT	720
QY	721	TGTTTTTGTTTTACCGATPATAATGAAATGATGTGTAAAAATATTTGTTTTACTAA	780
DB	721	TGTTTTTGTTTTACCGATPATAATGAAATGATGTGTAAAAATATTTGTTTTACTAA	780
QY	781	AACTCGTTTTATGTTAACTATATAATGTCTTCCGACATGTAATTTGAAACAAACTGTAA	840
DB	781	AACTCGTTTTATGTTAACTATATAATGTCTTCCGACATGTAATTTGAAACAAACTGTAA	840
QY	841	TACAAATTAATGTTAAGCAATGCAATTAATAAAATTCACGGGTAGTAATCTCGAGAGAT	900
DB	841	TACAAATTAATGTTAAGCAATGCAATTAATAAAATTCACGGGTAGTAATCTCGAGAGAT	900
QY	901	TATGTTAATGCTACAAATTTTCTCTTTAGATTAATGTAAGGTTTGACAAATTAATGTATA	960
DB	901	TATGTTAATGCTACAAATTTTCTCTTTAGATTAATGTAAGGTTTGACAAATTAATGTATA	960
QY	961	CTTCGACAGGGATTAAGATCACTGACATAGTCAGACTGAGATGAGCCAAAGAGTCGTC	1020
DB	961	CTTCGACAGGGATTAAGATCACTGACATAGTCAGACTGAGATGAGCCAAAGAGTCGTC	1020
QY	1021	TCTGTCTTAAGATATCTACAGCTGCTCGCTGTGAATAGAGAAATTTGAATGATGA	1080
DB	1021	TCTGTCTTAAGATATCTACAGCTGCTCGCTGTGAATAGAGAAATTTGAATGATGA	1080

QY	1081	GAGATCCCATCTAGGGTTTCAGSTTTGGGCTCTCGGTGCAACTTTGGCGGTGTGACT	1140
DB	1081	GAGATCCCATCTAGGGTTTCAGSTTTGGGCTCTCGGTGCAACTTTGGCGGTGTGACT	1140
QY	1141	TTTTTCTTAAGTGGTTGGTGAACTAATTTCTGAGGTGAGGTAACTAAGAAACT	1200
DB	1141	TTTTTCTTAAGTGGTTGGTGAACTAATTTCTGAGGTGAGGTAACTAAGAAACT	1200
QY	1201	AATATTCGAAAAGAAAAGAAAAAGGCAAGAAACTATTTGCGAAAAGACATAATGAC	1260
DB	1201	AATATTCGAAAAGAAAAGAAAAAGGCAAGAAACTATTTGCGAAAAGACATAATGAC	1260
QY	1261	ACTAAATTTGGATTATTAATAATGGTATATATGTTGGTGAATTTATATCATTCGAA	1320
DB	1261	ACTAAATTTGGATTATTAATAATGGTATATATGTTGGTGAATTTATATCATTCGAA	1320
QY	1321	AATCAAGAAAGAGAGAGGAGCCCTCTGCGCTTAATGATTTCCCTCGTAACAATGCT	1380
DB	1321	AATCAAGAAAGAGAGAGGAGCCCTCTGCGCTTAATGATTTCCCTCGTAACAATGCT	1380
QY	1381	CCCATATCTCTTTTATCTTCCAACAAAATATTCACACAGAAAATCTGCTCGTGATC	1440
DB	1381	CCCATATCTCTTTTACTTCCAACAAAATATTCACACAGAAAATCTGCTCGTGATC	1440
QY	1441	ACTTTCATGCAAAATTAACATAAATTTTGGTATTTTGTCAAGTCTTGCTGTTTAA	1500
DB	1441	ACTTTCATGCAAAATTAACATAAATTTTGGTATTTTGTCAAGTCTTGCTGTTTAA	1500
QY	1501	TGATATTTTGGTATTAATATATATGTTGGATATACATCCAAAGCTAATCAATAATGAT	1560
DB	1501	TGATATTTTGGTATTAATATATGTTGGATATACATCCAAAGCTAATCAATAATGAT	1560
QY	1561	CTCCTTCTGCTTAATCAATAAATTAACACACATTAAGCTAATCAAGCTAATAATTAACCA	1620
DB	1561	CTCCTTCTGCTTAATCAATAAATTAACACACATTAAGCTAATCAAGCTAATAATTAACCA	1620
QY	1621	CATTCTCTTAATCAATTTTATATGGTATTAATAAACAACGACTATATAGGCTACAGATT	1680
DB	1621	CATTCTCTTAATCAATTTTATATGGTATTAATAAACAACGACTATATAGGCTACAGATT	1680
QY	1681	GGTATTAAGGCAATTAATGCCCTTCTAGTTCGAAGAAATTTTGTATATATACACTGCTG	1740
DB	1681	GGTATTAAGGCAATTAATGCCCTTCTAGTTCGAAGAAATTTTGTATATATACACTGCTG	1740
QY	1741	GAAAAAAATCAGGCTTAATATGCTCAATTTAAAGATTAATGATTTAAAGCTTTAATCA	1800
DB	1741	GAAAAAAATCAGGCTTAATATGCTCAATTTAAAGATTAATGATTTAATATCTTAATCA	1800
QY	1801	TTAAATTAAGATTTTGTGCTTTTAAAGGTTACACACGCTTAATTCATTAAGAGAT	1860
DB	1801	TTAAATTAAGATTTTGTGCTTTTAAAGGTTACACACGCTTAATTCATTAAGAGAT	1860
QY	1861	ATTAACTTTGATCGAAATTCGAAATACTTTTAAACATTAAGAAAAATTTTCAGCAATT	1920
DB	1861	ATTAACTTTGATCGAAATTCGAAATACTTTTAAACATTAAGAAAAATTTTCAGCAATT	1920
QY	1921	TTAAATTAAGGCTCAATTAATGGGTTCAATAATGTTTCCAGTAAAGTTGGAGCT	1980
DB	1921	TTAAATTAAGGCTCAATTAATGGGTTCAATAATGTTTCCAGTAAAGTTGGAGCT	1980
QY	1981	TTAAACATGAAATGTTTTTGAATTTAAAAAAACATAAATTTTCTAGTATTTCAACTT	2040
DB	1981	TTAAACATGAAATGTTTTTGAATTTAAAAAAACATAAATTTTCTAGTATTTCAACTT	2040
QY	2041	TTTAAACGTCATCGAATGTATTAATAAGTGAACAATCTGAAAACATTTTTTTTTCTTG	2100
DB	2041	TTTAAACGTCATCGAATGTATTAATAAGTGAACAATCTGAAAACATTTTTTTTTCTTG	2100
QY	2101	AATCTGTGTTTAAATCTCTCTGCTGCAATCTTGAAGGCAATTTGACCAACGATTAACATA	2160
DB	2101	AATCTGTGTTTAAATCTCTCTGCTGCAATCTTGAAGGCAATTTGACCAACGATTAACATA	2160
QY	2161	TTGAAAGCAAAATATTCACACAGGATATATAGGTTAATCCACATTCATATCTTTTGT	2220

2161 TTGAAGCAAAATATCCACGAGGATGATAGGTTAGATCCCATTCATATCTTTGT 2220
2221 CTTTGTATTTATGAAAAACAATATTTATCAGAAAAAAAGCTTCTTCTAGTGGTA 2280
2222 CTTTGTATTTATGAAAAACAATATTTATCAGAAAAAAAGCTTCTTCTAGTGGTA 2280
2281 TAGGTATGATATATTAACAAATTTTAACTAGTTATGTATTTTCTATCTTCAACT 2340
2282 TAGGTATGATATATTAACAAATTTTAACTAGTTATGTATTTTCTATCTTCAACT 2340
2341 ACCATCCTTCACATTAATATTTGATCAATTTTATTTTATTTTAACTTAACTACTTCCA 2400
2342 ACCATCCTTCACATTAATATTTGATCAATTTTATTTTATTTTAACTTAACTACTTCCA 2400
2401 AAAAAATGCAAAAGAGATATATTTTAAAGTCAAAATTTTAAAGTGAATGGGTGAT 2460
2402 AAAAAATGCAAAAGAGATATATTTTAAAGTCAAAATTTTAAAGTGAATGGGTGAT 2460
2461 TCTTGACAAAAGGGGCGGTAGAGGTCTTATCCATCACTTACAGCTGGGTGTGGCAG 2520
2462 TCTTGACAAAAGGGGCGGTAGAGGTCTTATCCATCACTTACAGCTGGGTGTGGCAG 2520
2521 ACATCATAGGGCTTACGTATATTTGAGCTTTTACGTACGTAAAGCTTTTAACTATCTAGT 2580
2522 ACATCATAGGGCTTACGTATATTTGAGCTTTTACGTACGTAAAGCTTTTAACTATCTAGT 2580
2581 TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTATCATATATACATATCTAT 2640
2582 TAGTCTCACTGTACAAACAAACAAATCCAAATTCGTATCATATATACATATCTAT 2640
2641 GTATCATATCTTACAAACAAACAAATTCGTATCATATATACATATCTAT 2700
2642 GTATCATATCTTACAAACAAACAAATTCGTATCATATATACATATCTAT 2700
2701 CAAACTGTATGATTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTTGG 2760
2702 CAAACTGTATGATTTGTTTGTATTTATCTTAAACCAAGTTTGAATGTGCATTTGG 2760
2761 AGCTACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATCGACCGGTAAAGT 2820
2762 AGCTACACTGTAGTCCCTTTTCCCAAAATATCTCTTACATCGACCGGTAAAGT 2820
2821 ATTTAAACCAACAAATTTTATTTGTGTGCAAGGTACCAACATCATATATATGAGA 2880
2822 ATTTAAACCAACAAATTTTATTTGTGTGCAAGGTACCAACATCATATATATGAGA 2880
2881 CAGCATCGTTTATACAAATATATGTGATGTATTTGGAATTCAAATATATATGAGT 2940
2882 CAGCATCGTTTATACAAATATATGTGATGTATTTGGAATTCAAATATATATGAGT 2940
2941 GCGACTACTGTGTTTATATGTTTGGAGATATGAAATGAAATGAAATGAAATGAAATG 2999
2942 GCGACTACTGTGTTTATATGTTTGGAGATATGAAATGAAATGAAATGAAATGAAATG 2999
2999 GCGACTACTGTGTTTATATGTTTGGAGATATGAAATGAAATGAAATGAAATGAAATG 2999
3000 ACAGAGCTATATATGCGGTGATTTAGACCGGTGACCAAAAGTTTGTGTATTTCTA 3059
3001 ACAGAGCTATATATGCGGTGATTTAGACCGGTGACCAAAAGTTTGTGTATTTCTA 3059
3060 CCGTCCGTCATAGAAATTTTGAATTTTCTGACCTTTTATGAACTTCTATAGTTT 3119
3061 CCGTCCGTCATAGAAATTTTGAATTTTCTGACCTTTTATGAACTTCTATAGTTT 3119
3120 TTGTCCGATTAATATTTGATTCGATATATTTTGTCTAAATATGATAGTAAATTC 3179
3121 TTGTCCGATTAATATTTGATTCGATATATTTTGTCTAAATATGATAGTAAATTC 3179
3180 ACATTAAGAAAGCTTTTATTTATTTATTTGATTTTAACTTTTGTGTTTGGAAATGAC 3239
3181 ACATTAAGAAAGCTTTTATTTATTTATTTGATTTTAACTTTTGTGTTTGGAAATGAC 3239
3240 TCATTAACAAGTTTAAAGTTTGAATGATCAATTTTCAAAATGTTTGAAGTGGCTT 3299

3240 TCATTAACAAGTTTAAAGTTTGAATGATCAATTTTCAAAATGTTTGAAGTGGCTT 3299
3300 CGAGTCTTACCAACATGATCCAACTGTATGGGTATATATGATTTTCTTCT 3359
3301 CGAGTCTTACCAACATGATCCAACTGTATGGGTATATATGATTTTCTTCT 3359
3360 TTTTCCATGCTTTTATATGAAACCACTTAAATTTCTTTTAAATTTAGGTAAAG 3419
3361 TTTTCCATGCTTTTATATGAAACCACTTAAATTTCTTTTAAATTTAGGTAAAG 3419
3362 TTTTCCATGCTTTTATATGAAACCACTTAAATTTCTTTTAAATTTAGGTAAAG 3419
3420 TCTTGATTTTCTGTTGATTTTAAACCAAGTTTCAATCTTCTTACCAAAAAAAA 3479
3421 TCTTGATTTTCTGTTGATTTTAAACCAAGTTTCAATCTTCTTACCAAAAAAAA 3479
3480 AAAAAAGTTTCAATTAATTAAGAAATTTTAAAGTCTTAAAGTTTAAATGATGAG 3539
3481 AAAAAAGTTTCAATTAATTAAGAAATTTTAAAGTCTTAAAGTTTAAATGATGAG 3539
3540 TGAAGATTAATGATTAATGCAAGTTTGCAGAGATGCTGATGATGATGATGATGAT 3599
3541 TGAAGATTAATGATTAATGCAAGTTTGCAGAGATGCTGATGATGATGATGATGAT 3599
3600 ACATGATCAAAATATATATTTGCTGTAGCAAGAAACGATTTGAATTAACAGAAACA 3659
3601 ACATGATCAAAATATATATTTGCTGTAGCAAGAAACGATTTGAATTAACAGAAACA 3659
3660 TCGTTAACCACTTAAATATCTTGAATATTTTGTATGATATTTCTGTAAGAGAG 3719
3661 TCGTTAACCACTTAAATATCTTGAATATTTTGTATGATATTTCTGTAAGAGAG 3719
3720 GTATCATATCTTACAAACAAACAAATTCGTATCATATATACATATCTAT 3779
3721 GTATCATATCTTACAAACAAACAAATTCGTATCATATATACATATCTAT 3779
3780 AAGTATGTTTGTGCTGTACAGTTGATTTGATCTGCTCTTACCATATATGTTCTA 3839
3781 AAGTATGTTTGTGCTGTACAGTTGATTTGATCTGCTCTTACCATATATGTTCTA 3839
3840 GTTTTAAATGTTTGAAGCTTTCACAAATTAATTAATTAATTAATTAATTAATTAAT 3899
3841 GTTTTAAATGTTTGAAGCTTTCACAAATTAATTAATTAATTAATTAATTAATTAAT 3899
3900 GCTTAAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
3901 GCTTAAAGCAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 3959
3960 CAGATCCCAACGATTCAAACAGCAAAATTTGCTGCTCTTCTTATATATAT 4019
3961 CAGATCCCAACGATTCAAACAGCAAAATTTGCTGCTCTTCTTATATATAT 4019
4020 CCTTCAAAAAACCTTCTTATATCTTCTTAAAGCCCTTCTGTTCTTACCGCA 4079
4021 CCTTCAAAAAACCTTCTTATATCTTCTTAAAGCCCTTCTGTTCTTACCGCA 4079
4080 ACAAGAAAAAACAAGTTTGAAGAAATGCTGTTCTGTTGTTGTTGTTGTTGTTGTTG 4139
4081 ACAAGAAAAAACAAGTTTGAAGAAATGCTGTTCTGTTGTTGTTGTTGTTGTTGTTG 4139
4140 TTTTACCTTACTTCTGAGAGATTTATTAAGAAAGAGTGAATATATATATATAT 4199
4141 TTTTACCTTACTTCTGAGAGATTTATTAAGAAAGAGTGAATATATATATATATAT 4199
4200 AAGAGAGCAAGAAACCAAAAAAGAAACC 4228
4201 AAGAGAGCAAGAAACCAAAAAAGAAACC 4228

RESULT 5

AAAS9220

ID AAAS9220 standard; cDNA; 2148 BP.

XX AAAS9220;

XX

07-NOV-2000 (first entry)
 cDNA encoding an Arabidopsis aintegumenta (ANT) polypeptide.
 Aintegumenta; ANT; cell proliferation; growth; organ mass; fertility;
 asexual reproduction; plant; male sterile plant; female sterile plant;
 early flowering; se.
 Arabidopsis sp.
 Location/Qualifiers
 Key CDS
 269..1936
 /*tag= a
 /product= "aintegumenta polypeptide"
 WO200040694-A2.
 13-JUL-2000.
 07-JAN-2000; 2000NO-US000465.
 08-JAN-1999; 99US-00227421.
 (REGC) UNIV CALIFORNIA.
 Fischer RL, Mizukami Y;
 WPI; 2000-465969/40.
 P-PSDB; AAB07724.
 Modulating growth and cell proliferation in a plant used to alter organ
 mass, control fertility and enhance asexual reproduction in plants
 comprises modulating ANT activity and selecting plants with altered cell
 number.
 Claim 9; Page 40-41; 54pp; English.
 The present sequence encodes an aintegumenta (ANT) polypeptide. The ANT
 gene is expressed and functions not only in developing ovules but also in
 various developing organs. Growth and cell proliferation in plant can be
 modulated by modulating ANT activity. Modulation of ANT activity is used
 to alter organ mass, control fertility and enhance asexual reproduction
 in plants. Increased ANT activity can be used to produce male or female
 sterile plants. Inhibition of ANT activity can be used to truncate
 vegetative growth, resulting in early flowering
 Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
 Query Match 6.3%; Score 268; DB 3; Length 2148;
 Best Local Similarity 100.0%; Pred. No. 3.1e-35;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3961 AGATCCCAAGGATTCAAGCAAAATTTGCTTCTCTCTTATTAATATC 4020
 1 AGATCCCAAGGATTCAAGCAAAATTTGCTTCTCTCTTATTAATATC 60
 4021 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTCTCTTCTTAACGCAA 4080
 61 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTCTCTTCTTAACGCAA 120
 4081 CAAAGAAAAAAGTTGAGAAAAATGCTGCTTCTTGAACAATGAGGT 4140
 121 CAAAGAAAAAAGTTGAGAAAAATGCTGCTTCTTGAACAATGAGGT 180
 4141 TTTAGCTTACTCTTGAAGATTATTAAGAAAGAGTGAAGATCATTTAGAAAGA 4200
 181 TTTAGCTTACTCTTGAAGATTATTAAGAAAGAGTGAAGATCATTTAGAAAGA 240
 4201 AGAAGACAGAAACCAAAAGAAACC 4228
 241 AGAAGACAGAAACCAAAAGAAACC 268

RESULT 6
 ABX13437
 ID ABX13437 standard; DNA; 2148 BP.
 AC ABX13437;
 XX
 DT 04-JUN-2003 (first entry)
 XX
 DE A. thaliana AINTEGUMENTA DNA corresponding to Genbank U40256.
 XX
 KW Expression cassette; transgenic; promoter; LOX5; plant; food production;
 KW animal feed; seed; stress resistance; disease resistance; starch content;
 KW lipid content; dormancy; fibre content; pharmaceutical production;
 KW fine chemical production; sterile plant; vitamin; flavouring; perfume;
 KW dye; cotyledon; embryonic tissue; stress factor; LOX; de.
 XX
 OS Arabidopsis thaliana.
 XX
 PN DE10127882-A1.
 XX
 PD 12-DEC-2002.
 XX
 PF 11-JUN-2001; 2001DB-01027882.
 XX
 PR 11-JUN-2001; 2001DB-01027882.
 XX
 PA (BADI) BASF PLANT SCI GMBH.
 XX
 PI Bischoff F, Feussner I, Loyall LP;
 WPI; 2003-279966/28.
 DR
 PT Cassette for expressing transgene, useful e.g. in production of
 PT pharmaceuticals and fine chemicals, contains promoter from the LOX5 gene
 PT of Arabidopsis, provides cotyledon-specific expression.
 XX
 PS Claim 5; Page; 28pp; German.
 XX
 CC This invention describes a novel cassette for the transgenic expression
 CC of nucleic acid containing the promoter of the LOX5 gene from Arabidopsis
 CC thaliana or deletion variants of the LOX5 promoter which are functionally
 CC linked to the nucleic acid of the invention. The cassette is used to
 CC prepare transgenic organisms, especially plants, for production of foods,
 CC animal feeds, seeds (including those with increased resistance to stress
 CC and disease, altered starch/lipid contents or dormancy, or altered fibre
 CC content), pharmaceuticals (especially antibodies, vaccines, enzymes and
 CC pharmaceutical proteins) and fine chemicals (especially enzymes,
 CC vitamins, amino acids, sugars, (unsaturated fatty acids, flavourings,
 CC perfumes and dyes), also to produce sterile plants. The LOX5 promoter
 CC confers strong and specific expression in cotyledons and/or other early
 CC embryonic tissue, so can degrade, or protect against, stress factors to
 CC which these tissues are particularly sensitive. Since cotyledons are the
 CC main storage organs of seeds, expressing transgenes in them produces
 CC targeted increases/modifications in nutritional value. Expression in the
 CC cotyledons is homogeneous, there are no side effects on other plant
 CC organs (pollen) and the promoter is functional in a wide variety of
 CC plants (ornamentals or crops). This sequence represents a nucleic acid
 CC sequence associated with the Arabidopsis thaliana LOX gene described in
 CC the disclosure of the invention
 XX
 SQ Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
 Query Match 6.3%; Score 268; DB 8; Length 2148;
 Best Local Similarity 100.0%; Pred. No. 3.1e-35;
 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 3961 AGATCCCAAGGATTCAAGCAAAATTTGCTTCTCTCTTATTAATATC 4020
 1 AGATCCCAAGGATTCAAGCAAAATTTGCTTCTCTCTTATTAATATC 60
 4021 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTCTCTTCTTAACGCAA 4080
 61 CTCTCAAAACCCCTCTATATCTCTTAAGCCCCCTCTCTTCTTAACGCAA 120

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QY 4081 CAAAGAAAAACAAGTTGAGAAAAATGCTGTTGTTGTTAACAATGATTGGGT 4140
DB 121 CAAAGAAAAACAAGTTGAGAAAAATGCTGTTGTTGTTAACAATGATTGGGT 180
QY 4141 TTTAGCTTACTACTTGAAGAGATTATAGAAAAAGAGTAGAATACATTATAGAAAAGA 4200
DB 181 TTTAGCTTACTACTTGAAGAGATTATAGAAAAAGAGTAGAATACATTATAGAAAAGA 240
QY 4201 AGAGAAAGCAGAAACCAAAAAAGAAACC 4228
DB 241 AGAGAAAGCAGAAACCAAAAAAGAAACC 268

RESULT 7
ADG25135
ID ADG25135 standard; cDNA; 2148 BP.
AC ADG25135;
XX
XX 26-FEB-2004 (first entry)
DT
XX Thalecress cDNA encoding Aintegumenta, ANT.
XX Thalecress; ss; gene; Aintegumenta; ANT; AP2 domain; plant; seed mass;
XX asexual reproduction; reduced fertility.
OS Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX CDS 269..1936
XX FT /*tag= a
XX FT /product= "Aintegumenta, ANT"

PN US639128-B1.
XX
XX 28-OCT-2003.
PD
XX 07-JAN-2000; 2000US-00479855.
PF
XX 08-JAN-1999; 99US-00227421.
PR
XX (NASC-) NAT SCI FOUND.
PA
XX Fischer RL, Mizukami Y;
XX
XX WPI; 2003-842795/78.
XX P-PSDB; ADG25136.
DR
XX
XX New nucleic acid, useful in conferring desired traits on plants, such as
XX increased seed mass, asexual reproduction or reduced fertility.
XX
XX Example 1; SEQ ID NO 1; 25pp; English.
XX
XX The invention relates to an isolated nucleic acid comprising a
XX polynucleotide encoding a polypeptide having at least 90% identity with a
XX Cnola Aintegumenta, ANT, (appearing as ADG25139) as determined using a
XX BLAST algorithm and comprising two AP2 domains. Also included are an
XX expression cassette comprising a plant promoter operably linked to a
XX heterologous polynucleotide encoding the polypeptide, a vector comprising
XX the expression cassette, a plant comprising the plant promoter operably
XX linked to the heterologous polynucleotide, a method of asexually
XX reproducing a plant and a method of reducing fertility in a plant. The
XX nucleic acid is useful in conferring desired traits on plants, such as
XX increased seed mass, asexual reproduction or reduced fertility. The
XX present sequence encodes Thalecress Aintegumenta, ANT.
XX
XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
XX
XX Query Match 6.3%; Score 268; DB 10; Length 2148;
XX Best Local Similarity 100.0%; Prid. No. 3.1e-35;
XX Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 3961 AGATCCCAACGAGATTCAACACAGCAATTTGCTGTTGCTCTCTATTATTAATATC 4020
DB 1 AGATCCCAACGAGATTCAACACAGCAATTTGCTGTTGCTCTCTCTATTATTAATATC 60
QY 4021 CTCTCAAAAACCTCTCTCTATATCTCTCTTAAGCCCCCTTCTCTCTCTACCGCA 4080
DB 61 CTCTCAAAAACCTCTCTCTATATCTCTCTTAAGCCCCCTTCTCTCTCTACCGCA 120
QY 4081 CAAAGAAAAACAAGTTGAGAAAAATGCTGTTGTTGTTAACAATGATTGGGT 4140
DB 121 CAAAGAAAAACAAGTTGAGAAAAATGCTGTTGTTGTTAACAATGATTGGGT 180
QY 4141 TTTAGCTTACTACTTGAAGAGATTATAGAAAAAGAGTAGAATACATTATAGAAAAGA 4200
DB 181 TTTAGCTTACTACTTGAAGAGATTATAGAAAAAGAGTAGAATACATTATAGAAAAGA 240
QY 4201 AGAGAAAGCAGAAACCAAAAAAGAAACC 4228
DB 241 AGAGAAAGCAGAAACCAAAAAAGAAACC 268

RESULT 8
ADG88430
ID ADG88430 standard; cDNA; 2148 BP.
AC ADG88430;
XX
XX 11-MAR-2004 (first entry)
DT
XX Arabidopsis thaliana aintegumenta (ANT) cDNA.
XX
XX Plant; genetic engineering; cell proliferation; aintegumenta; ANT;
XX transgenic; transgenic plant; organ mass alteration; fertility;
XX asexual reproduction; gene; ss.
OS Arabidopsis thaliana.
XX
XX Key Location/Qualifiers
XX CDS 269..1936
XX FT /*tag= a
XX FT /product= "Arabidopsis thaliana ANT protein"

PN US2003159180-A1.
XX
XX 21-AUG-2003.
PD
XX 28-JAN-2002; 2002US-00059911.
PF
XX 28-JAN-2002; 2002US-00059911.
PR
XX (REGC ) UNIV CALIFORNIA OFFICE TECHNOLOGY.
PA
XX Fischer RL, Mizukami Y;
XX
XX WPI; 2003-787370/74.
XX P-PSDB; ADG88431.
DR
XX
XX Increasing cell proliferation in a plant by introducing into the plant an
XX expression cassette containing a plant promoter operably linked to a
XX nucleic acid encoding a modified ANT polypeptide and selecting plants
XX with increased mass.
XX
XX Example 1; SEQ ID NO 1; 51pp; English.
XX
XX The present invention relates to plant genetic engineering. The invention
XX particularly relates to a method of increasing cell proliferation in a
XX plant. The method involves introducing into the plant an expression
XX cassette containing a plant promoter operably linked to a nucleic acid
XX encoding a modified aintegumenta (ANT) polypeptide comprising an ANT AP2
XX domain and selecting plants the with increased size or mass. The
XX invention is useful to generate transgenic plants. The method is useful
XX for increasing cell proliferation in a plant for altering organ mass,
XX controlling fertility or enhancing asexual reproduction. The present

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CC sequence is Arabidopsis thaliana ANT cDNA.
XX Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
SQ Best Local Similarity 100.0%; Score 268; DB 10; Length 2148;
Query Match 6.3%; Pred. No. 3.1e-35;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3961 AGATCCCAAGGATTCAACGCAAAATTGCTGCTTGTCTCTTATTAATATC 4020
Db 1 AGATCCCAAGGATTCAACGCAAAATTGCTGCTTGTCTCTTATTAATATC 60
QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCTCTGTTCTTACCGCAA 4080
Db 61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCTCTGTTCTTACCGCAA 120
QY 4081 CAAAGAAAAACAAGTTTGAGAAAAATGCTGTCTGTGTAAACAATGATGGGT 4140
Db 121 CAAAGAAAAACAAGTTTGAGAAAAATGCTGTCTGTGTAAACAATGATGGGT 180
QY 4141 TTATGCTTACTCTTCGAGAGATTATAGAAAGAGTGAAGATCATTATAGAAAG 4200
Db 181 TTATGCTTACTCTTCGAGAGATTATAGAAAGAGTGAAGATCATTATAGAAAG 240
QY 4201 AGAGAACGAGAAACCAAAAAAGAAACC 4228
Db 241 AGAGAACGAGAAACCAAAAAAGAAACC 268
RESULT 9
ABZ10246/c
ID ABZ10246 standard; DNA; 8056 BP.
XX ABZ10246;
AC
XX 25-JUN-2005 (first entry)
DT
XX A. thaliana aintegumenta (ANT) cDNA, seq id 1.
DE
XX Plant engineering; growth; cell proliferation; organ mass; fertility;
KM asexual reproduction; aintegumenta; ANT; plant; gene; ss.
XX Arabidopsis thaliana.
OS
XX Key location/Qualifiers
FH 269. .1936
FT CDS /*tag= a
FT /product= "aintegumenta protein"
FT
XX US2005132445-A1.
XX PN 16-JUN-2005.
XX PD 18-JUL-2003; 2003US-00623477.
XX PR 07-JAN-2000; 2000US-00479855.
XX PA (REGC) UNIV CALIFORNIA.
XX PI (REGC) UNIV CALIFORNIA.
XX PI Fischer RL, Mizukami Y;
XX WPI; 2005-424635/43.
XX DR P-PSDB; ABZ10246.
XX DR
XX PT Modulating growth and cell proliferation in a plant, useful in plant
PT genetic engineering; comprises modulating aintegumenta (ANT) gene
PT activity and selecting plants with altered cell number.
XX Claim 9; SEQ ID NO 1; 27pp; English.
XX
XX The invention relates to modulating growth and cell proliferation in a
CC plant comprising modulating aintegumenta (ANT) gene activity and
CC selecting plants with altered cell number. Further disclosed is a method

CC for directing expression of a heterologous nucleic acid in meristematic
CC cells of a plant. The method is useful in plant genetic engineering,
CC specifically for altering organ mass, controlling fertility and enhancing
CC asexual reproduction in plants. The current sequence represents A.
CC thaliana ANT cDNA.
SQ Sequence 2148 BP; 659 A; 431 C; 460 G; 598 T; 0 U; 0 Other;
Query Match 6.3%; Score 268; DB 14; Length 2148;
Best Local Similarity 100.0%; Pred. No. 3.1e-35;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3961 AGATCCCAAGGATTCAACGCAAAATTGCTGCTTGTCTCTTATTAATATC 4020
Db 1 AGATCCCAAGGATTCAACGCAAAATTGCTGCTTGTCTCTTATTAATATC 60
QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCTCTGTTCTTACCGCAA 4080
Db 61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCTCTGTTCTTACCGCAA 120
QY 4081 CAAAGAAAAACAAGTTTGAGAAAAATGCTGTCTGTGTAAACAATGATGGGT 4140
Db 121 CAAAGAAAAACAAGTTTGAGAAAAATGCTGTCTGTGTAAACAATGATGGGT 180
QY 4141 TTATGCTTACTCTTCGAGAGATTATAGAAAGAGTGAAGATCATTATAGAAAG 4200
Db 181 TTATGCTTACTCTTCGAGAGATTATAGAAAGAGTGAAGATCATTATAGAAAG 240
QY 4201 AGAGAACGAGAAACCAAAAAAGAAACC 4228
Db 241 AGAGAACGAGAAACCAAAAAAGAAACC 268
RESULT 10
ABZ10246/c
ID ABZ10246 standard; DNA; 8056 BP.
XX ABZ10246;
AC
XX 16-JAN-2003 (first entry)
DT
XX Haematopoietic cell proliferation disorder related DNA sequence #386.
DE
XX Human; haematopoietic cell proliferation disorder; cytostatic;
KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
KW cytosine methylation state; gene; ds.
XX Homo sapiens.
XX OS
XX WO200277272-A2.
XX PN 03-OCT-2002.
XX PD 26-MAR-2002; 2002WO-EP003401.
XX PR 26-MAR-2001; 2001US-0278333P.
XX PA (EPIC-) EPIGENOMICS AG.
XX PI Berlin K, Braun A, Distler J, Guefig D, Howe A, Mueller J;
PI Olex A, Piependrock C, Adorjan P, Grabs G, Lesche R, Leu E, Pelet C;
PI Lewin A, Lipscher B, Mater S, Model F, Mueller V, Otto T, Pelet C;
PI Schwabe I, Ziebarth H;
XX WPI; 2003-018942/01.
XX DR
XX Detecting and differentiating between haematopoietic cell proliferative
PT disorders, comprises contacting a target nucleic acid with a reagent that
PT distinguishes between methylated and non-methylated CpG dinucleotides.
XX Claim 28; SEQ ID NO 386; 117pp; English.
XX
XX The present invention describes a method for detecting and


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Db 2243 A-----TTTTTAAATAATTTTTTTTTTTTTTTTTTTTTTTTCAATTTTTTTA 2190
Qy 1848 TCATTAGAGAAATTAATTAATTGATCGAAATTCGAAAATCTTTTTTAAACATAGAAA 1907
Db 2189 AATTTTAAATAAATTAATTTTTTTTTTTTTTTTTTTTTTTTAAATTTAAATAAAA 2130
Qy 1908 AATTTGCGATTTTTAAATAAGGTCATTATTTGGTCAATAAATATGTTCCAGT 1967
Db 2129 AATTAATAAATTAATTAATAATTAATTAATTAATTAATTAATTAATTAATTAATTTTA 2070
Qy 1968 AAGTTTGAGGTTTAAACAATGAATGTTTTGATTTAAAAAACAATTAATTTCTA 2027
Db 2069 AATATAATTTTAAATAAATAAATAATTAATAAATAATTAATTAATTAATTAATTAATA 2010
Qy 2028 GATTAATACATTTTAAACCGTCATCGAATGTAATAGTGAACAATCTGAAAACAT 2087
Db 2009 AATTTAATAATTTTAAATAAATAATTAATTAATTAATTTAATTAATAAATAATTAATTTT 1950
Qy 2088 TTTTTTTCTGATCTGTTTAAATTCCTGCTGCAATCTTGACGATTTGACCA 2147
Db 1949 TTTTATTAATTAATTAATTAATTAATTAATTTTAAATAATTTTAAATAATTAATA 1890
Qy 2148 ACGATATACATATTTGAAGCAAAATATCCACAGGATGATAGGTTAGATCCCAT 2207
Db 1889 AAAAAATAAAAATTAATTAATTAATTTTTTTTTTTTTTTTTTTTTTTTTTAAACA 1830
Qy 2208 CAATATCTTTGCTTGTATTAATGAAAAACA-----ATATTAATCAG 2253
Db 1829 AATTTAATTTTAAATTAATTAATAATTAATAATTAATTAATTTTAAATTTTAAAT 1770
Qy 2254 GAAAAAAAGCTTCTGCTAGTGTATAGTATAGATTAATTAACAATTAATCTTA 2313
Db 1769 TTTAAATAATTTTAAATTTTAAATTTTAAATAATTAATAATTAATTAATTAAT 1710
Qy 2314 GTTAATGTA---TTTACATCTTCAAACTTACATCCCTCAACTTAATTAATGTAAT 2370
Db 1709 AATTAATTAATTTTAAATTTTAAATAAATAAATAATTTTATCAATTAATTAATAAT 1650
Qy 2371 TTTATTTTTTAACTTAACATCTTCACTAATAAATAAGCAAAAGATATTAATTTA 2430
Db 1649 TTTTTTTAATTTTAACTATCAATTTTCAATTTTAAATAATTAATAATTAATAATA 1590
Qy 2431 AGTCAAAGTAATTAAGATGATGGTATTTCTGACGAAACGGCCGCGTAGGCTC 2490
Db 1589 AATTAATAAT-ATTAATAATTAATAATTTTAAATAAATAATTAATTTAATAAATTTT 1531
Qy 2491 TTAATCTACATTCAGCTGGGTTGCGACATCATAGGCTCAGATTAATTTGACTT 2550
Db 1530 TTTAACTAATTTTAAATTTTAAATTAATTAATTAATTTAATTAATTAATTTAATA 1471
Qy 2551 TACTGATCGTAAGCTTAAATATCTAGTATGTTCTCACTGTAACAACAATAATC 2610
Db 1470 TAAATTTATTAATAAATAAATAATTTTATTTTTTTTTTA-----AAAAAATAAATAA 1415
Qy 2611 CAATTCGTAATATATATACAATACTAAGTACTAGATTAACGCTAGATATACGCTT 2670
Db 1414 AATAAATAAATAAATAATTAATTTTAAATAAATAAATAATTTAATAAATAAATAA 1355
Qy 2671 TTTTCGAAATTTCTAACTAATCTATACAACAATCTGAATGTTGTTTGTATTAATC 2730
Db 1354 AATTTAAATTAATTTTAAATAAATAATTAATAATTTTAAATAATTTAATAATTTTAA 1295
Qy 2731 TTAATAAGTAATTTGAATGTCATTTGGAGTACACTAGTCCCTTTTTTCCCAA 2790
Db 1294 AAAAAATTTTCAATTTTATATATTAAT-ATTAATTAATCAATTAATTTTATTAATCAAAA 1236
Qy 2791 AATTAATCTCTTATACGACCGGTTAAAGTATTAACAACAATAATTTAATTTGTTGCT 2850
Db 1235 AATTAATTTTATTA-TTAATAAATAATTAATAATTAATAATTTTAAATAATAATTA 1177
Qy 2851 GAAGGTCAAAACATGTCATATATAGACAGATGTTTATCAATATATGTTCAATG 2910
Db 1176 TAAATTAATAAATAATTAATTTTAAATTTTCAAAATTAACAAAAAATAT-AAAAA 1119

Qy 2911 TTAATGGAATCAAAATTAATTAATAGATTTAGCACTCACTGGTTAATAGTTGAGAA 2970
Db 1118 CAATATATTAATTAATTTTAAACAATTAATAAATAAATAAATAAATAAATAATTTTAAAT 1059
Qy 2971 TAAATGAATTAATAAATGAATTAAGGATACAGATATATATGCGGCTCATTAAGAC 3030
Db 1058 TTACATATTAATTAATTTCAAAATTAATAAATAATTAATAAATAAATAATTAATTTT 999
Qy 3031 CGTACCAAAAGTTTCTGCTAATTTCTAGCGTGGCTCATAGAAATTTGACTTTCT 3090
Db 998 AAAAAATTAATTAATTAATTAATTTTATTCATTTAATAAATAAATAAATAATTTTAA 939
Qy 3091 TCACCTTTTATGAATCTCTGATATGTTTGTGCGATTAATATTTGATTCGTATAT 3150
Db 938 AAAAAATTAATTAACAATAAACAATAATTAATAATTAATAATTAATAATTAACAAT 879
Qy 3151 TTTTGTCTAATAATGATACGTAAATTCAGATTAAGAAAGACTTCTTTTATTAATTT 3210
Db 878 TTTTATACATTAATAAATAAATAAATAAACAATTTTAAATAAATAATTAATAAT 819
Qy 3211 GATTTAAACTTTTGTGTTTGAATGATCATACACAAGTTAAAGTTGATGATCC 3270
Db 818 CATTAATAATTAATTTAATAATTAATTAATTAATAATTAATTAATTAATTAATTAAT 759
Qy 3271 AATTTAACAATAATGTTTGAAGTGGTGAAGTGTCAACATGTAACAATCTGT 3330
Db 758 TAAATTAATAAATAATTAATTAATTAATTAATTAATTTTAAATAATTTTAAATAA 699
Qy 3331 ATGGTTTATTAATAGTTTCTTCTCTCTTTTCCATGCTTAAATTAATGAACACTCT 3390
Db 698 AATTTTAAATAATTAATTAATTTTAAATTTTAAATAATTAATAATTAATAATTAAT 639
Qy 3391 AATTTCTTTTAAATTAATGTTAAGATCTGAATTTTCTGATATTTAAACAAG 3450
Db 638 TTTAATAAATAATTTAATAATTAATTAATTTTAAATAATTAATTAATTAATTAAT 579
Qy 3451 TTTTCAATCTCTTGAACAATAAATAAATAAATAAAGTTTCAATTAATAAAGACTTAA 3510
Db 578 AATTTAATAAACAATTAATTAATTAATTAATTAATAATTTAATTAATTAATTAAT 519
Qy 3511 TTTTGAATCAAGATTTAATGATAGCTGAAGATTAATGAATGATGCAAGTTGCA 3570
Db 518 ATATTAATAAT-ATTAATAATTTTAAATTTTAAATTAATTAATTTTAAATAA 460
Qy 3571 CAGATGCTGATGATATCATATCAAAACATGATCAAAATTAATTAATCGTGTAGC 3630
Db 459 TTAATTTTATTTATTTTAAATAAATAAATAAATAAATAATTAATTAATTAATTAAT 400
Qy 3631 AAGGAAACGATTAATAATAAACAACAATCGTTAACCACTTAAATCTTAGATTAAT 3690
Db 399 AATTTAATAATTAATAATTAATTAATTTTAAATAAATAAATAAATAAATAATTTT 340
Qy 3691 TTGTAGATTAATTTTCTGTAAGAGAGATATCATCTTACAAAAAATCAATTTT 3750
Db 339 AATTAATTTTAAATTAATTAATTTTAAATAAATAAATAAATAAATAAATAATTTT 280
Qy 3751 AGATTAATAATGATGTCGAATGTTCAAGATGTTTT---GCTGATCAGTTGTA 3807
Db 279 TATTAATAAATAATTTAATAAATAATTTTAAATTTTAAATAAATAAATAATTTT 220
Qy 3808 TTGTAATCTCTCTTAGCATATAGTCTTAAGTTTAAATGTTTCAAAAGACTTAA 3867
Db 219 TTAATAATTAATTAATTAATTAATAATTAATAATTAATAAATAAATAAATAAATAA 160
Qy 3868 AATTAATAATTAATTAAGTGAATTTGTAGGCTAAGCGAAATAAATAAATAATA 3927
Db 159 AATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAATTAATTAATAA 100
Qy 3928 AAGTAAGAA 3938
Db 99 AATTAATAAATAA 89
```

RESULT 11
 ABZ10246
 ID ABZ10246 standard; DNA; 8056 BP.
 XX ABZ10246;
 AC
 XX 16-JAN-2003 (first entry)
 DT
 XX Haematopoietic cell proliferation disorder related DNA sequence #386.
 DE
 XX Human; haematopoietic cell proliferation disorder; cytostatic;
 KM Gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KM cytosine methylation state; gene; ds.
 XX Homo sapiens.
 OS
 XX MO20027272-A2.
 PN
 XX 03-OCT-2002.
 PD
 XX 26-MAR-2002; 2002MO-EP003401.
 PF
 XX 26-MAR-2001; 2001US-0278333P.
 PR
 XX (EPIC-) EPIGENOMICS AG.
 PA
 XX Berlin K, Braun A, Dietler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Plegenbrock C, Adorjan P, Grabs G, Lesche R, Leu E;
 PI Lewin A, Lipscher E, Meier S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwobe I, Ziebarth H;
 XX
 DR WPI; 2003-018942/01.
 XX
 PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 PS
 XX Claim 28; SEQ ID NO 386; 117bp; English.
 XX
 CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy haematopoietic cells and proliferative
 CC disorder haematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of haematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC haematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of haematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 CC
 XX
 SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;
 Query Match 2.5%; Score 107.8; DB 8; Length 8056;
 Best Local Similarity 43.4%; Pred. No. 1.4e-08;
 Matches 1170; Conservative 0; Mismatches 1477; Indels 46; Gaps 13;
 QY 1505 TTATTTGGTAATCTATATGCTGATATACACATCCAGCTATCAATATGATCTCC 1564
 DB 1868 TAATTAATATTTTATTTTATTTATATTAATAAATTAATTTATTAATAAATAAATAA 1927

QY 1565 TTCTGCTATCAATTAATTAACACCATAGCTATCAAGCTATTAATTAATTAACACCAT 1624
 DB 1928 TTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1987
 QY 1625 CTCTTATCAATTTTATATGATATTAATTAACACCGACTATAGCTACAGTTGGTA 1684
 DB 1988 TTTATTTTAAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2044
 QY 1685 TTAAGCATTAATGCTTCAGTCGAAAGAAATTTTGTATGATTAACCTCGTGGAA 1744
 DB 2045 ATTTTATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2104
 QY 1745 AAAATCCAGCCATATATGCTCATTTTAAAGATTAATTAATTAATGCTTTAATCAATTA 1804
 DB 2105 AATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2162
 QY 1805 AATTAAGGTTTGTGTTTAAAGTTACACCGCTTAATTCATCTAGAGAAATTTA 1864
 DB 2163 AAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2222
 QY 1865 ACTTGATGAAATCCAAATCTTTTAAACATTAAGAAATTTTCAGATTTTAA 1924
 DB 2223 AATTTAATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2282
 QY 1925 ATTAAGGTATCAATTTATGCTTCATTAATATGTTCCAGCTAAAGTTGAGTTTAA 1984
 DB 2283 TTTTAAATTTTATTAATTTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAA 2342
 QY 1985 CCACATGAATGTTTGTGATTTTAAACACATTAATTTCTAGTATTAACATTTTAA 2044
 DB 2343 TTAATTTTAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2402
 QY 2045 ACCGTCCATCCAGATTTGTAATTAAGTCAAAATCTGAAACATTTTCTGTAATC 2104
 DB 2403 GAAATTAATTAATTAATTAATTAATTTATTTTAAATTAATTTTATTTATTTAT 2462
 QY 2105 T--TGTTAAATTTCTCTGCTGCATCTGACGAGCATTTGACCAAGCTATTAATTA 2161
 DB 2463 TATATATTTTATTAATTTTGTGTTTAAATTAATTAATTAATTAATTAATTAATTA 2522
 QY 2162 TGAAGCAAAATATCCACAGAGGATATAGGTTAGATCCCATTCATATCTTTGTC 2221
 DB 2523 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2582
 QY 2222 TTTGTTATTTAAGAAACAAATATTTATCAGGAAATTAAGCTTCTGCTAGTGTAT 2281
 DB 2583 TAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2639
 QY 2282 AAGTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2341
 DB 2640 AAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2699
 QY 2342 CCAATCTGCAATTAATTAATTAATTAATTTTATTTTAACTAACTATCCACTAA 2401
 DB 2700 TATTTTATTTTATTAATTAATTAATTAATTTGTTAAATTAATTAATTAATTAATTA 2755
 QY 2402 AAAAATGCAAAAGAAAGATATATTTAAGTCAAGTATTAAGATGATGGTGAT 2461
 DB 2756 AAAAAATTAATTAATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAAT 2815
 QY 2462 CTTCAGCAAAAGCGCGGATGAGTGTCTATCTACATTAACAGCTGGGTGTGCGAGA 2521
 DB 2816 ATTAATTAATTAATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTAATTA 2875
 QY 2522 CATCATAGGCGCTACATTAATTTGAGCT--TTACGTACGTAATTTTAAATTAATTAAT 2580
 DB 2876 AATTTTGTGTAATTAATTAATTAATTTGTAATTAATTAATTAATTAATTAATTAATTA 2935
 QY 2581 TAGTTCTACGTACAAACAAATTCGAATTTGTAACATTAATTAACAAATTAATTA 2640
 DB 2936 AATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 2995
 QY 2641 GTACTAGATTAGCTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2700

Db	2996	GATATATTTTAAATGATGATGTTAAATTTATTAATATAATTAATAATAATAATAAT	3055
Oy	2701	CAAACTGAATGTTGTTTGTATTAATTCTTAAACCAAGTTTGAATGCTGGG	2760
Db	3056	GTTATTAATGGAATGAATTTGATATTTGTATTTTATGTGTAATTTAATATAAAT	3115
Oy	2761	AGCTACACTGATGCCCTTTTCCCAATAATCTCTTACATGACCGGTTAAGT	2820
Db	3116	TAAATTTTTTAAATGAATTTTAATGATGATGAAAAATGTTTTATATATATTTAAAT	3175
Oy	2821	ATTTAACCAAAATTTTAAATTTGTGCTGAAGTCAAAACGTCTCATATATAGGA	2880
Db	3176	AATATATATTTTAAATAAAATTTTGTGTTGAATGTAATGTAATTTTAAATTTTA	3231
Oy	2881	CAGCATCGTTATACAAATTAATGTCGATATGTAATGAAATCAATATTAATACGAATTA	2940
Db	3232	TTATATTTTTTTTAAATTAATTTGATATATTTTAAATTAATGATGTAATAAAATTTT	3291
Oy	2941	GCGACTACTGTGTTAAATAGTTTGAAGATATGAAATTAATAAATGAATTTCAAGAT-	2999
Db	3292	TGTTATGTGTGTTATTTTGTGAAAAAATAATATGTAATGTAATAAATG	3351
Oy	3000	-ACAGAGTATATATGTCGGGTCATTTAGACCGGACCAAAAGTTGCTGTATTTCT	3058
Db	3352	AATATAATTTGAATGATTAATAAATAAATAAATAAATAAATAATTAATTTGAATTTT	3411
Oy	3059	ACGGTCGGTCAAGAATTTTGGACTTTTCTCACCCCTTTATGAACCTGTATAGTT	3118
Db	3412	TTTAAATTTTTTGTATTAATGTAATAATTTATTTTATTTATTTATTTAATTA	3471
Oy	3119	TTTGTGGATTATATATTTGTATTCGATTAATTTTGTGTTCTAATATGATACGTAATT	3178
Db	3472	AATTTTTTTTTTGTGTATTAATAAATAATGATTAATGATGTAATGTAATAATTAAT	3531
Oy	3179	CACGATAGAAGACTCTTTTATTTAATTTGATTTAAACTTTGTTTGGAAATGA	3238
Db	3532	TTTTATTAATATAATTAATGTTAAATAATTTGTGAAAAAATTAATTAATATAAT	3591
Oy	3239	CTCATACACAAGTTTAAAGTTGATGTAATCAATTTACAAAANGTTGAGAGTGGT	3298
Db	3592	ATTA-----ATGAAAAATTAATTTAAATTAATAAATAATTTTATATGAAAAATTT	3640
Oy	3299	TCGAGTGTCTACCAACCATGTAACCATGTAATGAGTTTATTAATAGTTTTTCTC	3358
Db	3641	AATGTAATGTGAATATGATGTTAATAATTTGAAATTTTTTTTATTAATAATATTTT	3700
Oy	3359	TTTTTCCATGTCTTTAATTAATTTGAACCACTTAATTTCTTTTTTAATTAAGTTAAG	3418
Db	3701	AAATGATTAATAATTTTAATTAATAAATAAATAAATAAATTTTATTTTAAATA	3760
Oy	3419	ATCTGAAATTTTGTGTTGATTTTAAACAAGTTTCAATCTCTTAAGCAAAAAA	3478
Db	3761	ATTTTATTAAT-----TTGAAAATGTAATTAATAATTAATGTTTAATTTGTTG	3814
Oy	3479	AAAAAAGTTTTCATTAATTAAGATCTAATTTTTTGAAGTTCAAGGTTAATGATAG	3538
Db	3815	AATTTTGTTTTTTGAATAATTTGAATGTAAATTTGAATAATTTGTTGTATGATTA	3874
Oy	3539	CTGAAAAGTTATGATGATTTGCAAGTTTGCAACGAATGTCGATGTATGATCAATCAAA	3598
Db	3875	AAAAATGAAATTTGAT--TTTAATGTTTTTAAAAAATTTGAAAAATTAATGATAAAAAT	3932
Oy	3599	AAACATGATCAAAATTAATATTTGTCGCTTACCAAGAAAGATTTGAATTAACAGAA	3658
Db	3933	ATTAATTTATTAATAATTTAAATATTAATAATTTTAATGTTTAAATAAATAATGAAAT	3992
Oy	3659	ATCGTTAACCACTTAATAAATCTTGAATTAATTTGTAGTGAATAATTTCTGTAAAGAGA	3718
Db	3993	GTTTAAATGAAATGATTAATGTAATTTTGTGTTGTGTAATAATTTTGTAT-----G	4048
Oy	3719	GGTATCATATCTTACAAAAAACTCATTTTCAGATTAATAATGTTGTCCATGTTAC	3778

Db	4049	ATTATTTTAAATTTGCTTTTAAAGTTTATTTTATTTTGTGTAATTTGTAATTTTATTTT	4108
Oy	3779	CAAGATGTTTGTGTCATCAGTGTGATTTGTAACGTCTCTTACCATATAGTTCTA	3838
Db	4109	ATTTTATTTTATTTATGTTTTTGTTTTTATTTTAAATATATTTTGTATTAATTTTTT	4168
Oy	3839	AGTTTAAATGTTTCAAAAGCTTTACAAAATATAATATATAGGTGAATTTGTAG	3898
Db	4169	TTATTAATTTTATTTTATTTTGTGATTTAAATATGAAATTTAATGTGAATTTTAA	4228
Oy	3899	GGCTAAAGCAAAAATATAATATAATATAAGTAAGAAACGCTTTCGAATAGAC	3958
Db	4229	TATTTTATTAATATAATATAAAAAATATAATATAATATAATATTTTATTTTGTATT	4288
Oy	3959	ACAGATCCCAAGGATTCAAACAGCAAAATTTGTGCTTGTCTCTCTATTAATATA	4018
Db	4289	TAAATATGAAATATATATATATTTGTAATAATTTT-TGTATGATATTTTTTGGAAATATTT	4347
Oy	4019	TCCTCTCAAAACCCCTCTCTATATCTCTTAAAGCCCTCTCTGTTTCTCTACCGC	4078
Db	4348	TATTAATAATATATATATATTTTAAATTTGTTTAAATTTGTTTGTATTTTATTTTGTG	4407
Oy	4079	AACAAAGAAAACAAAGTTTGAGAAAATCGTGTCTGTGTGTATACCAATGATTCG	4138
Db	4408	ATTTTGAATGTGAAAATATTTTGGAAATGATTTGATTAATAATTAATTAATTAATGA	4467
Oy	4139	GTTTATGCTTACTCTCGAGAGATTATTAAGAAAGAAAGAGTGAAGATACATT	4191
Db	4468	AATTTGTTTAAATTTTATTTTAAATTAATGATTAATAAAAAATGAATATATTTT	4520

RESULT 12
 ABZ10100/C
 ID ABZ10100 standard; DNA; 8056 BP.

AC ABZ10100;
 AC
 AC
 DT 16-JAN-2003 (first entry)
 DT
 XX
 XX
 DE Haematopoietic cell proliferation disorder related DNA sequence #240.
 DE
 XX
 XX
 KM Human; haematopoietic cell proliferation disorder; cytostatic;
 KM
 KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KM cytosine methylation state; gene; ds.
 XX
 XX
 OS Homo sapiens.
 OS
 XX
 XX
 FN WO200277272-A2.
 FN
 PD 03-OCT-2002.
 PD
 XX
 XX
 PF 26-MAR-2002; 2002WO-EP003401.
 PF
 XX
 XX
 PR 26-MAR-2001; 2001US-0278333P.
 PR
 PA (EPIG-) EPIGENOMICS AG.
 PA
 XX
 XX
 PI Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu B, Pelet C;
 PI Lewin A, Lipscher B, Mater S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwöbe I, Ziebarth H;
 XX
 XX
 DR WPI, 2003-018942/01.

PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 CC
 CC Claim 28; SEQ ID NO 240; 117bp; English.
 CC
 CC The present invention describes a method for detecting and
 CC differentiating between haematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a

CC subject. The method comprises contacting a target nucleic acid in a
CC biological sample obtained from the subject with at least 1 reagent,
CC which distinguishes between methylated and non-methylated CpG
CC dinucleotides within the target nucleic acid. AB209861 to AB211118
CC represent specifically claimed nucleotide sequences from the present
CC invention. Oligonucleotides from the present invention can be used: for
CC differentiating between healthy haematopoietic cells and proliferative
CC disorder haematopoietic cells; for differentiating between acute
CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
CC determining the cytosine methylation state and/or single nucleotide
CC polymorphisms (SNPs) of haematopoietic cell proliferation disorder
CC related sequences and their complements; and as primers for the
CC amplification of haematopoietic cell proliferation disorder related DNA
CC sequences. The nucleotide sequences from the present invention can also
CC be used for detecting a predisposition to, differentiation between
CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
CC haematopoietic cell proliferative disorders. The present method enables a
CC highly specific classification of haematopoietic cell proliferative
CC disorders allowing for improved and informed treatment of patients

SO Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;

Query Match 2.5%; Score 106.8; DB 8; Length 8056;

Best Local Similarity 41.8%; Pred. No. 2.1e-08;

Matches 1210; Conservative 0; Mismatches 1652; Indels 32; Gaps 8;

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QY 1140 TTTTCTTCTTCTGCTGTTGCTATCTATTTCTCGAGTGAAGTATCAAGAAAC 1199
DB 2890 TTTTCGACGAATTTTTCGTAAATTAATTCGAATTTTAATTTTAATAAATAA 2831
QY 1200 TAAATTCGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAA 1259
DB 2830 TCGTTTATTTATTAATAACGATTTTAATAACGAAATTCGTTAAATTTAATAA 2771
QY 1260 CACTAAATTCGATTAATAAATGATATATGTTGCGAATTATATCAATACCA 1319
DB 2770 CGATTAATTTTATTTTATTTATTAATTAATTTTAACGAATTTATTTTAA 2711
QY 1320 AATTCGAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGAAAGTGC 1379
DB 2710 AAAAAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 2652
QY 1380 TCCCATCTCTCTTTTACTTCCAACTAATCATCTACAGAAATCTGCTCGAT 1439
DB 2651 TAACTGTTTTTTTATTTTATTTTAAATTTATTTATTTAATTTTATTTTCTG 2592
QY 1440 CACTTCATGCAAAATTAATTAATTTTGGTATTTTTCGAAGTTCTGCTGTTAA 1499
DB 2591 TATTTTATTTTATTTTAAATTTTATTTAATTTTAAATTTTAAATTTTAAAT 2532
QY 1500 GTGATTTTGTGATATCTATATGCTGATATACATCCAAAGCTAATCATATGTA 1559
DB 2531 TTAATTTATTTTATTTTATTTTATTTTATTTTATTTTAAATTTTAAATTT 2472
QY 1560 TCTCTTCTGCTATCAATTAATTAACACATTAAGTATCAAGTATTAATTAAC 1619
DB 2471 AAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2412
QY 1620 ACATCTCTTATCAATTTTATATGTAATTAATTAATTAATTAATTAATTAAT 1679
DB 2411 TTAATTTTGAATAATTAATTAATTAATTAATTAATTAATTAATTAATTT 2352
QY 1680 TGTATTTAAGGCAATATGCTCTAGTCGAAGAAATTTTGTATGTAACATCGT 1739
DB 2351 AAAAAATTAATTAATTTATTTAATTAATTAATTAATTAATTTAATAATTA 2292
QY 1740 GGGAAAAATTCAGCTATATGCTAATTAAGTATTAATTTAATGCTTAATC 1799
DB 2291 AATTAATTAATTAATTTTATTTAATTTATTTAATTAATTAATTAATTAAT 2238
QY 1800 AATTAATTAATTAATTTTGTCTTTAAGGTTACACCGCTAATCATTAAGGAA 1859
DB 2237 AATTAATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTAAATTTTAA 2178
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QY 1860 TATTAACCTTGAATCGAAATTCGAAATTAATTAATTAATTAATTAATTAAT 1919
DB 2177 AATTAATTAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTAAT 2118
QY 1920 TTTAAATTAAGGTCATTTATTTGGTCAATTAATTAATTTTCCAGTAAAGTTGAGC 1979
DB 2117 AATTAATTAATTAATTTAATTTATTTAATTAATTTAATTAATTTAATTTT 2058
QY 1980 TTTAACCAGATGAAGTTTATTTGATTTAATAAACAATAAATTTTCTAGTAATACAT 2039
DB 2057 AAAAAATTAATTAATTTAATAATTAATTTAATTTAATTAATTTAATTTAAT 1998
QY 2040 TTTTAAACCTTCATCCAGATTTGTAATTAAGTGAATTAATTCGAAACATTTTCTT 2099
DB 1997 TTTAAATTAATAATTAATTAATTAATTTATTTTAAATAATTAATTTTATTAAT 1938
QY 2100 GAATCTGTTTAATTCCTCTGCTGCATACCTTGACGCAATTTGACCAACGACTATACAT 2159
DB 1937 TATTAATTTAATTTTATTTTATTTTAAATTTTATTTTAAATTAATTAATTA 1878
QY 2160 ATTGAAGAAATTAATTCACAGGATGAATAGGTTAGATCCACATTCATATCTTTG 2219
DB 1877 TAAATTAATTAATTAATTTTATTTTATTTTATTTTATTTTAAACGAAATTTAT 1818
QY 2220 TCTTGTATTTATGAAATTAACAA-----ATATTATCGAGAAATTAATCGTT 2265
DB 1817 ATTAATTAATTAATTAATTAATTAATTAATTAATTAATTTTAAATTTTAAATTT 1758
QY 2266 TCTTCTCTAGGTATTAAGTATTAATTAATTAATTAATTAATTAATTAATTAAT 2322
DB 1757 TTTATTTATTTTATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1698
QY 2323 TTTACTATCTCAAACTTAACATCTTCAACATTAATTAATTAATTTTATTTTATTT 2382
DB 1697 TTTATTAATTTTAAATTAATTAATTTTATCGATTAATTAATTAATTTTATTT 1638
QY 2383 ACTAACTACTCTCACTAATAAATAATGCAAAAGAAAGATATTAATTTAAGTCAAGTAAT 2442
DB 1637 TACGATTCGTTTATTTTCGATTTTATTTTAAATTTATTAATTTATTAATTTAAAT -AT 1579
QY 2443 TAAAGATGATGGGTATTTCTTCAAGAAACGGCGGTAGAGTGTCTATCTATCTAT 2502
DB 1578 TAAATTAATTAATTAATTTTAAATAATTAATTTATTTAATAATTTTAAATTTT 1519
QY 2503 AAGCTGGGTGGGAGCATCATAGGCTTAATTAATTTGAGCTTATCTAGTATA 2562
DB 1518 ATATTTATTAATTAATTAATTAATTAATTAATTAATTAATTTAATTTAATTT 1459
QY 2563 AGCTTAACATTAATCTAGTATGTTCTCACTGTACAAACAAACAAATCCAAATCGTACA 2622
DB 1458 AAAAAATTAATTTTATTTTATTTTATTTTAA-----AAAAAATAAATAAATAA 1403
QY 2623 TATTAACAAATTAATCTAGTATGATTAACGCTACGTAATTAATTAATTTTTCGAAATTT 2682
DB 1402 TCGATATTTATTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATTTAT 1343
QY 2683 CTAATTAATCTATACAACTGAATGTTGTTGTAATTTATCTTAAACAAAGT 2742
DB 1342 TTTTATTAATAATTAATTAATTAATTTTATTAATTTAATTTAATAAATAATTA 1283
QY 2743 TTTGAATGTCATGGGAGCTACACTAGTCCCTTTTCCCAATAATATCTCCTT 2802
DB 1282 TTTTATTAATTAATTAATTAATTTTATTTTATTTTATTTTAAATAATTTATTTAT 1225
QY 2803 ACATCGACCGGTTAAAGTATTTTAAACCAATTTAATTTGTTGCTGAGGTACAAAC 2862
DB 1224 TATTAATAAATAATTAATTAATTAATTTAATTTTAAATAATTAATTAATTAAT 1165
QY 2863 ATGTCATATTAATGAGACGATCGTTATTAACAAATTAATTTGATTTGAAATC 2922
DB 1164 ATATATTAATTTTAAATTTTTCGATATTCGAAATAAATAATTAATAAATAACG-AAATATTAACG 1106
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QY 2923 AATATATATACGATTTAGGAGTCACTGGTTTATAGTTGGAGATATAGATATAA 2982
 DB 1105 TTTTAAACGTTAAAAAAGCAATTTAAACGAAATTTTATTTTACGTATATATAA 1046
 QY 2983 AATGATTCAGAAAGATACAGAGCTATATATGTCGGGTCACTTGAACCGTACAAAG 3042
 DB 1045 TTTCGAAATTTAAAAATATATAAAAATTTTAAATATATTTTAAAAAATATATA 986
 QY 3043 TTTCGTCGTAATTTCTACGGTCGTAAAGAAATTTTGGACTTTCTTCACTTTTAT 3102
 DB 985 TATATATTTTATTCGTTTAAATAAAAATAAAAATTTTAAAAAATTTATTTAC 926
 QY 3103 GAATCTGTATGTTTGTTCGATATATATTTGATTCGTATTTTGTTCCTAA 3162
 DB 925 GAAATACGAGAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 866
 QY 3163 TAAATGATTCAGAAATTTACAGATTAAGAAAGCTTCTTTTATTTTAAATTTGAATTTAA 3222
 DB 865 AAAAAATAAAAAAGCAATTTTATTAATAAATTTTAAATTAATCGTTATTAATTT 806
 QY 3223 TTGTTTGGAAATGACTCATACAAAGTTAAAGTTGATGTCATTCATTAAGAAA 3282
 DB 805 ATTTTAAATTAATTAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTAA 746
 QY 3283 TGTTCGAGAGTCGCTCGAGTCCTACCACTGCTACCACTGCTATGGCTTATTA 3342
 DB 745 TTTTAAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 686
 QY 3343 TTAGTTTTTTTCTCTTTTCCAAATGCTTTATATTTGAAGCACTCAAAATTTCTTTT 3402
 DB 685 TTATTTATTTTATTTTATTTTAAATTAATTAATTTTAAATTTTAAATTTTAA 626
 QY 3403 TTAATTTAGTTAAGAACTTGAATTTCTGTTGATTTTAAACCAAGTTTCAATTTCT 3462
 DB 625 AATATTAATTAATTTTATTTTAAATTAATTAATTAATTAATTAATTTTAA 566
 QY 3463 CTTAGCACAAAAAAGAGTTTCAATTTTAAAGAACTTAATTTTGAAGTTC 3522
 DB 565 CGTTTAAATTAATTAATTAATTTTAAATTTTAAATTAATTAATTTTAA 506
 QY 3523 AAGAGTTAATGATGAGTGAAGGTTATGATGATTCAGATTTGCAACGAATGTCGA 3582
 DB 505 TATTAATTTTAAATTTTATTTTAAATTAATTTTAAATTTTAAATTTTAA 446
 QY 3583 TGTAGTACATATCAAAAAATGATCATCAAAATTAATTTGCTGCTTACCAAGAAAGAT 3642
 DB 445 TTATTTTAAAAAATTAATTAATTAATTAATTTTAAATTTTAAATTTTAA 386
 QY 3643 TGAATTAACAGAAATCGTTAACCTTAAATTTTGAATTAATTTTGTAGTATA 3702
 DB 385 AATATTTTATTTGTTTTTTTTTTTTTAAATTAATTTTAAATTTTAA 326
 QY 3703 TTTTCTGTAAGAGAGTATCAATTTTCAAAAAAATCTCAATTCAGATTAATTAAT 3762
 DB 325 ATTAATTTTAAAAAATTAATTTTAAAAAATTTTATTTTAAATTTAAAT 266
 QY 3763 GTTGTCATATCGTTACCAAGATGTTTGTGCTGTCATCAGTGTATTTGTAAGTCTCT 3822
 DB 265 TAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 206
 QY 3823 TAGCCATATAGTTCTAAAGTTTAAAGTTTCAAGACTTTACAAAAATTAATTAAT 3882
 DB 205 AATTAATTTAAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTAA 146
 QY 3883 AAGGTGAATTTGAGGCTTAAAGCAAAATTAATTAATTAATTAATTAATTAAGAAAGT 3942
 DB 145 ATAAAAAATTAATTAATTTTAAATTAATTTTAAATTTTAAATTTTAA 86
 QY 3943 CTTTTCATATAGAACACAGATCCCAAGATTCAAACAGCAATTTGTGCTTGTCTT 4002
 DB 85 AAAAAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAA 26
 QY 4003 CTCTCTTATTAATA 4016

DB 25 TTTATTTTATTTTAA 12
 RESULT 13
 ABZ10100
 ID ABZ10100 standard; DNA; 8056 BP.
 XX
 AC ABZ10100;
 XX
 DT 16-JAN-2003 (first entry)
 XX
 DE Hematopoietic cell proliferation disorder related DNA sequence #40.
 XX
 KM Human; hematopoietic cell proliferation disorder; cytostatic;
 KM gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KM cytosine methylation state; gene; de.
 XX
 OS Homo sapiens.
 XX
 PN W02002772-2.
 XX
 PD 03-OCT-2002.
 XX
 PE 26-MAR-2002; 2002NC-EP003401.
 XX
 PR 26-MAR-2001; 2001US-0278333P.
 XX
 PA (EPig-) EPIGENOMICS AG.
 PI Berlin K, Braun A, Dietler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepdrock C, Adorjan P, Grabs G, Lesche R, Leu B;
 PI Lewin A, Lipscher B, Mater S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwope I, Ziebarth H;
 PI
 DR WPI; 2003-018942/01.
 XX
 PT Detecting and differentiating between hematopoietic cell proliferative
 PT disorders, comprises contacting a target nucleic acid with a reagent that
 PT distinguishes between methylated and non-methylated CpG dinucleotides.
 XX
 PS Claim 28; SEQ ID NO 240; 117bp; English.
 XX
 CC The present invention describes a method for detecting and
 CC differentiating between hematopoietic cell proliferative disorders
 CC associated with at least 1 gene and/or their regulatory regions in a
 CC subject. The method comprises contacting a target nucleic acid in a
 CC biological sample obtained from the subject with at least 1 reagent,
 CC which distinguishes between methylated and non-methylated CpG
 CC dinucleotides within the target nucleic acid. ABZ09861 to ABZ1118
 CC represent specifically claimed nucleotide sequences from the present
 CC invention. Oligonucleotides from the present invention can be used: for
 CC differentiating between healthy hematopoietic cells and proliferative
 CC disorder hematopoietic cells; for differentiating between acute
 CC lymphocytic leukaemia and acute myelogenous leukaemia; as probes for
 CC determining the cytosine methylation state and/or single nucleotide
 CC polymorphisms (SNPs) of hematopoietic cell proliferation disorder
 CC related sequences and their complements; and as primers for the
 CC amplification of hematopoietic cell proliferation disorder related DNA
 CC sequences. The nucleotide sequences from the present invention can also
 CC be used for detecting a predisposition to, differentiation between
 CC subclasses, diagnosis, prognosis, treatment and/or monitoring of
 CC hematopoietic cell proliferative disorders. The present method enables a
 CC highly specific classification of hematopoietic cell proliferative
 CC disorders allowing for improved and informed treatment of patients
 XX
 SQ Sequence 8056 BP; 3711 A; 371 C; 371 G; 3603 T; 0 U; 0 Other;
 Query Match 2.4%; Score 99.4; DB 8; Length 8056;
 Best Local Similarity 42.6%; Pred. No. 3.5e-07;
 Matches 1195; Conservative 0; Mismatches 156; Indels 46; Gaps 11;
 QY 1138 ACTTTTCTTATGTCGTTGTTGACTAAATTTCTCAGAGTGAAGTGTAAATCAAGAA 1197

QY 2473 CGGCGCGTAGAGGTGCTTATCTTACATTACAGCTGGGTGGGAGACATCATAGGCG 2532
DB 926 AATTATTATATATAGATATAATATATCTATATATATATATTTTACATATATTTAAT 985
QY 2533 CTACGTATATATTTAGCTTTACTGTACGTAAAGCTTTAACATATCTAGTTAGTTCTACTG 2592
DB 986 ATATGATATATTTTATATCATATATATATATATATATATATATTTTATATCATATAT 1045
QY 2593 TACAAACAAACAAATCCATTCGTACATATATACAAATCTACTAGTACGTATAC 2652
DB 1046 AAT 1105
QY 2653 GCTACGTATACATCGCTTTTGGCAATTTCTTAACTATCTATACAAACAACTGATG 2712
DB 1106 TATCAT 1165
QY 2713 TTTGTTTGTATATATCTTAAACCAAGTTTGAATGTGCAATGGAGCTACACTCA 2772
DB 1166 TATATCTACAT 1225
QY 2773 GTCCCTTTTCCCAAAATATCTCTTACATCGACCGGTAAAGTATTTAAACCAAC 2832
DB 1226 TATACATATATATCTATATATATATATATATATATATATATATATATATAT 1285
QY 2833 AATTTTATATTTGTCTGTGAAGGTACAAACATGTACATATATAGACAGCATCGT-- 2890
DB 1286 TATATATATATATCTTTTATATATATATATATATATATATATATATATATAT 1345
QY 2891 -TATACAAATATATGTTTGCATGTTATTTGAAATCAAAATATATATATATATATAT 2949
DB 1346 ATATATAATGAT 1405
QY 2950 TTGGTTTATATAGTTTGGAAAGATATAGAAATATAAAATGAAATCCAAAGATACAGACTA- 3008
DB 1406 TTTATTTTATATATATAAATGATATATATATATATATATATATATATATATAT 1465
QY 3009 TATATGTGCGGTCAATTTAGAGCGGTGACCAAAAGTTTCGTGCAATTTTCTACGCGT 3068
DB 1466 TAT 1525
QY 3069 ATTAAGAAATTTTGGACTTTTCTTACCCCTTTATGAAAC-----TTCGTATATGTTT 3122
DB 1526 ATATGAT 1585
QY 3123 TCGGATATATATATTTGATATGATATATTTTGTCTATATATGATAGTAAATTCACG 3182
DB 1586 AT 1645
QY 3183 ATTAAGAAAGCTCTTTTATATATATATATATATATATATATATATATATATATAT 3242
DB 1646 ATATATTTTGTAT 1705
QY 3243 TACACAAGGTTAAAGTTTGAATGATCAATTTACAAAATGTTTGAAGTGGCTTCA 3302
DB 1706 TAT 1765
QY 3303 GTCTCTACACATATGATACCACTGATAGGCTTATATATGTTTCTTCTTCTT 3362
DB 1766 AT 1825
QY 3363 TCCATGTCCTTATATATGAAACACTTAAATTTCTTTTATATATATATATATATAT 3422
DB 1826 TTTAT 1885
QY 3423 TGAATTTTCTGTGATTTTAAACCAAGTTTCAATCTTCTTGAACAAAAA 3482
DB 1886 TAT 1945
QY 3483 AAGGTTTCAATATATTAAGATCTAAATTTTGGAGTCAAGGTTTAA--ATGATAGC 3539
DB 1946 AATATGAT 2005
QY 3540 TGAATAAGTATGATGATTTGCAAGTTTGAACGAAGTGTGATATATATATATATAT 3598

DB 2006 TAAAATGAT 2065
QY 3599 -----ACATGATCAACAAATATATATTTGCTGCTTACGACGAAGAAAGTGAATTAAC 3652
DB 2066 GTAT 2125
QY 3653 AGAACATGCTTAAACACTTAAATCTTGAATATATTTGTAGATATATTTCTGTAA 3712
DB 2126 TGTAT 2185
QY 3713 GAGAGGATATCATATCTTACAAAAAATCTCAATTCAGATATATATATATATATAT 3772
DB 2186 AAT 2245
QY 3773 CGTTACCAAGTATGTTTGTGCTGATCATGCTGATATGTTAGTACCTGCTTACCATTA 3832
DB 2246 TAT 2305
QY 3833 GTTCTAAGTTTAAATGTTTCAAGACTTTCAAAAAATATATATATATATATATATAT 3892
DB 2306 -TTTAT 2364
QY 3893 TTGTAGGCTTAAAGGAAAAATATAAATATAAAGTAAAGAAACGTTCTCAAT 3952
DB 2365 AT 2424
QY 3953 AAGACACACA 3963
DB 2425 TAT 2435

RESULT 15
ABN80291
ID ABN80291 standard; DNA; 7306 BP.
XX
AC ABN80291;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human chemically modified disease associated gene SEQ ID NO 308.
XX
KW Human; development; homeobox gene; HOX; diabetes; cancer; apoptosis;
KW heart disease; epilepsy; histone deacetylation; muscular dystrophy;
KW dwarfism; single nucleotide polymorphism; SNP; cytosine methylation;
KW antidiabetic; cyclostatic; anticonvulsant; ds.
XX
OS Homo sapiens.
OS Synthetic.
PN MO200200927-A2.
XX
PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP007536.
XX
PR 30-JUN-2000; 2000DE-01032529.
PR 01-SEP-2000; 2000DE-01043826.
XX
PA (EPIG-) EPIGENOMICS AG.
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI; 2002-130908/17.
XX
XX Novel nucleic acid useful for diagnosis and therapy of diseases
PT associated with development genes such as diabetes, comprises a sequence
PT of a segment of chemically pretreated DNA of genes associated with
PT development.
XX
XX Claim 1; SEQ ID NO 308; 27bp; English.
XX
XX The invention relates to a nucleic acid (I) comprising a sequence at

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GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: February 27, 2006, 09:02:01 ; Search time 20772 Seconds
(Without alignments)

11570.100 Million cell updates/sec

Title: US-10-623-477-3

Perfect score: 4228
Sequence: 1 gtgcactctgcgcctcactg.....agaaccaaaaaagaacc 4228

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 5083141 seqs, 28421725653 residues

Total number of hits satisfying chosen parameters: 11766282

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Genembl:.*
1: gb_ba:.*
2: gb_in:.*
3: gb_env:.*
4: gb_ov:.*
5: gb_ov:.*
6: gb_pat:.*
7: gb_ph:.*
8: gb_pr:.*
9: gb_ro:.*
10: gb_ste:.*
11: gb_sy:.*
12: gb_un:.*
13: gb_vl:.*
14: gb_hcg:.*
15: gb_pl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4228	100.0	4228	6	BD274517 Methods f
2	4228	100.0	4228	6	AR316368 Sequence
3	4228	100.0	4228	6	AR427902 Sequence
4	4072.2	96.3	110766	15	ATT28119 Arabidops
5	4072.2	96.3	198493	15	ATCHR188 Arabidops
6	366.4	8.7	371	15	ATHS30550 Arabidops
7	366.4	8.7	371	15	ATHS30550 Arabidops
8	268	6.3	2148	6	BD274516 Sequence f
9	268	6.3	2148	6	AR316367 Sequence
10	268	6.3	2148	6	AR427901 Sequence
11	268	6.3	2148	15	ATU60256 Arabidops
12	155	3.7	2056	15	AY080706 Arabidops
13	147	3.5	8056	6	AX599046 Sequence
14	120.6	2.9	349751	2	PFMAL4P3 Plasmodi
15	114	2.7	178670	8	AC104073 Homo sapi
16	107.8	2.5	8056	6	AX599046 Sequence
17	107.8	2.5	313050	2	PFAL929352 Plasmodi
18	106.8	2.5	8056	6	AX599046 Sequence

19	105.2	2.5	86826	2	PFMAL3P5	AL034556 Plasmodi
20	105	2.5	104992	14	AC005504	AC005504 Plasmodi
21	105	2.5	169546	14	AC004157	AC004157 Plasmodi
22	105	2.5	250421	2	AE014849	AE014849 Plasmodi
23	105	2.5	349751	2	PFMAL4P3	AL035476 Plasmodi
24	104.6	2.5	205130	14	AC105425	AC105425 Homo sapi
25	104	2.5	4601	2	DMU11584	U1584 Drosophila
26	104	2.5	19517	2	DMU17541	U17541 Drosophila
27	103.8	2.5	257757	2	AE014837	AE014837 Plasmodi
28	102.8	2.4	313050	2	PFAL929352	AL034556 Plasmodi
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30	101	2.4	67970	2	PFMAL1P3	AL031746 Plasmodi
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34	98.6	2.3	122168	8	AC127383	AC127383 Homo sapi
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41	95	2.2	175559	14	AC145101	U17541 Drosophila
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43	94.2	2.2	86826	2	PFMAL3P5	AL034556 Plasmodi
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ALIGNMENTS

RESULT 1
BD274517
LOCUS
DEFINITION
Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant.

ACCESSION
BD274517
VERSION
BD274517.1 GI:33084285
KEYWORDS
JP 2002534078-A/2.
SOURCE
Arabidopsis thaliana (thale cress)
ORGANISM
Arabidopsis thaliana

REFERENCE
Fischer, R.L. and Mizukami, Y.
1 (bases 1 to 4228)
TITLE
Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant

JOURNAL
Patent: JP 2002534078-A 2 15-OCT-2002;
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
COMMENT
OS Arabidopsis thaliana (thale cress)
PN JP 2002534078-A/2
PD 15-OCT-2002 JP 2000592392
PF 07-JAN-2000 JP 2000592392
PR 08-JAN-1999 US 09/227421
PI ROBERT L FISCHER, YUKIKO MIZUKAMI
PC A01H1/00, C12N5/10, C12N5/09, C12N5/00 CC ANT

FEATURES
source
FT promoter
Location/Qualifiers
1..4228
/organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/db_xref="taxon:3702"

ORIGIN

Query Match 100.0%; Score 4228; DB 6; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Q	y		61	GTTAGAAAAA	120
D	b		61	GTTAGAAAAA	120
Q	y		121	ACATGTGATATACAAATATATATATTTGAAATTGGAATATATCATTTATATGATTAAGT	180
D	b		121	ACATGTGATATACAAATATATATATTTGAAATTGGAATATATCATTTATATGATTAAGT	180
Q	y		181	TAATATATATACGCTGACATTAACAACCAATATGTTCTGCTTTATAGGATAGTCTATAT	240
D	b		181	TAATATATATACGCTGACATTAACAACCAATATGTTCTGCTTTATAGGATAGTCTATAT	240
Q	y		241	GTTGCACTTGATTTAGATTAATAATAAACTGGATTTATTTAAATCCGATCCCATTAAC	300
D	b		241	GTTGCACTTGATTTAGATTAATAATAAACTGGATTTATTTAAATCCGATCCCATTAAC	300
Q	y		301	AAAAGTGACCAAAACGAGATCCATGCTTTGTGTTTCTTTGTTGGTTAACCGATAT	360
D	b		301	AAAAGTGACCAAAACGAGATCCATGCTTTGTGTTTCTTTGTTGGTTAACCGATAT	360
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Q	y		481	CTAGAGTTGATATATCATTAACACGTGATATTTTAAACGACCGTATCATTAACATGAT	540
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Q	y		541	CGATCAATTCAAATTTATATGACATGAATCAAGATGAGATGCTCTAGACGAATA	600
D	b		541	CGATCAATTCAAATTTATGACATGAATCAAGATGAGATGCTCTAGACGAATA	600
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Q	y		781	AACTGTTTTATGTTAATATATATATGCTTTCCGATGTAATTTGAAACAAACTGTAA	840
D	b		781	AACTGTTTTATGTTAATATATATATGCTTTCCGATGTAATTTGAAACAAACTGTAA	840
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D	b		901	TATGTTAAGCTACAAATTTTCTCTTTAGATTAAGTTAGAAAGTTTATATATTA	960
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D	b		961	CTTTCAGGGGTATTAAGTCACTGCAATGACACTCAGCATAGACCAAAAGAGTGTCT	1020
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Db	1201	AATATTCGAAAAGAAAAGAAAAAGCGCAAGAAACTATGTCGAAAAGCATAAATGAC	1260
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Db	1321	AATCAAGAGAGAGAGAGGAGCCTCTTCGTGCTTAGATTTCCCTCTAAACAACCTGCT	1380
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Db	1381	CCCATATCCCTTTTATCTCCACAAAATCATCACAGAGAAAATCTGCTCTCGATC	1440
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Db	1441	ACTTCATGCAAAATTTAACTAAATTTGGTAATTTTGTCAAGTCTTGCTGTTTAA	1500
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Db	1501	TCGATTAATTTGGTAATTAATTAATGTGTGTGATATACATCCAGCTAATCAATTAATGAT	1560
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Qy	1861	ATTAATCTTGATCGAAATTCGAAAATCTTTTTTAAACATTAAGAAAATTTTCAGACTTT	1920
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Qy	1981	TTAACCAATGAATGTTTTTTGATTAAABAAACATAAATTTTTCAGTAATTAACACTT	2040
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Db	2161	TTGAAGCAAAATATCCACAGAGGATGATAGGGTTAGATCCCACTCAATATCTTTTGT	2220

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4228)
AUTHORS Fischer, R.L. and Mizukami, Y.
TITLE Methods for altering mass and fertility in plants
JOURNAL Patent: US 6559357-A 3 06-MAY-2003;
The Regents of the University of California; Oakland, CA
FEATURES
source 1..4228
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ORIGIN
Query Match 100.0%; Score 4228; DB 6; Length 4228;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy	2641	GTACTAGATTAACGTACGTATACATCGCTTTTCCCAATTTCTTAACTAATCTATACAA	2700
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ORGANISM Unknown.
REFERENCE 1 (bases 1 to 4228)
AUTHORS Fischer,R.L. and Mizukami,Y.
TITLE Methode for altering organ mass, controlling fertility and
enhancing asexual reproduction in plants
JOURNAL Patent: US 6639128-A 3 28-OCT-2003;
National Science Foundation; Arlington, VA
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 JOURNAL
 REFERENCE
 AUTHORS
 2 (bases 3704 to 114469)
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 JOURNAL
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 3 (bases 114416 to 198493)
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 EU Arabidopsis sequencing project.
 Submitted (10-MAR-2000) MIPS, at the Max-Planck-Institut fuer
 Direct Submission
 Biochemie, Am Klopfersteitz 18a, D-82152 Martinsried, FRG, E-mail:
 lemcke@mpi.biochem.mpg.de, mayer@mpi.biochem.mpg.de Project
 Coordinator: Mike Bevan, Molecular Genetics Department, Cambridge
 Laboratory, John Innes Centre, Colney Lane, NR4 7JY Norwich, UK,
 E-mail: michael.bevan@biotec.ac.uk
 Information on performance of analysis and a more detailed
 annotation of this entry and other sequences of chromosomes 3, 4
 and 5 can be viewed at: <http://www.mips.biochem.mpg.de/proj/thal/>
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DB 38046 GATCCTTAGTAAAGAAAACCTTCTTGTAGCGTGTGTGTTTAAGTCAATTAA 38105
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41816 ATATGTTCTAAGTTTAAATGTTTCAAGACCTTTACAAACAAATTAATTAATAGT 41875
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42116 AATGATTTGTTTGTGATTTACTTCTGAGATTTTAAAGAAAGATGATGATGAT 42175
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42176 TTATAGAAAGAGAGAGCAAAACCAAAAGAAAGAAC 42214

RESULT 6
ATHS30550 371 bp DNA linear pln 29-MAR-2003
LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone
DEFINITION 21206.
ACCESSION AJ530550
VERSION AJ530550.1 GI:26798810
KEYWORDS left border; T-DNA flanking sequence.
SOURCE Arabidopsis thaliana (thale cress)
ORGANISM Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.
1
REFERENCE
AUTHORS Brunaud, V., Balzergue, S., Dubreucq, B., Aubourg, S., Samson, F.,
Chauvin, S., Bechold, N., Cruaud, C., DeRose, R., Pelletier, G.,
Lepoint, L., Caboche, M. and Lecharny, A.

TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED 12446565

REFERENCE 2 (bases 1 to 371)

AUTHORS Balzerque, S.

TITLE Direct Submission

JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobio.gen.fr>).

FEATURES

Source

1..371

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="212A06"

/clone_1lb="Arabidopsis thaliana T-DNA insertion lines"

/ecotype="Wassilewskija"

1..371

/note="T-DNA flanking sequence

left border"

ORIGIN

Query Match 8.7%; Score 366.4; DB 15; Length 371;

Best Local Similarity 99.7%; Pred. No. 2.5e-39;

Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2457 TGAATTCCTGCGAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGTGTG 2516

DB 4 TCAATTCCTGCGAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGTGTG 63

QY 2517 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTACGTAAAGCTTTAAACATATC 2576

DB 64 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTACGTAAAGCTTTAAACATATC 123

QY 2577 TAGTTAGTTCTCACTGTACAAACAAACAAATCAATTCGTACATATATACAAATATCT 2636

DB 124 TAGTTAGTTCTCACTGTACAAACAAACAAATCAATTCGTACATATATACAAATATCT 183

QY 2637 ACTAGTACTAGTATGAGCTACGTATACATCGCTTTTCGCAAAATTTCTAAACTATCTAT 2696

DB 184 ACTAGTACTAGTATGAGCTACGTATACATCGCTTTTCGCAAAATTTCTAAACTATCTAT 243

QY 2697 ACAACAACTGTAATGTTGTTTGTATATTATCTTAAACAAAGTTTGAATTTGGCAT 2756

DB 244 ACAACAACTGTAATGTTGTTTGTATATTATCTTAAACAAAGTTTGAATTTGGCAT 303

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DB 304 TGGAGCTACACTCTAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTTA 363

QY 2817 AAGTATTT 2824

DB 364 AAGTATTT 371

RESULT 7

ATHS31085 371 bp DNA linear PLN 29-MAR-2003

LOCUS Arabidopsis thaliana T-DNA flanking sequence, left border, clone

DEFINITION 225808.

ACCESSION AJ531085

VERSION AJ531085.1 GI:26799345

KEYWORDS left border; T-DNA flanking sequence.

SOURCE Arabidopsis thaliana (thale cress)

ORGANISM Arabidopsis thaliana

REFERENCE 1

AUTHORS Brunaud, V., Balzerque, S., Dubreucq, B., Aubourg, S., Samson, F., Chauvin, S., Bechtold, N., Cruaud, C., Denose, R., Pelletier, G., Lepoint, L., Caboche, M., and Lecharny, A.

TITLE T-DNA integration into the Arabidopsis genome depends on sequences of pre-insertion sites

JOURNAL EMBO Rep. 3 (12), 1152-1157 (2002)

PUBMED 12446565

REFERENCE 2 (bases 1 to 371)

AUTHORS Balzerque, S.

TITLE Direct Submission

JOURNAL Submitted (21-NOV-2002) Balzerque S., UMRGV, INRA/CNRS, 2 rue Gaston Cremieux, 91057 Evry cedex, FRANCE

COMMENT PCR was performed on DNA from transformants of Arabidopsis thaliana plants from INRA (Versailles). The DNA fragment(s) resulting from the PCR were directly sequenced from the left or the right border to determine the genomic sequence flanking the insertion. T-DNA derived sequences were removed. Information to order the corresponding mutant line and a link to a database providing a graphical display of the insertion site are available at <http://dbsgap.versailles.inra.fr/publiclines/>. This sequence has been generated in the framework of the French plant genomics program 'Genoplante' (<http://www.genoplante.com> and <http://genoplante-info.infobio.gen.fr>).

FEATURES

Source

1..371

/organism="Arabidopsis thaliana"

/mol_type="genomic DNA"

/db_xref="taxon:3702"

/clone="225808"

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/ecotype="Wassilewskija"

1..371

/note="T-DNA flanking sequence

left border"

ORIGIN

Query Match 8.7%; Score 366.4; DB 15; Length 371;

Best Local Similarity 99.7%; Pred. No. 2.5e-39;

Matches 367; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2457 TGAATTCCTGCGAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGTGTG 2516

DB 4 TCAATTCCTGCGAAACGGCGCGGTAGAGTGTCTTATCTTACATTAACAGCTGGTGTG 63

QY 2517 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTACGTAAAGCTTTAAACATATC 2576

DB 64 GCAGACATCATAGGGCGCTACGTATATTGAGCTTTACGTAAAGCTTTAAACATATC 123

QY 2577 TAGTTAGTTCTCACTGTACAAACAAACAAATCAATTCGTACATATATACAAATATCT 2636

DB 124 TAGTTAGTTCTCACTGTACAAACAAACAAATCAATTCGTACATATATACAAATATCT 183

QY 2637 ACTAGTACTAGTATGAGCTACGTATACATCGCTTTTCGCAAAATTTCTAAACTATCTAT 2696

DB 184 ACTAGTACTAGTATGAGCTACGTATACATCGCTTTTCGCAAAATTTCTAAACTATCTAT 243

QY 2697 ACAACAACTGTAATGTTGTTTGTATATTATCTTAAACAAAGTTTGAATTTGGCAT 2756

DB 244 ACAACAACTGTAATGTTGTTTGTATATTATCTTAAACAAAGTTTGAATTTGGCAT 303

QY 2757 TGGAGCTACACTCTAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTTA 2816

DB 304 TGGAGCTACACTCTAGTCCCTTTTCCCAAAATTAATCTCTTACATGACCGGTTA 363

QY 2817 AAGTATTT 2824

Db 364 AAGTATT 371

RESULT 8
BD274516

DEFINITION
BD274516 2148 bp DNA linear PAT 17-JUL-2003
Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant.

ACCESSION
BD274516

VERSION
BD274516.1 GI:33084284

KEYWORDS
JP 2002534078-A/1.
Arabidopsis thaliana (thale cress)

SOURCE
Arabidopsis thaliana

ORGANISM
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE
1 (bases 1 to 2148)
Fischer, R.L., and Mizukami, Y.
Methods for modifying weight of organ, controlling fertility and enhancing asexual reproduction in plant
Patent: JP 2002534078-A 1 15-OCT-2002;

JOURNAL
THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

COMMENT
OS Arabidopsis thaliana (thale cress)
PN JP 2002534078-A/1
PD 15-OCT-2002
PF 07-JAN-2000 JP 2000592392
PR 08-JAN-1999 US 09/2237421
PI ROBERT L FISCHER, YUKIKO MIZUKAMI
PC A01H1/00, C12N5/10, C12N15/09, C12N5/00, C12N15/00 CC
A1NTEGUMENTA (ANT)

FEATURES
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Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTCTTTCTCTACCGCA 120

Db 4081 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTTCTGTTGTAACCAATATGGGT 4140
121 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTTCTGTTGTAACCAATATGGGT 180

QY 4141 TTATGCTTACTACTTGAGAGATTATAGAAAAGAGGAGATACATTATAGAAAG 4200
181 TTATGCTTACTACTTGAGAGATTATAGAAAAGAGGAGATACATTATAGAAAG 240

Db 4201 AGAGAACGAGAAACCAAAAAGAAACC 4228
241 AGAGAACGAGAAACCAAAAAGAAACC 268

RESULT 9
AR316367

LOCUS AR316367 2148 bp DNA linear PAT 12-JUN-2003

DEFINITION
Sequence 1 from patent US 6559357.
AR316367
AR316367.1 GI:31711158

ACCESSION
AR316367

VERSION
AR316367.1

KEYWORDS
Unknown.

SOURCE
Unknown.

ORGANISM
Unknown.

REFERENCE
1 (bases 1 to 2148)
Fischer, R.L., and Mizukami, Y.
Methods for altering mass and fertility in plants
Patent: US 6559357-A 1 06-MAY-2003;
The Regents of the University of California; Oakland, CA

JOURNAL
The Regents of the University of California; Oakland, CA

FEATURES
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/mol_type="genomic DNA"

ORIGIN

Query Match 6.3%; Score 268; DB 6; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3961 AGATCCCAACGAGATTCAACAGCAAAATTTGCTTTGCTTCTCTCTATTATTAATATC 4020
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QY 4021 CTCTCAAAAACCTCTCTATATCTCTTAAGCCCCCTTCTCTTTCTCTACCGCA 4080
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121 CAAAGAAAAACAAAGTTGAGAAAAATGCTGTTCTGTTGTAACCAATATGGGT 180

QY 4141 TTATGCTTACTACTTGAGAGATTATAGAAAAGAGGAGATACATTATAGAAAG 4200
181 TTATGCTTACTACTTGAGAGATTATAGAAAAGAGGAGATACATTATAGAAAG 240

Db 4201 AGAGAACGAGAAACCAAAAAGAAACC 4228
241 AGAGAACGAGAAACCAAAAAGAAACC 268

RESULT 10
AR427901

LOCUS AR427901 2148 bp DNA linear PAT 18-DEC-2003

DEFINITION
Sequence 1 from patent US 6639128.
AR427901
AR427901.1 GI:40186930

ACCESSION
AR427901

VERSION
AR427901.1

KEYWORDS
Unknown.

SOURCE
Unknown.

ORGANISM
Unknown.

REFERENCE
1 (bases 1 to 2148)
Fischer, R.L., and Mizukami, Y.
Methods for altering organ mass, controlling fertility and enhancing asexual reproduction in plants
Patent: US 6639128-A 1 28-OCT-2003;
National Science Foundation; Arlington, VA

JOURNAL
National Science Foundation; Arlington, VA

FEATURES
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ORIGIN

Query Match 6.3%; Score 268; DB 6; Length 2148;
Best Local Similarity 100.0%; Pred. No. 1.6e-26;
Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4021 CTCTCAAAAACCTCTCTATATCTCTAAAGCCCCCTTCTGTTTCTCTACGGCA 4080
 DB 61 CTCTCAAAAACCTCTCTATATCTCTAAAGCCCCCTTCTGTTTCTCTACGGCA 120
 QY 4081 CAAAGAAAAACAAAGTTTGAGAAAAATGGTGTCTGTTGTAAACCAATGATGGGT 4140
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 QY 4141 TTTAGCTTACTCTTCAGAGATTATTAAGAAAGAGTGAAGATCATTTATGAAAGA 4200
 DB 181 TTTAGCTTACTCTTCAGAGATTATTAAGAAAGAGTGAAGATCATTTATGAAAGA 240
 QY 4201 AGAAGACGAGAAACCAAAAAGAAACC 4228
 DB 241 AGAAGACGAGAAACCAAAAAGAAACC 268
 RESULT 11
 ATU40256 2148 bp mRNA linear PLN 10-JAN-2005
 LOCUS Arabidopsis thaliana ovule development protein (AINTEGUMENTA) mRNA,
 complete cds.
 ACCESSION U40256
 VERSION U40256.1 GI:1209098
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2148)
 REFERENCE Klucher K.M., Chow H., Reiser L. and Fischer R.L.
 TITLE The AINTEGUMENTA gene of Arabidopsis required for ovule and female
 gametophyte development is related to the floral homeotic gene
 APETALA2
 JOURNAL Plant Cell 8 8 (2), 137-153 (1996)
 PUBMED 8742706
 REFERENCE 2 (bases 1 to 2148)
 AUTHORS Klucher, K.
 TITLE Direct Submission
 JOURNAL Submitted (07-NOV-1995) L. Reiser, Plant Biology, UC Berkeley, 111
 Koshland Hall, Berkeley, CA 94720, USA
 FEATURES
 SOURCE
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 Matches 268; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 4201 AGAAGACGAGAAACCAAAAAGAAACC 4228
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 RESULT 12
 AY080706 2056 bp mRNA linear PLN 18-SEP-2002
 LOCUS Arabidopsis thaliana putative ovule development protein
 aintegumenta (At4g37750) mRNA, complete cds.
 ACCESSION AY080706
 VERSION AY080706.1 GI:19310586
 KEYWORDS
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2056)
 REFERENCE Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bower L.,
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B.,
 Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T.,
 Satou M., Seki M., Shim P., Southwick A., Shinozaki K.,
 Davis R.W., Ecker J.R. and Theologis A.
 TITLE Arabidopsis Full Length cDNA Clones
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2056)
 AUTHORS Yamada K., Banh J., Chan M.M., Chang C.H., Chang E., Dale J.M.,
 Deng J.M., Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L.,
 Tang C.C., Toriumi M., Wu H.C., Yamamura Y., Yu G., Bower L.,
 Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B.,
 Lin J., Meyer M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
 Sakurai T., Satou M., Seki M., Shim P., Southwick A.,
 Shinozaki K., Davis R.W., Ecker J.R. and Theologis A.
 TITLE Direct Submission
 JOURNAL Submitted (19-FEB-2002) Plant Gene Expression Center, 800 Buchanan
 Street, Albany, CA 94710, USA
 COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the
 collection and clustering of RFL cDNAs (RFL cDNA: 'RIKEN
 Arabidopsis Full-length cDNA'): Seki M., Narusaka M., Ishida J.,
 Satou M., Kamiya A., Sakurai T., Carninci P., Kawai J.,
 Hayashizaki Y. and Shinozaki K.
 The Salk, Stanford, PGSC (SSP) Consortium members carried out the
 sequencing and annotation of the RFL cDNAs: Yamada K., Banh J.,
 Chan M.M., Chang C.H., Chang E., Dale J.M., Deng J.M.,
 Goldsmith A.D., Lee J.M., Onodera C.S., Quach H.L., Tang C.C.,
 Toriumi M., Wu H.C., Yamamura Y., Yu G., Bower L., Chen H.,
 Cheuk R., Jones T., Karlin-Neumann G., Kim C., Lam B., Lin J.,
 Meyer M.C., Miranda M., Nguyen M., Palm C.J., Shim P.,
 Southwick A., Davis R.W., Ecker J.R. and Theologis A.
 Yamada K. (SSP/PGSC) and Seki M. (RIKEN GSC) contributed equally to
 this work. Shinozaki K. (RIKEN GSC) and Theologis A. (SSP/PGSC)

Oy	891	CTGAGACATTAATGTTAGTCTACAAATTTTCTCTTGGATTGTAAGSTTTGACACAA	950
Dp	3142	ATCATTAATTCATTTTTAAAAAATTAATTTTATTAATAATTTCACATPAAAAATPACAT	3083
Oy	951	ATTATGTATTCCTGACAGGGATATPAAAGTCACTGACATGTCAGACTCAGCATGAGCCA	1010
Dp	3082	AATTCMAATTCATTCCACAAATTTATACATTTATTTTATTTTAAATTTATTTATPAAAT	3023
Oy	1011	AAGAGTCGTCTCTGTCCPMAAGATATCTACAGCTGCTCGCCTGTGAATPAGAGAAAT	1070
Dp	3022	TTAAACATCATCATTTTAAATAATATCAATTTTCAATPAAATTTTTTTTATTTTTTAAAC	2963
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Dp	2962	AATATATATTCATTTAAATTTTACATTTTCATPAAATTTTAACATTTTTTTTTCATTTTCA	2903
Oy	1131	GTTGTGACTTTTTTTCTTATGTGCTGTGACATA---ATTTCCTGAGGTGAGAGCT	1187
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Dp	2722	TTTTTATTTAAAAAATPAAATPAAATTTTAAAAAATTTTAAAAATTTATTTATTTTAA	2663
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Dp	2603	TTTTTTTTCATTTATTTTTTATTTTTTAAAAATTTTATTTAAATTTTAAATTTTTTAA	2544
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Dp	2543	TTATTTTATTAATTAATTTATTTTATTTTTTTTCAATTAATTTTATTAATTTTAA	2484
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Dp	2483	CAAAATATATAAAAATATATPAAATPAAATPAAATPAAATPAAATPAAATPAAATPAA	2424
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Oy	1788	AATGCTTAAATCATTTAAATPAAAGSTTTTGCTTTTAAAGSTTAAACACGCGCTAAATCA	1847
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Dp	2189	AATTTTATATAAATTAATTAATTTTTTTTTTTTTTATTTTATTTTAAATPAAATPAA	2130
Oy	1908	ATTTTCAGCATTTTAAATPAAAGGCTACATTTATGGGTCAATPAAATATGTTTCCAGCT	1967
Dp	2129	ATTATTAATAATTAATTAATAATTTTATTAATTTATTTATTTATTAATTTTAAATATTTT	2070
Oy	1968	AAAGTTTGAGGTTTAAACCAATGATGTTTTTTGATTTTAAAAAACAATAAATTTCTA	2027

Db	2069	ATTAATAATTTTAAATAATAAAAATATTTAAATAATATTTTAAATTTTAAATATTTTAA	2010
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Db	2009	ATTTTATTAATTTTAAATAAATAATTAATATTAATATTTTAAATTTTAAATAATATATTTT	1955
Oy	2088	TTTTTTTTCTGGAATCTGTTTAAATCTCTGCTGCATGACTTGCAGCAATTTGACCA	2147
Db	1949	TTTTATTTAAATATTAATTTAAATATTTTAAATTTTAAATAATTTTAAATTTTAAATTA	1890
Oy	2148	ACGACTATACATATGGAAGCAAAATATCCACGAGATGATAGGTTAGATCCCACTAT	2207
Db	1889	AAAAAATTAATAATTAATTAATTAATTTTAAATTTTAAATTTTAAATTTTAAATTA	1830
Oy	2208	CAATATCTTTGTCTTTGTATTTATATGAAAAACAA-----ATATTTATGAG	2253
Db	1829	AAATTTTATTTTATTTATTTAAATTTAAAAATTAATTAACATTAATTTTAAATTTTAAAT	1770
Oy	2254	GAAAAAATCGTTCTCTAGTGTATAGGTATAGATTAATTAACAAATTTTAATCTTA	2313
Db	1769	TTAAAAAATTTTAAATTTTAAATTTTAAATTTTAAATTTAAATTAATTAATTAAT	1711
Oy	2314	GTTAATATGA--TTTACATCTTCAAACTTACCATCTTCAACATTAATATTTGATCATY	2370
Db	1709	ATTAATAATTAATTTTAAATTTTAAATTAATAAATAAATTTTATCATTTAAATTAATAAT	1655
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Db	1649	TTTTTTTATTTTACAAATTCATTTATTTCAATTTTAAATTTTAAATTTTAAATTAATTA	1590
Oy	2431	AGTCAAGATTAATAAGATGAGTGGTGAATCTTACAGCAAAACGGCCGTAGAGGTCTC	2490
Db	1589	AATTAATAAT-ATTAATAATTAATAATTAATAATTTTAAATAATTTTAAATTTTAAATATTT	1531
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Db	1530	TTTAACTATTTAATTTAATTTAATTAATTAATTAATTTAATTAATTAATTAATTTAATTA	1471
Oy	2551	TACGTACGTAAAGCTTTTAACTATCTAGTAGTTCTCATCTGTCAACAAACAAACAAATCT	2610
Db	1470	TAAATTTATTAATAAATAATATTTTATTTTATTTTAA-----AAAAAATAAATAAATAA	1415
Oy	2611	CAATTCGTACATATATATACAAATCTACTAGTACAGATTACGCTACGATATACATCGCTT	2670
Db	1414	ATTAATAAATAAATAATCAATTTATTTTAAATAAATAAATAAATAATTTTAAATAAATAATTA	1355
Oy	2671	TTTGCAGAAATTTCTAACTAACTATATACACAAACCTGAAATGTTGTGTTGTAATTTATC	2733
Db	1354	AATTTAAATATTTTAAATTAATAATTAATAATTTTAAATTAATTTTAAATTTTAAATTTTAA	1295
Oy	2731	TTTAAACCAAGTTTGAATGTGCAATTTGGAGCTACACTCAGTCCCTTTTCCCAAC	2799
Db	1294	AAAAATATTTACATTTTAAATTAATTAATTAAT-ATTAATTAACATTAATTTTAAATTA	1236
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Db	1058	TTTACATTAATTTAAATTTCAAAATTTAAAAATAAATAAATAAATTTTAAATAATTAATTTT	999
Oy	3031	CGTGAACAAAGTTTCGTCTGAATTTCTACGGTCGTCATAGAAATTTTGACATTTTCT	3090

D	b		998	AAAAAATATATATATATATTTTATCTATTAAATAAAAAAAATAAAATTTATTTTTTAA	933
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D	b		938	AAAAATTATATCAAAAAACAACAAAAATTAATTAATTAATTTAAATTTACAAAT	879
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D	b		878	TTTATATACATAAAAAATAAAAAAACAAATTTTTTAAATAAAAATATTTTAATAT	819
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D	b		818	CATTATATAAATTTATTTTAAATATATATTAATTAATTTTATATTTTAAATTT	759
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D	b		758	TAAATTTAAAAATTAATTAATTAATTAATTAATTTTAAATTTAAATTTAAATAA	699
O	y		3331	ATGGGTTTATTTATATAGTTTTTTTCTCTTTTCCATGCTTTTATATGACACATCT	3390
D	b		698	AATTTTTTATATATATATATTTTTTTTTTTTTTAAATTAATTAATTTAAATAATAT	639
O	y		3391	AAATTTCTTTTATTTAAATTAGGTAAAGATCTGAATTTTCGTGATTTTAAACAAG	3456
D	b		638	TTTAAAAAATTTTAAATTTTATATATATTTTTTTTAAATATATTTTAAATATAT	579
O	y		3451	TTTTCAATCTCTCTTACACAAAAAATAAAGTTTCAATATTTAAAGATCTAA	3510
D	b		578	AATTTTATTAATAACATTTATATATATATATTAATTAATTTTAAATATATTAATTTA	519
O	y		3511	TTTTTTGAGTTCAAGAGTTTATGATAGCTGAAAAGTTATGATGATTTGCAAGTTGCA	3570
D	b		518	ATATTTATTAAT-AATTAATTAATTTTATTTTATTTTAAATATATTTATTTTAA	460
O	y		3571	CAGATGGTCAGTAGTACATATCAAAAACATGATCAAAAATTAATTTGCTGTAC	3630
D	b		459	TTAAATTTTTTTTATTTATTTTAAAAAATAAATAATTAATTAATATATTTAAAT	400
O	y		3631	AAGAGAAACGATGTGAATTAACAGAACATGTTTACACCTTAAATAATCTTGAATAT	3690
D	b		399	AAATTTTAAATTAATTAATATTTTATTTTCAATTTTTTTTTTTTATATATATATTTT	340
O	y		3691	TTGTATGATATATTTCTGTAAAGAGAGTATCATATCTTACAAAAAATTCATTTTC	3750
D	b		339	ATTTATTTTATTTATTTATTTTAAAAAATAATTTAAAAAATAATTTATTTT	280
O	y		3751	AGATTAATAATATNGTTCGCAATCGTTACCAAGTATGTTTT--CGCTCATCGTGTGA	3807
D	b		279	TATTAATAATTAATTAATTAATTTTAAATTTTTTAAATTTTTTAAATAATTTT	220
O	y		3808	TTGTACTCGTCTCTTACCATATATAGTCTAAGTTTAAATGTTTCAAAGACTTACAA	3867
D	b		219	TTAATAAATTAATTAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	160
O	y		3868	AAATTAATAATTAATAGCTGAATTTGTAGGCTTAAAGCAAAATTAATAATTAATA	3927
D	b		159	AAAAATTAATAATTAATTAATAAATAATTAATAAATAATTAATTAATTAATAATA	100
O	y		3928	AAAGTAAAGAA 3938	
D	b		99	AAATATTAATAA 89	
<hr/>					
RESULT_14					
PFMAL4P3/c					
LOCUS	PFMAL4P3	349751 bp	DNA	linear	INV 16-APR-2005
DEFINITION	Plasmidium falciparum MAL4P3.				
ACCESSION	AL035476 AL844503				
VERSION	AL035476.7 GI:23498195				
KEYWORDS					
SOURCE	plasmidium falciparum 3D7				
ORGANISM	Plasmidium falciparum 3D7				
	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.				

REFERENCE	AUTHORS	TITLE	JOURNAL	PUBMED	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	SOURCE	gene	CDS																				
1	Hall, N., Pain, A., Berriman, M., Churcher, C., Harris, B., Harris, D., Mungall, K., Bowman, S., Atkin, R., Baker, S., Barton, A., Brooks, K., Buckee, C. O., Burrows, C., Cheever, I., Chillingworth, C., Chillingworth, T., Christodoulou, Z., Clark, L., Clark, R., Cotton, C., Cronin, A., Davies, R., Davis, P., Dear, P., Dearden, F., Doggett, J., Felwell, T., Goble, A., Goodhead, I., Gwilliam, R., Hamlin, N., Hance, Z., Harper, D., Hauser, H., Hornsby, T., Holroyd, S., Horrocks, P., Humphray, S., Jagsels, K., James, K. D., Johnson, D., Karhounou, A., Knights, A., Konfortov, B., Kyes, S., Lake, N., Lawson, D., Lennard, N., Line, A., Maddison, M., McLean, J., Mooney, P., Moul, S., Murphy, L., Oliver, K., Ormond, D., Price, C., Quail, M. A., Rabinovitch, E., Rajandream, M. A., Rutter, S., Rutherford, K. M., Sanders, M., Simmonds, M., Seeger, K., Sharp, S., Smith, R., Squares, R., Squares, S., Stevens, K., Taylor, K., Tiley, A., Unwin, L., Whitehead, S., Woodward, J., Sulston, J. E., Craig, A., Newbold, C. and Barrett, B. G.	Sequence of Plasmodium falciparum chromosomes 1, 3-9 and 13	Nature	419 (6906), 527-531 (2002)	2	(bases 1 to 349751)	1236867	On Oct 3, 2002 this sequence version replaced gi:5763808. For more information about this sequence or the Malaria Project, see http://www.sanger.ac.uk/Projects/P_falciparum .	location/Qualifiers	1. 349751	/organism="Plasmodium falciparum 3D7"	/mol_type="genomic DNA"	/isolate="3D7"	/db_xref="taxon:36329"	/chromosome="4"	/clone="MAL4P3"	complement (join(2130..3551,4472..3988))	/gene="PF0630C"	/note="synonym: VAR"	complement (join(2130..3551,4472..3988))	/gene="PF0630C"	/note="Similar to Plasmodium falciparum var. mal4p2.58	mal4p2.58, var. SWAL:Q9U0G5 (EMBL:U05475) (2277 aa)	fasta scores: E(): 1.5e-143, 52.77% id in 2486 aa, and to Plasmodium falciparum variant-specific surface protein var-7 SWAL:026034 (EMBL:U42656) (2182 aa) fasta scores: E(): 1.9e-126, 46.72% id in 2412 aa"	/codon_start=1	/product="erythrocyte membrane protein 1 (pFEMP1)"	/protein_id="CAD49166.1"	/db_xref="GI:23498196"	/db_xref="NCBA:Q811V7"	/db_xref="InterPro:IPR004258"	/db_xref="UniProt/TREMBL:Q811V7"	/translation="MGPPSTADPYSSAKHLADISIGKRVHVAQVONKQSGNDLKGILLTSYLTSGESAFTENPCELIKDQGDILGSDRGKQSGNSAEKSPFVSGCEDKDKTIGNRNNGGACAPRYRLFCNKMKEKMGRTSTTGILLDVCMAVYAGSLIRYHDOYDAYPSGDSKCTMLARSPADIDITRGDLVIGAKKKKKTETTERDDESLKTLFSGIYVELTNGRNGVDHYODDNGSNYFOLREBDMTRNATVWKAITCRADTGNAPFRPTCSNRQGSQAHYRCNCRGDKPDNDKPNTPDPTFYDYQVYLAWPEBMAEDCRKKKIYVIGIYVYCREKTKSGENPRYCSRNGYDCTKTRAIIGKRVNQCISCIYACNPYVDWINOKRQPDROKKKTYTDELTENASRSRSGRNGARASGSNTDGVESKYRNLIKDQYGTDDPKLILNKRSQCAVYNDNGGTLINTEKRDQNNNNKDKGCTPYRSYCOVCPDGVTYNSGWEKERRKNDQCNITKLYPKKDAHPHTIKLKSSEGBEIKBLKBAFCDDKDGASDLSFLYDPMQCYDPOLEKDKKEGVDNRYDNDVYRGGLCTILQKNGENKQKQKTYNSGFLYFVFWVAHMLKDSIHMKKKEKLCLONTYKTRCNNEKCNKECECFQWVEKKKKTWEMKIKDHFQNTONIGDETNCDEPIVTLBEGVLTLOFANEDSTODKNSLDEELIKLKHSEMGILQETSNGDGLTGSASNEKETIMDKTLIHBEIGIAKCLARKNCEKKAKPEGSSDSMDHDPQPPDADNEDDLDEDEDEBEERQVANDYNOBEBOGVYVQOEGSSSPYPAAPADIVSYQLFSDPSQFSDACTLTKYIVGKNGKCLIPSGNTSTGTSGESATYGAQRDPTDSGDTGGTGKGAATGCLIPRRRLYVGGISQWASQRTQSTGTSQSENLLE

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		Query Match	2.9%; Score 120.6; DB 2; Length 349751;
		Best Local Similarity 43.7%; Pred. No. 9.8e-08;	
		Matches 1062; Conservative % 0; Mismatches 1344; Indels 25; Gaps 11;	
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Oy	1726	ATGATAACAACCTCGTGGAAAAAATCCAGCCTAATATGTCATTTAAAGATAATGATT	1785
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Oy	1786	TAAATGCTTAATCATTAATAATAAGGTTTGCT--TTTAAAGGTTAACCAAGCTTAA	1843
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D	b	69046	TAAATGTTAAATATATTTATTTTTTTTTTAAATTAATTTTAAATATATATATATTAAT	68988
Q	y	1904	GAATAATTTTTCAGCATTTTAAATTAAGGGTACATTTATGGTTCATAATAATATGTTCC	1963
D	b	68986	AACAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA	68927
Q	y	1964	ACGTAAGTTTGGAGGTTTAAACCAATGATTTTTTGATTTAAAAACACTAAATT	2023
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D	b	68808	TTTAAAT	68749
Q	y	2144	ACCAACGACTATACATATTTGAAAGCAAAATATCCACAGGATGATAGGTTATCCCA	2203
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Q	y	2324	TTACTATCTTCAACCTTACATCTCTTCAACATTAATATGCAATTTTATTTTTTTTA	2383
D	b	68568	TTTTTAAATTA	68509
Q	y	2384	CTAAACACTTCCACTTAAATAAATGCAAGAGAGATATATATTTAATGCAAGTAAT	2443
D	b	68508	ATATTTATTTAATTAATTTATTTATATATTTTAAATTAATTAATTAATTAATTAAT	68449
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D	b	68088	ACATATATATTTATTTATTTATTTATTTATTTAATTTAAGTATATATTTATTTAT-	68030
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Matches 1134; Conservative 0; Mismatches 1480; Indels 22; Gaps 11;

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Db 91291 ATTAATATATATATATATATATATATATATATATATATATATATATATATAT 91232

Qy 1262 CTAAATTCGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1319
Db 91231 TATTAATATATATATATATATATATATATATATATATATATATATATATAT 91172

Qy 1320 AATCAAGAGAGAGAGAGAGCTCTTCGTCGCTTAATTCCTCTCAAGCACTGC 1379
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